

09/699580

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2004, 20:32:14 ; Search time 4065 Seconds  
(without alignments)  
5576.484 Million cell updates/sec

Title: US-08-864-955-2  
Perfect score: 2769  
Sequence: 1 MEIGSPAPRRLLFACSPPP.....SRTAGEKSKREWSRLKXL 523

Scoring table: BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167516995 residues  
Total number of hits satisfying chosen parameters: 1676830

Minimum DB seq length: 10  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xih  
-O/cgnt 1/USPTO.spool/US08864955/runat 07092004 144930 24476/app query.fasta\_1.711  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=45 -MODE=LOCAL  
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=10 -MAXLEN=60  
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-NO\_MMAP -IARGOUTERY -NEG\_SCORES=0 -WAIT -DSPLITLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: gb\_pr:\*  
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17: em\_hum:\*  
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19: em\_in:\*  
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30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rdt:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	1.7	50	AX752284	AX752284 Sequence
2	48	1.7	53	AR068881	AR068881 Sequence
3	47	1.7	54	BD271047	BD271047 Method an
4	47	1.7	54	BD271048	BD271048 Method an
5	47	1.7	54	AR258453	AR258453 Sequence
6	47	1.7	54	AR258454	AR258454 Sequence
7	45	1.6	43	BD073435	BD073435 Membrane-
8	45	1.6	51	AX161875	AX161875 Sequence
9	45	1.6	58	AX197541	AX197541 Sequence
10	44.5	1.6	49	AX441045	AX441045 Sequence
11	44	1.6	45	MDTRVDJA	MDTRVDJA
12	44	1.6	46	AX3507	AX3507 M.domesticu
13	44	1.6	51	AX161284	AX161284 Sequence
14	44	1.6	51	AX40794	AX40794 Sequence
15	44	1.6	59	AX657102	AX657102 Sequence
16	43	1.6	52	ATHS25205	ATHS25205 Sequence
17	43	1.6	52	HO1086805	HO1086805 Sequence
18	42.5	1.5	42	AR362812	AR362812 Sequence
19	42.5	1.5	54	AR362812	AR362812 Sequence
20	42.5	1.5	60	AX811366	AX811366 Sequence
21	42	1.5	34	AR261278	AR261278 Sequence
22	42	1.5	34	AR400541	AR400541 Sequence
23	42	1.5	34	AR405808	AR405808 Sequence
24	42	1.5	34	AX201058	AX201058 Sequence
25	42	1.5	34	AX267857	AX267857 Sequence
26	42	1.5	36	AX003471	AX003471 Sequence
27	42	1.5	36	BD087087	BD087087 Erythrovi
28	42	1.5	40	AR099144	AR099144 Sequence
29	42	1.5	40	AR361794	AR361794 Sequence
30	42	1.5	40	AX591271	AX591271 Sequence
31	42	1.5	40	AX591416	AX591416 Sequence
32	42	1.5	40	BD136532	BD136532 Therapeut
33	42	1.5	48	AX12209	AX12209 EBI 643. 12
34	42	1.5	48	AR363935	AR363935 Sequence
35	42	1.5	55	AX453980	AX453980 Sequence
36	42	1.5	56	HMMTCVDICT	HMMTCVDICT
37	42	1.5	60	HSRAULB	HSRAULB
38	41.5	1.5	48	AR306664	AR306664 Sequence
39	41.5	1.5	48	AR306665	AR306665 Sequence
40	41.5	1.5	48	AR340099	AR340099 Sequence
41	41.5	1.5	48	AR340100	AR340100 Sequence
42	41.5	1.5	48	AR412168	AR412168 Sequence
43	41.5	1.5	48	AR412169	AR412169 Sequence
44	41.5	1.5	60	AR182231	AR182231 Sequence
45	41	1.5	29	AX082967	AX082967 Sequence

RESULT 1

## ALIGNMENTS

AX752284/C  
LOCUS AX752284 50 bp DNA linear PAT 20-JUN-2003  
DEFINITION Sequence 116 from Patent WO03035693.  
ACCESSION AX752284  
VERSION AX752284.1 GI:32134325  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1 Williams, P.A., Cosme, J.M., Ward, A., Brewerton, S.C., Hamilton, B.J.,  
AUTHORS Uchli, H., Jones, M.A., Villard, L.M., and Williams, M.G.  
TITLE Crystals of cytochrome P450 2C9, structures thereof and their use  
JOURNAL Patent: WO 03035693-A 116 01-MAY-2003;  
Astex Technology Limited (GB)  
FEATURES  
source Location/Qualifiers  
1..50  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.4e+04 Length: 50  
Score: 48.00 Matches: 8  
Percent Similarity: 76.92% Conservative: 2  
Best Local Similarity: 61.54% Mismatches: 3  
Query Match: 1.73% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX752284 (1-50)

Qy 12 LeuLeuPheAlaCySerProProAlaSerGlnPro 24  
Db 41 CTGCTTCATTCCTGTCCACGACACGACACTGAGTCGACCG 3

RESULT 2  
LOCUS AR068881 53 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5854081.  
ACCESSION AR068881  
VERSION AR068881.1 GI:6001088  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE  
1 (bases 1 to 53)  
AUTHORS Linder, J., Taylor, H., Robeva, A., Woodard, R. and Jin, X.  
TITLE Stable expression of human A. sub. 2B adenosine receptors, and assays  
employing the same  
JOURNAL Patent: US 5854081-A 3 29-DEC-1998;  
FEATURES  
source Location/Qualifiers  
1..53  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.67e+04 Length: 53  
Score: 48.00 Matches: 8  
Percent Similarity: 73.33% Conservative: 3  
Best Local Similarity: 53.33% Mismatches: 4  
Query Match: 1.73% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AR068881 (1-53)

Qy 489 HisHisGluAspPheLysGluAspLeuLysLysPheArgThrLys 503  
Db 53 CATCACCATGACTACAGACGACGATGACAACTGTAAGAACGGCT 9

RESULT 3

BD271047  
LOCUS BD271047 54 bp DNA linear PAT 17-JUN-2003  
DEFINITION Method and polynucleotides for determining translational efficiency  
of a codon.  
ACCESSION BD271047  
VERSION BD271047.1 GI:33080815  
KEYWORDS JP 2002534133-A/89.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1 (bases 1 to 54)  
AUTHORS Zhou, J. and Frazer, I.H.  
TITLE Method and polynucleotides for determining translational efficiency  
of a codon  
JOURNAL Patent: JP 2002534133-A 89 15-OCT-2002;  
THE UNIVERSITY OF QUEENSLAND  
COMMENT  
OS Artificial Sequence  
PN JP 2002534133-A/89  
PD 15-OCT-2002  
PF 07-JAN-2000 JP 2000593772  
PI 08-JAN-1999 AU PP 8078  
PI JIAN ZHOU, IAN HECTOR FRAZER  
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12N15/  
CC Description of Artificial Sequence: His(CAC)5 primer FH Key  
FT source 1..54  
Location/Qualifiers  
1..54  
/organism="Artificial Sequence".  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Alignment Scores:  
Pred. No.: 4.44e+04 Length: 54  
Score: 47.00 Matches: 8  
Percent Similarity: 70.59% Conservative: 4  
Best Local Similarity: 47.06% Mismatches: 5  
Query Match: 1.70% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x BD271047 (1-54)

Qy 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyLysAspLeuPheThr 172  
Db 1 CGGGGTACCATGCACACACACGACGAGGCGAGGAACTGTCACT 51

RESULT 4  
LOCUS BD271048 54 bp DNA linear PAT 17-JUN-2003  
DEFINITION Method and polynucleotides for determining translational efficiency  
of a codon.  
ACCESSION BD271048  
VERSION BD271048.1 GI:33080816  
KEYWORDS JP 2002534133-A/90.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1 (bases 1 to 54)  
AUTHORS Zhou, J. and Frazer, I.H.  
TITLE Method and polynucleotides for determining translational efficiency  
of a codon  
JOURNAL Patent: JP 2002534133-A 90 15-OCT-2002;  
THE UNIVERSITY OF QUEENSLAND  
COMMENT  
OS Artificial Sequence  
PN JP 2002534133-A/90  
PD 15-OCT-2002  
PF 07-JAN-2000 JP 2000593772  
PI 08-JAN-1999 AU PP 8078  
PI JIAN ZHOU, IAN HECTOR FRAZER  
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12N15/

PC 00, C12N5/00  
 CC Description of Artificial Sequence: His(CAT)5 primer FH Key  
 FT source Location/Qualifiers  
 1.54  
 /organism='Artificial Sequence'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32630'

FEATURES  
 source Location/Qualifiers  
 1.54  
 /organism='synthetic construct'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32630'

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.44e+04 Length: 54  
 Score: 47.00 Matches: 8  
 Percent Similarity: 70.59% Conservative: 5  
 Best Local Similarity: 47.06% Mismatches: 4  
 Query Match: 1.70% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x BD271048 (1-54)

QY 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyLysAspLeuPheThr 172  
 DB 1 CGGGGTACCATGATCATCATCATATGCAAGGCGAGAACTGTTCACT 51

RESULT 5  
 AR258453 54 bp DNA linear PAT 20-DEC-2002  
 LOCUS AR258453  
 DEFINITION Sequence 184 from patent US 6489141.  
 ACCESSION AR258453  
 VERSION AR258453.1 GI:27308740  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 54)  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Frazer, I.H. and Zhou, J.  
 TITLE Nucleic acid sequence and methods for selectively expressing a protein in a target cell or tissue  
 JOURNAL Patent: US 6489141-A 184 03-DEC-2002;  
 FEATURES Location/Qualifiers  
 1.54  
 /organism='unknown'  
 /mol\_type='genomic DNA'

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.44e+04 Length: 54  
 Score: 47.00 Matches: 8  
 Percent Similarity: 70.59% Conservative: 4  
 Best Local Similarity: 47.06% Mismatches: 5  
 Query Match: 1.70% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AR258453 (1-54)

QY 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyLysAspLeuPheThr 172  
 DB 1 CGGGGTACCATGATGACACACACACACACAGGCGAGAACTGTTCACT 51

RESULT 6  
 AR258454 54 bp DNA linear PAT 20-DEC-2002  
 LOCUS AR258454  
 DEFINITION Sequence 185 from patent US 6489141.  
 ACCESSION AR258454  
 VERSION AR258454.1 GI:27308741  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 54)  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Frazer, I.H. and Zhou, J.

TITLE Nucleic acid sequence and methods for selectively expressing a protein in a target cell or tissue  
 JOURNAL Patent: US 6489141-A 185 03-DEC-2002;  
 FEATURES Location/Qualifiers  
 1.54  
 /organism='unknown'  
 /mol\_type='genomic DNA'

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.44e+04 Length: 54  
 Score: 47.00 Matches: 8  
 Percent Similarity: 70.59% Conservative: 4  
 Best Local Similarity: 47.06% Mismatches: 5  
 Query Match: 1.70% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AR258454 (1-54)

QY 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyLysAspLeuPheThr 172  
 DB 1 CGGGGTACCATGATCATCATCATATGCAAGGCGAGAACTGTTCACT 51

RESULT 7  
 BD073435/C 43 bp DNA linear PAT 27-AUG-2002  
 LOCUS BD073435  
 DEFINITION Membrane-bound cytokine composition and method for modulating an immune response using it.  
 ACCESSION BD073435  
 VERSION BD073435.1 GI:22619038  
 KEYWORDS JP 2001512009-A/3.  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 1 (bases 1 to 43)  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS Hou, W.S.  
 TITLE Membrane-bound cytokine composition and method for modulating an immune response using it  
 JOURNAL Patent: JP 2001512009-A 3 21-AUG-2002;  
 COMMENT THE IMMUNE RESPONSE CORP  
 OS Unidentified  
 PN JP 2001512009-A/3  
 PD 21-AUG-2001  
 PF 28-JUL-1998 JP 2000505285  
 PR 29-JUL-1997 US 08/902516  
 PI WILLIAM SOU HOU  
 PC C12N15/08, A61K35/12, A61K35/66, A61K39/00, A61K48/00, A61P35/00, A61P37/02  
 PC C07K14/475, C07K14/52, C07K14/705, C12N15/00  
 CC Strandedness: Single;  
 CC Topology: linear;  
 CC Membrane-bound cytokine composition and method for modulating an immune response using it  
 CC response using it  
 CC Key  
 FT source Location/Qualifiers  
 1.43  
 /organism='Unidentified'.  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.61e+04 Length: 43  
 Score: 45.00 Matches: 9  
 Percent Similarity: 76.92% Conservative: 1  
 Best Local Similarity: 69.23% Mismatches: 3  
 Query Match: 1.63% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x BD073435 (1-43)

Cy 145 PhagubelysProvalArgProvalSerArgely 157  
 Db 39 TTGAATGCAAAAACCAATCAAAAGTCGACCGCGGT 1

RESULT 8  
 LOCUS AX161875 51 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 5203 from Patent WO0140521.  
 ACCESSION AX161875  
 VERSION AX161875.1 GI:14543206

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Shimkets, R.A. and Leach, M.  
 Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof  
 Patent: WO 0140521-A 5203 07-JUN-2001;

JOURNAL Curagen Corporation (US)

FEATURES  
 source Location/Qualifiers

1..51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

misc\_feature 26  
 /note="1 of 2 allelic variants (5204 is other entry)"  
 Accession number cg43986519"

ORIGIN

Alignment Scores:

Pred. No.: 5.76e+04 Length: 51  
 Score: 45.00 Matches: 7  
 Percent Similarity: 62.50% Conservative: 3  
 Best Local Similarity: 43.75% Mismatches: 6  
 Query Match: 1.63% Indels: 0  
 DB: Gaps: 0

US-08-864-955-2 (1-523) x AX161875 (1-51)

Cy 235 CyMeMetAlaSerLeuTPThrAlaProLeuValMetArgThrThraSn 250

Db 50 TGTGTGTTCTTATGACACCTGCTGCTGCTGCTGCTTAAT 3

RESULT 9  
 LOCUS AX197541 58 bp DNA linear PAT 29-AUG-2001

DEFINITION Sequence 11 from Patent WO0151045.  
 ACCESSION AX197541  
 VERSION AX197541.1 GI:15387858

KEYWORDS synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1 Lehmann, J.M. and Shiau, A.K.  
 Modulators of the constitutive androstane receptor (car): screening  
 and treatment of hypercholesterolemia  
 Patent: WO 0151045-A 11 19-JUL-2001;

JOURNAL Tularik Inc. (US)

FEATURES  
 source Location/Qualifiers

1..58  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="overlapping Oligo 2931"

ORIGIN

Alignment Scores:

Pred. No.: 6.81e+04 Length: 58  
 Score: 45.00 Matches: 7

Percent Similarity: 71.43% Conservative: 3  
 Best Local Similarity: 50.00% Mismatches: 4  
 Query Match: 1.63% Indels: 0  
 DB: Gaps: 0

US-08-864-955-2 (1-523) x AX197541 (1-58)

Cy 481 GIUPProSerTyArgProMetHisGlnAspPheLys 494  
 Db 6 CAGCTCCAGCCTATCTGTCATGCAATCAACGCGCTTCCAG 47

RESULT 10

LOCUS AX441045 49 bp DNA linear PAT 28-JUN-2002  
 DEFINITION Sequence 71 from Patent WO0204664.  
 ACCESSION AX441045  
 VERSION AX441045.1 GI:21665661

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 von Knebel Doeberitz, M., Bork, P., Yuan, Y.P., Gebert, J., Woerner, S.  
 and Linnebacher, M.  
 Genes and their genetic products pertinent to microsatellite  
 instable (msi+) tumors  
 Patent: WO 0204664-A 71 17-JAN-2002;

JOURNAL Von Knebel Doeberitz, Magnus (DE)

FEATURES  
 source Location/Qualifiers

1..49  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
 Pred. No.: 5.94e+04 Length: 49  
 Score: 44.50 Matches: 10  
 Percent Similarity: 58.82% Conservative: 0  
 Best Local Similarity: 58.82% Mismatches: 0  
 Query Match: 1.61% Indels: 7  
 DB: Gaps: 1

US-08-864-955-2 (1-523) x AX441045 (1-49)

Cy 5 ProSerProAlaProArgArgLeuPheAlaCysSerProProAla 21

Db 4 CCGTCCCTGCTGCTCC-----AGCCCCCCCCAGCT 33

RESULT 11

LOCUS MTRVDJA 45 bp mRNA linear ROD 07-MAR-1993  
 DEFINITION M.domesticus DBA/2 rearranged T-cell receptor  
 (Vbeta8.2-N-Dbeta1.1-N-Jbeta2.7).  
 ACCESSION X63590  
 VERSION X63590.1 GI:57902

KEYWORDS Ig D-segment; joining region; N-region; T-cell receptor; variable  
 region.

ORGANISM Mus musculus domesticus (western European house mouse)  
 Mus musculus domesticus

REFERENCE 1 (bases 1 to 45)  
 Roger, T.R.  
 Unpublished

JOURNAL 2 (bases 1 to 45)  
 Roger, T.  
 Direct Submission

TITLE Submitted (16-DEC-1991) T. Roger, Laboratoire  
 d'immunodifférenciation, Service du Pr SEMAN, Institut J.MONOD, 2,  
 Place JUSSIEU, 75251 PARIS CEDEX 05, FRANCE

FEATURES  
 Location/Qualifiers



Score: 44.00 Matches: 6  
 Percent Similarity: 88.89% Conservative: 2  
 Best Local Similarity: 66.67% Mismatches: 1  
 Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX840794 (1-51)

QY 382 IleaSPCYsArgTYrProTYrGluTYr 390  
 DB 40 GTCGACTGTCTGCTACTGCTAGAGATTTC 14

RESULT 15  
 AX657102 59 bp DNA linear PAT 22-MAR-2003  
 LOCUS Sequence 45 from Patent WO2103010.  
 DEFINITION AX657102  
 ACCESSION AX657102  
 VERSION AX657102.1 GI:29159884  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Gust, B., Chater, K.F. and Kieser, T.E.  
 TITLE Methods and materials for targeted gene disruption in actinomycete bacteria  
 JOURNAL Patent: WO 02103010-A 45 27-DEC-2002;  
 FEATURES  
 source  
 1. 59  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

ORIGIN

Alignment Scores:  
 Pred. No.: 8.18e+04 Length: 59  
 Score: 44.00 Matches: 8  
 Percent Similarity: 76.92% Conservative: 2  
 Best Local Similarity: 61.54% Mismatches: 3  
 Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX657102 (1-59)

QY 272 LeuLYsArgProGluArgSerGlnGluUserProPro 284  
 DB 1 GTCAGGCGCGCGGACGACGACGAGAGAGACCACCC 39

RESULT 16  
 ATH525205 52 bp DNA linear PIN 29-MAR-2003  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 090F11.  
 DEFINITION  
 ACCESSION AJ525205  
 VERSION AJ525205.1 GI:26793441  
 KEYWORDS left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samsom, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
 MEDLINE 22363535  
 PUBMED 12446565  
 REFERENCE 2 (bases 1 to 52)

AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
 1. 52  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /cultivar="wassilewskija"  
 /db\_xref="taxon:3702"  
 /clone="090F11"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 1. 52  
 /note="T-DNA flanking sequence  
 left border"

misc\_feature

ORIGIN

Alignment Scores:  
 Pred. No.: 8.2e+04 Length: 52  
 Score: 43.00 Matches: 7  
 Percent Similarity: 62.50% Conservative: 3  
 Best Local Similarity: 43.75% Mismatches: 6  
 Query Match: 1.55% Indels: 0  
 DB: 8 Gaps: 0

US-08-864-955-2 (1-523) x ATH525205 (1-52)

QY 375 LeuLYsGluPheValIleIleaSPCYsArgTYrProTYrGluTYr 390  
 DB 5 TTAATTAAGAAGCTTGCTGCTGATATTGTCGTTAAATTTATT 52

RESULT 17  
 H010868S05/c 52 bp DNA linear PRI 17-AUG-2001  
 LOCUS Homo sapiens Ca2+/calmodulin-dependent protein kinase beta (CAMKK2) gene, exon 5.  
 DEFINITION  
 ACCESSION AF321392  
 VERSION AF321392.1 GI:15192746  
 KEYWORDS  
 SEGMENT  
 SOURCE  
 5 of 18  
 Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 52)  
 Hsu, L.-S., Chen, G.-D., Lee, L.-S., Chi, C.-W., Cheng, Y.-F. and Chen, J.-Y.  
 TITLE Human Ca2+/calmodulin-dependent protein kinase beta gene encodes multiple isoforms that display distinct kinase activity  
 JOURNAL J. Biol. Chem. 276 (33), 31113-31123 (2001)  
 MEDLINE 21391903  
 PUBMED 11395482

REFERENCE 2 (bases 1 to 52)  
 Hsu, L.-S. and Chen, J.-Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2000) Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan, ROC

FEATURES  
 source  
 1. 52  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="12"

QY 8 ALAProARGLeuPheAlaCysSerProProAlaSer 22

Db 57 CTCGGGCCCCCGCCCCCG-----GCCCGGCCCGCCCG 25

RESULT 21  
LOCUS AR261278 34 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 831 from patent US 6321716.  
ACCESSION AR261278  
VERSION AR261278.1 GI:28072041  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Mashiki, Z. and Harada, J.  
TITLE Negative pressure control apparatus for engine mounted in vehicle  
JOURNAL Patent: US 6321716-A 831 27-NOV-2001;  
FEATURES Location/Qualifiers  
source 1..34  
/organism="Unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.61e+04 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 90.91% Conservative: 3  
Best Local Similarity: 63.64% Mismatches: 1  
Query Match: 1.52% Indels: 0  
Gaps: 0  
DB: 0

US-08-864-955-2 (1-523) x AR261278 (1-34)

Qy 90 ProLeuaspSerLySGluasnLeuGluasnPro 100  
Db 1 CCGCTCGAGATATAGGAAATGAGACATCCA 33

RESULT 22  
LOCUS AR400541 34 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 831 from patent US 6620922.  
ACCESSION AR400541  
VERSION AR400541.1 GI:40144011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6620922-A 831 16-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..34  
/organism="Unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.61e+04 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 90.91% Conservative: 3  
Best Local Similarity: 63.64% Mismatches: 1  
Query Match: 1.52% Indels: 0  
Gaps: 0  
DB: 0

US-08-864-955-2 (1-523) x AR400541 (1-34)

Qy 90 ProLeuaspSerLySGluasnLeuGluasnPro 100  
Db 1 CCGCTCGAGATATAGGAAATGAGACATCCA 33

RESULT 23  
LOCUS AR405808 34 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 831 from patent US 6630305.  
ACCESSION AR405808  
VERSION AR405808.1 GI:40154645  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6630305-A 831 07-OCT-2003;  
FEATURES Location/Qualifiers  
source 1..34  
/organism="Unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.61e+04 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 90.91% Conservative: 3  
Best Local Similarity: 63.64% Mismatches: 1  
Query Match: 1.52% Indels: 0  
Gaps: 0  
DB: 0

US-08-864-955-2 (1-523) x AR405808 (1-34)

Qy 90 ProLeuaspSerLySGluasnLeuGluasnPro 100  
Db 1 CCGCTCGAGATATAGGAAATGAGACATCCA 33

RESULT 24  
LOCUS AX201058 34 bp DNA linear PAT 29-AUG-2001  
DEFINITION Sequence 688 from Patent WO0151633.  
ACCESSION AX201058  
VERSION AX201058.1 GI:15390863  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: WO 0151633-A 688 19-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..34  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PCR Primer"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.61e+04 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 90.91% Conservative: 3  
Best Local Similarity: 63.64% Mismatches: 1  
Query Match: 1.52% Indels: 0  
Gaps: 0  
DB: 0

US-08-864-955-2 (1-523) x AX201058 (1-34)

QY 90 Proleusapserilysgluasnleugluasnpro 100  
Db 1 CCGCTCGAGATAAGAAAATGAGACATCCA 33

RESULT 25  
AX267857 34 bp DNA linear PAT 26-OCT-2001  
LOCUS Sequence 831 from Patent WO0173032.  
DEFINITION AX267857  
ACCESSION AX267857  
VERSION AX267857.1 GI:16516500  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  
Katos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,  
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.  
and Henderson,R.A.  
Compositions and methods for the therapy and diagnosis of prostate  
cancer  
Patent: WO 0173032-A 831 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
1. .34  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PCR Primer"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.61e+04 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 90.91% Conservative: 3  
Best Local Similarity: 63.64% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX267857 (1-34)

QY 90 Proleusapserilysgluasnleugluasnpro 100  
Db 1 CCGCTCGAGATAAGAAAATGAGACATCCA 33

RESULT 26  
AX003471/c 36 bp DNA linear PAT 07-SEP-2000  
LOCUS Sequence 51 from Patent WO9928439.  
DEFINITION AX003471  
ACCESSION AX003471  
VERSION AX003471.1 GI:9927324  
KEYWORDS  
SOURCE B19 virus  
ORGANISM B19 virus  
REFERENCE  
1 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.  
AUTHORS Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.  
TITLE Erythrovirus and its applications  
JOURNAL Patent: WO 9928439-A 51 10-JUN-1999;  
ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERNIQUE (FR); GARBARG  
CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)  
FEATURES  
1. .36  
Location/Qualifiers  
/organism="B19 virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10798"

ORIGIN  
Alignment Scores:  
Pred. No.: 6.04e+04 Length: 36  
Score: 42.00 Matches: 5  
Percent Similarity: 88.89% Conservative: 3  
Best Local Similarity: 55.56% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x BD087087 (1-36)

QY 482 ProProserTyArgProMechishis 490  
Db 35 CCACCAACTTTTCCCGGTACATCAT 9

RESULT 28  
AR099144/c 40 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 9 from patent US 6077692.  
DEFINITION AR099144  
ACCESSION AR099144  
VERSION AR099144.1 GI:12808910  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 Unclassified.  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.,Roxanne., Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.  
and Gentz,R.L.

Best Local Similarity: 55.56% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX003471 (1-36)

QY 482 ProProserTyArgProMechishis 490  
Db 35 CCACCAACTTTTCCCGGTACATCAT 9

RESULT 27  
BD087087/c 36 bp DNA linear PAT 27-AUG-2002  
LOCUS Erythrovirus and application thereof.  
DEFINITION BD087087  
ACCESSION BD087087.1 GI:22632697  
VERSION JP 2001525163-A/51.  
KEYWORDS Erythrovirus  
SOURCE Erythrovirus  
ORGANISM Erythrovirus  
REFERENCE  
1 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae.  
1 (bases 1 to 36)  
AUTHORS Nguyen,Q.T., Garbarg,C.A. and Auguste,V.  
TITLE Erythrovirus and application thereof  
JOURNAL Patent: JP 2001525163-A 51 11-DEC-2001;  
ASSISTANCE PUBLIQUE HOPITAUX DE PARIS  
COMMENT  
OS Erythrovirus  
PN JP 2001525163-A/51  
PD 11-DEC-2001  
PF 03-DEC-1998 JP 2000523317  
PR 03-DEC-1997 FR 97/15197  
PI QUANG TRI NGUYEN, CHENON ANTOINE, GARBARG, VERNIQUE, AUGUSTE, PC  
C12N15/09, A61K39/12, A61K48/00, C07K14/015, C07K16/08, C12Q1/68, PC  
G01N33/53,  
PC C12N15/00  
CC Erythrovirus and application thereof  
FT Key Location/Qualifiers  
FT source 1. .36  
FT /organism="Erythrovirus".  
FEATURES  
1. .36  
Location/Qualifiers  
/organism="Erythrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:40121"

ORIGIN  
Alignment Scores:  
Pred. No.: 6.04e+04 Length: 36  
Score: 42.00 Matches: 5  
Percent Similarity: 88.89% Conservative: 3  
Best Local Similarity: 55.56% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x BD087087 (1-36)

QY 482 ProProserTyArgProMechishis 490  
Db 35 CCACCAACTTTTCCCGGTACATCAT 9

RESULT 28  
AR099144/c 40 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 9 from patent US 6077692.  
DEFINITION AR099144  
ACCESSION AR099144  
VERSION AR099144.1 GI:12808910  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 Unclassified.  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.,Roxanne., Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.  
and Gentz,R.L.

TITLE Keratinocyte growth factor-2  
JOURNAL Patent: US 6077692-A 9 20-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..40  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 6.89e+04 Length: 40  
Score: 42.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AR099144 (1-40)

QY 384 CysargTYrProTYrGluTYrGluGly 393  
DB 39 TGTCAATATCATTTCCACATGATGCGGA 10

RESULT 29  
AR361794/c 40 bp DNA linear PAT 17-AUG-2003  
LOCUS  
DEFINITION Sequence 9 from patent US 6599879.  
ACCESSION AR361794  
VERSION AR361794.1 GI:33769764  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE  
AUTHORS Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.  
TITLE Therapeutic uses of keratinocyte growth factor-2  
JOURNAL Patent: US 6599879-A 9 29-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..40  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 6.89e+04 Length: 40  
Score: 42.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AR361794 (1-40)

QY 384 CysargTYrProTYrGluTYrGluGly 393  
DB 39 TGTCAATATCATTTCCACATGATGCGGA 10

RESULT 30  
AX591271/c 40 bp DNA linear PAT 27-JAN-2003  
LOCUS  
DEFINITION Sequence 9 from Patent EPI247530.  
ACCESSION AX591271  
VERSION AX591271.1 GI:27949742  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Duan,R.D., Ruben,S.M., Jimenez,P., Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2 (Kgf-2 or fibroblast growth factor-12,  
fgf-12)  
JOURNAL Patent: EP 1247530-A 9 09-OCT-2002;

HUMAN GENOME SCIENCES, INC. (US)  
FEATURES Location/Qualifiers  
source 1..40  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 6.89e+04 Length: 40  
Score: 42.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX591271 (1-40)

QY 384 CysargTYrProTYrGluTYrGluGly 393  
DB 39 TGTCAATATCATTTCCACATGATGCGGA 10

RESULT 31  
AX591416/c 40 bp DNA linear PAT 27-JAN-2003  
LOCUS  
DEFINITION Sequence 9 from Patent EPI247862.  
ACCESSION AX591416  
VERSION AX591416.1 GI:27949863  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Duan,R.D., Ruben,S.M., Jimenez,P., Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2 (Kgf-2 or fibroblast growth factor-12,  
fgf-12)  
JOURNAL Patent: EP 1247862-A 9 09-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..40  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 6.89e+04 Length: 40  
Score: 42.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX591416 (1-40)

QY 384 CysargTYrProTYrGluTYrGluGly 393  
DB 39 TGTCAATATCATTTCCACATGATGCGGA 10

RESULT 32  
BD136532/c 40 bp DNA linear PAT 18-SEP-2002  
LOCUS  
DEFINITION Therapeutic utilization of horny cell growth factor-2.  
ACCESSION BD136532  
VERSION BD136532.1 GI:23231477  
KEYWORDS JP 2002507546-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 40)

AUTHORS Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.  
 TITLE Therapeutic utilization of horny cell growth factor-2  
 JOURNAL Patent:JP 2002507546-A 8 12-MAR-2002;  
 HUMAN GENOME SCIENCES INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002507546-A/8  
 PD 12-MAR-2002  
 PR 13-FEB-1999 JP 2000531473  
 PAELO JIMENEZ,MARK A RAMPY,DONNA MENDRICK,DEBORAH RUSSELL, PT  
 ARTHUR LOUIE  
 PC A61K38/00,A61P1/00,A61P7/00,A61P7/04,A61P7/06,A61P11/00,A61P11/02,  
 02, A61P13/08,A61P13/10,A61P27/02,A61P27/16,A61P35/02,C07K14/475,  
 PC C07K14/50//  
 PC A61K48/00,C12N15/09,A61K37/02,C12N15/00  
 CC Therapeutic utilization of horny cell growth factor-2 FH Key  
 TITLE Location/Qualifiers  
 JOURNAL Location/Qualifiers  
 FEATURES 1..40 /organism='Homo sapiens (human)'.  
 source /organism='Homo sapiens'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 6.88e+04 Length: 40  
 Score: 42.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4  
 Best Local Similarity: 50.00% Mismatches: 1  
 Query Match: 1.52% Indels: 0  
 DB: 6 Gaps: 0  
 US-08-864-955-2 (1-523) x BD136532 (1-40)  
 QY 384 CysArgTyrProTyrGluTyrGluGly 393  
 Db 39 TGTCAGTATCATTCATTCACATGATGCGCA 10  
 RESULT 33  
 LOCUS A12209 48 bp DNA linear PAT 10-DEC-1993  
 DEFINITION EBI 643.  
 ACCESSION A12209  
 VERSION A12209.1 GI:492577  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 48)  
 AUTHORS Heckl,K., Spevak,W., Ostermann,E., Zophel,A., Krystek,E.,  
 TITLE Maurer-Fogy,I., Wiche-Castanon,M.J., Stratowa,C. and Hauptmann,R.  
 JOURNAL Human manganese superoxide dismutase (hmn-SOD)  
 Patent: EP 0282899-A 31 21-SEP-1988  
 FEATURES BOEHRINGER INGELHEIM INTERNATIONAL GmbH  
 source Location/Qualifiers  
 1..48 /organism='unidentified'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:32644'  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.73e+04 Length: 48  
 Score: 42.00 Matches: 7  
 Percent Similarity: 81.82% Conservative: 0  
 Best Local Similarity: 63.64% Mismatches: 2  
 Query Match: 1.52% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x A12209 (1-48)  
 QY 9 ProArgArgLeuLeuPheAlaCysSerProPro 19  
 Db 2 CCAGAGAGGAGTGTGTCATTCATTCACCA 34  
 RESULT 34  
 LOCUS AR363935 48 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 31 from patent US 5240847.  
 ACCESSION AR363935  
 VERSION AR363935.1 GI:34426042  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 48)  
 AUTHORS Heckl,K., Spevak,W., Ostermann,E., Zophel,A., Krystek,E.,  
 TITLE Maurer-Fogy,I., Wiche-Castanon,M.J., Stratowa,C. and Hauptmann,R.  
 JOURNAL Human manganese superoxide dismutase (hmn-SOD)  
 Patent: US 5240847-A 31 31-AUG-1993;  
 FEATURES Location/Qualifiers  
 source 1..48 /organism='unknown'  
 /mol\_type='genomic DNA'  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.73e+04 Length: 48  
 Score: 42.00 Matches: 7  
 Percent Similarity: 81.82% Conservative: 2  
 Best Local Similarity: 63.64% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
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 Db 2 CCAGAGAGGAGTGTGTCATTCATTCACCA 34  
 RESULT 35  
 LOCUS AX453980 55 bp DNA linear PAT 06-JUL-2002  
 DEFINITION Sequence 6 from Patent WO0200883.  
 ACCESSION AX453980  
 VERSION AX453980.1 GI:21713632  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Parks,C.J., Sidhu,M.S., Walpita,P., Kovacs,G.R. and Udem,S.A.  
 TITLE Rescue of canine distemper virus from cdna  
 JOURNAL Patent: WO 0200883-A 6 03-JAN-2002;  
 AMERICAN CYANAMID COMPANY (US)  
 FEATURES Location/Qualifiers  
 source 1..55 /organism='synthetic construct'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:32630'  
 /note='Synthetic construct'  
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 Pred. No.: 1.04e+05 Length: 55  
 Score: 42.00 Matches: 8  
 Percent Similarity: 61.54% Conservative: 0  
 Best Local Similarity: 61.54% Mismatches: 5  
 Query Match: 1.52% Indels: 0  
 DB: 6 Gaps: 0  
 US-08-864-955-2 (1-523) x AX453980 (1-55)



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RESULT 39
AR306665/c AR306665 48 bp DNA linear PAT 12-JUN-2003
LOCUS AR306665
DEFINITION Sequence 79 from patent US 6548642.
ACCESSION AR306665
VERSION AR306665.1 GI:31696867
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kieleszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 79 15-APR-2003;
FEATURES
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                     /mol_type="genomic DNA"
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Pred. No.: 9.49e+04 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
Query Match: 1.50% Indels: 7
DB: 6 Gaps: 1
US-08-864-955-2 (1-523) x AR306665 (1-48)
QY 5 ProSerProAlaProArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 39 CCATCTCCCCACCT-----TCCCTCCACCATCACCACCACT 1
RESULT 40
AR340099 AR340099 48 bp DNA linear PAT 17-AUG-2003
LOCUS AR340099
DEFINITION Sequence 78 from patent US 6570062.
ACCESSION AR340099
VERSION AR340099.1 GI:33731393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kieleszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 78 27-MAY-2003;
FEATURES
    source          Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 9.49e+04 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
Query Match: 1.50% Indels: 7
DB: 6 Gaps: 1
US-08-864-955-2 (1-523) x AR340099 (1-48)
QY 5 ProSerProAlaProArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCTTCACCACTCTCA-----TCTCCCCACCTTCCCTCCACCA 45
RESULT 41
AR340100/c AR340100 48 bp DNA linear PAT 17-AUG-2003
LOCUS AR340100
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DEFINITION Sequence 79 from patent US 6570062.
ACCESSION AR340100
VERSION AR340100.1 GI:33731394
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kieleszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 79 27-MAY-2003;
FEATURES
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Alignment Scores:
Pred. No.: 9.49e+04 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
Query Match: 1.50% Indels: 7
DB: 6 Gaps: 1
US-08-864-955-2 (1-523) x AR340100 (1-48)
QY 5 ProSerProAlaProArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCTTCACCACTCTCA-----TCTCCCCACCTTCCCTCCACCA 45
RESULT 42
AR412168 AR412168 48 bp DNA linear PAT 18-DEC-2003
LOCUS AR412168
DEFINITION Sequence 78 from patent US 6639050.
ACCESSION AR412168
VERSION AR412168.1 GI:40166812
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kieleszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6639050-A 78 28-OCT-2003;
FEATURES
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                     /mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 9.49e+04 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
Query Match: 1.50% Indels: 7
DB: 6 Gaps: 1
US-08-864-955-2 (1-523) x AR412168 (1-48)
QY 5 ProSerProAlaProArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCTTCACCACTCTCA-----TCTCCCCACCTTCCCTCCACCA 45
RESULT 43
AR412169 AR412169 48 bp DNA linear PAT 18-DEC-2003
LOCUS AR412169
DEFINITION Sequence 79 from patent US 6639050.
ACCESSION AR412169
VERSION AR412169.1 GI:40166813
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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Kelliszewski, M.J.  
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins  
JOURNAL Patent: US 6639050-A 79 28-OCT-2003;  
FEATURES  
Location/Qualifiers  
1..48  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.49e+04 Length: 48  
Score: 41.50 Matches: 9  
Percent Similarity: 50.00% Conservative: 3  
Best Local Similarity: 45.00% Mismatches: 3  
Query Match: 1.50% Indels: 7  
DB: 6 Gaps: 1

US-08-864-955-2 (1-523) x AR412169 (1-48)

OY 5 ProSerProAlaProAlaGArgLeuPheAlaCysSerProProProAlaSerGlnPro 24  
Db 39 CCATCTCCCCACCT-----TCCCTCCACCATCACCACCT 1

RESULT 44  
AR182231  
LOCUS AR182231 60 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 15 from patent US 6337200.  
ACCESSION AR182231  
VERSION AR182231.1 GI:20225147  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 60)  
AUTHORS Morin, G.B.  
TITLE Human telomerase catalytic subunit variants  
JOURNAL Patent: US 6337200-A 15 08-JAN-2002;  
FEATURES  
Location/Qualifiers  
1..60  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Alignment Scores:  
Pred. No.: 1.27e+05 Length: 60  
Score: 41.50 Matches: 10  
Percent Similarity: 54.55% Conservative: 2  
Best Local Similarity: 45.45% Mismatches: 5  
Query Match: 1.50% Indels: 5  
DB: 6 Gaps: 1

US-08-864-955-2 (1-523) x AR182231 (1-60)

OY 4 G1yProSerProAlaProAlaGArgLeuPheAlaCysSerProProProAlaSerGln 23  
Db 6 GGCCCGGCCGCCGCCACACGC-----TAGCCTGCTCGCCGACACACAG 50

OY 24 ProVal 25  
Db 51 CCCCTG 56

RESULT 45  
AX082967/c 29 bp DNA linear PAT 28-FEB-2001  
LOCUS AX082967  
DEFINITION Sequence 3 from Patent WO011053.  
ACCESSION AX082967  
VERSION AX082967.1 GI:13184888

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Deibel, M.R., Klein, R.D. and Yem, A.W.  
TITLE Soluble, active recombinant human mao-b  
JOURNAL Patent: WO 011053-A 3 15-FEB-2001;  
FEATURES  
Location/Qualifiers  
1..29  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.39e+04 Length: 29  
Score: 41.00 Matches: 7  
Percent Similarity: 88.99% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 1.48% Indels: 0  
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x AX082967 (1-29)

OY 156 ArgGlyCysLeuHisSerHisGlyLeu 164  
Db 28 AGAGGGTGTCTGAATTCACACTCTCTT 2

Search completed: September 9, 2004, 22:48:52  
Job time : 4069 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2004, 19:32:39 / Search time 432 Seconds

(without alignments)  
5143.073 Million cell updates/sec

Title: US-08-864-955-2

Perfect score: 2769

Sequence: 1

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3297956

Minimum DB seq length: 10  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: genesegn1990s:\*  
3: genesegn2000s:\*  
4: genesegn2001as:\*  
5: genesegn2001bs:\*  
6: genesegn2002as:\*  
7: genesegn2003as:\*  
8: genesegn2003bs:\*  
9: genesegn2003cs:\*  
10: genesegn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	3.4	60	6	ABN40154 Human spl
2	73	2.6	60	6	ABN40193 Human spl
3	49	1.8	60	6	ABN40217 Human spl
4	48	1.7	53	2	AAV83902 Human spl
5	48	1.7	60	6	ABN32725 Human spl
6	47	1.7	54	3	AAA73939 GFP Hs(C
7	47	1.7	54	3	AAA73940 GFP Hs(C
8	46	1.7	60	6	ABN58762 Human spl

9	45.5	1.6	60	5	AAE89452 Human gen
10	45.5	1.6	60	7	AAD50221 Human GAL
11	45	1.6	40	2	AAV04087 Enkephali
12	45	1.6	43	2	AAK27070 PCR prime
13	45	1.6	50	6	ABZ04528 Human leu
14	45	1.6	51	4	AAI78262 Human sll
15	45	1.6	57	3	AAH95764 HIV envcl
16	45	1.6	58	4	AAH42540 Human FTL
17	44.5	1.6	49	6	ABN75019 Human FTL
18	44	1.6	50	4	AAI33848 Human SNP
19	44	1.6	50	4	AAI29098 Human SNP
20	44	1.6	50	4	AAI29098 Human SNP
21	44	1.6	50	6	ABZ07506 Human leu
22	44	1.6	50	6	ABZ07133 Human leu
23	44	1.6	50	6	ABZ07427 Human leu
24	44	1.6	51	4	AAI29072 Human SNP
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26	44	1.6	52	7	ACD94372 Human col
27	44	1.6	59	7	ADA88986 S. coelic
28	44	1.6	60	6	ABN35109 Human spl
29	44	1.6	60	6	ABN37833 Human spl
30	44	1.6	60	6	ABN42974 Human spl
31	44	1.6	60	6	ABN59321 Human spl
32	44	1.6	60	6	ABN42357 Human spl
33	44	1.6	60	6	ABN58779 Human spl
34	44	1.6	60	6	ABN58502 Human spl
35	44	1.6	60	6	ABN35318 Human spl
36	44	1.6	60	6	ABN38507 Human spl
37	44	1.6	60	6	ABN59505 Human spl
38	43	1.6	39	9	AAI61489 Human MWP
39	43	1.6	50	4	AAI33854 Human SNP
40	43	1.6	54	3	AAI60434 Plasmid P
41	43	1.6	60	6	ABN40897 Human spl
42	43	1.6	60	6	ABN59521 Human spl
43	43	1.6	60	6	ABN40259 Human spl
44	43	1.6	60	6	ABN46250 Human spl
45	43	1.6	60	6	ABN35538 Human spl

## ALIGNMENTS

RESULT 1	ABN40154	standard; DNA; 60 BP.
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AC	ABN40154	
DT	15-JUL-2002 (first entry)	
XX		
DE	Human spliced transcript detection oligonucleotide SEQ ID NO:12902.	
XX		
KW	Human; mouse; rat; splice transcript; detection; RNA transcript;	
XX	splice variant; transcriptome; oligonucleotide library; ss.	
OS	Homo sapiens.	
XX		
PN	WO200210449-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	20-JUL-2001; 2001WO-1B001903.	
XX		
PR	28-JUL-2000; 2000US-0221607P.	
XX		
PR	02-MAY-2001; 2001US-0287724P.	
XX		
PA	(COMP-) COMPUGEN INC.	
XX		
PI	Shoshan A, Wasserman A, Mintz E, Faigler S;	
XX		
DR	WPI; 2002-257383/30.	
XX		
PT	New oligonucleotide libraries comprising oligonucleotides which	
	selectively hybridize to mRNAs transcribed from a transcription unit of a	

PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
PS Example 1; SEQ ID NO 12902; 47bp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 15 A; 20 C; 9 G; 16 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 4.26 Length: 60  
Score: 95.00 Matches: 19  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.43% Indels: 0  
Gaps: 0  
DB: 6  
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Db 2 ACTAATCCAGAGAGAGGCCCATGAGACTCTTCATCATGCTTATCCCTGCAGCTCTCC 58  
RESULT 2  
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ID ABN40193 standard; DNA; 60 BP.  
XX  
AC ABN40193;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12941.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
PR 02-MAY-2001; 2001US-0287724P.  
PA (COMP-) COMPUGEN INC.  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX

DR WPI; 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
PS Example 1; SEQ ID NO 12941; 47bp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 17 A; 18 C; 15 G; 10 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 290 Length: 60  
Score: 73.00 Matches: 12  
Percent Similarity: 85.00% Conservative: 5  
Best Local Similarity: 60.00% Mismatches: 3  
Query Match: 2.64% Indels: 0  
Gaps: 0  
DB: 6  
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QY 488 MetHisHisGluAspPheLysGluAspLeuLysPheArgThrLysSerArgThrTyr 507  
Db 1 ATGAACCAAGAGAGGCTTCAAGATGACGTAAAGACCTCCGCCCTCAGACTCGACGCTGG 60  
RESULT 3  
ABN40217  
ID ABN40217 standard; DNA; 60 BP.  
XX  
AC ABN40217;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12965.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
PR 02-MAY-2001; 2001US-0287724P.  
PA (COMP-) COMPUGEN INC.  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX

PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX  
PS Example 1; SEQ ID NO 12965; 47bp; English.  
XX  
XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini-  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABRN27253 to ABRN9589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 19 A; 13 C; 17 G; 11 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 2.89e+04 Length: 60  
Score: 49.00 Matches: 8  
Percent Similarity: 77.78% Conservative: 6  
Best Local Similarity: 44.44% Mismatches: 4  
Query Match: 1.77% Indels: 0  
DB: Gaps: 0  
US-08-864-955-2 (1-523) x ABRN40217 (1-60)  
OY 488 Methisgluaspheylsgluaspheulysypheargthylserrarg 505  
DB 2 ATGCTCATCTGACGACACAGACTGAGTCTGCTGAGTGTGCAACCGAGACAA 55  
RESULT 4  
AAV83902/C  
ID AAV83902 standard; DNA; 53 BP.  
XX  
AC AAV83902;  
XX  
DT 03-MAR-1999 (first entry)  
XX  
DE Oligonucleotide used to construct a His6-Flag sequence.  
XX  
XX [3H]1,3-diehy1-8-phenyl-xanthine; [3H]DPX, human A2B adenosine receptor;  
XX competitive binding assay; ss.  
XX  
OS Synthetic.  
XX  
FN US5854081-A.  
XX  
PD 29-DEC-1998.  
XX  
PF 20-JUN-1996; 96US-00670175.

XX  
XX 20-JUN-1996; 96US-00670175.  
XX  
XX (UYPA-) UNIV PATENT FOUND.  
XX  
PA Jin X, Woodard R, Linden J, Taylor H, Robeva A;  
XX  
PI WPI; 1999-094922/08.  
XX  
DR  
XX  
PT Detecting binding of tritiated 1,3-di-ethyl-8-phenyl-xanthine - to human  
PT A2B adenosine receptors.  
XX  
XX  
PS Disclosure; Col 5; 24pp; English.  
XX  
XX Oligonucleotides AAV99228 and AAV83902 were used to construct a His6-Flag  
CC sequence, which is used to produce an expression vector that can be used  
CC to express the proteins of the invention. The specification describes a  
CC method for detecting binding of [3H]1,3-diehy1-8-phenyl-xanthine  
CC ([3H]DPX) to a human A2B adenosine receptor. The method comprises  
CC contacting the receptor, which is present in an amount of at least 5  
CC pmole/mg protein, with [3H]DPX, washing the receptor to remove any  
CC unbound material, and inspecting the resulting sample to determine the  
CC presence of [3H]DPX, where the presence and amount of [3H]DPX correlates  
CC with the presence and amount of binding of [3H]DPX to the receptor. The  
CC method is used for detecting binding where it is a competitive binding  
CC assay and the target compound is a potentially therapeutically active  
CC compound  
XX  
SQ Sequence 53 BP; 9 A; 13 C; 14 G; 17 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 2.96e+04 Length: 53  
Score: 48.00 Matches: 8  
Percent Similarity: 73.33% Conservative: 3  
Best Local Similarity: 53.33% Mismatches: 4  
Query Match: 1.73% Indels: 0  
DB: Gaps: 0  
US-08-864-955-2 (1-523) x AAV83902 (1-53)  
OY 489 Hishisgluaspheylsgluaspheulysypheargthyls 503  
DB 53 CATCACCATGACTACAGACGACGATGACCAAGTCTAAGACCGCT 9  
RESULT 5  
ABRN32725  
ID ABRN32725 standard; DNA; 60 BP.  
XX  
AC ABRN32725;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:5473.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200210449-A2.  
XX  
PN 07-FEB-2002.  
XX  
PD 20-JUL-2001; 2001WO-1B001903.  
XX  
PF 26-UTL-2000; 2000US-0221607F.  
XX  
PR 02-MAY-2001; 2001US-0287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.

```

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 5473; 47bp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN29589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 60 BP; 13 A; 14 C; 16 G; 17 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.5e+04 Length: 60
Score: 48.00 Matches: 11
Percent Similarity: 63.64% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 1.73% Indels: 6
DB: Gaps: 1
XX
US-08-864-955-2 (1-523) x ABN2725 (1-60)
XX
CY 200 PheThrProGlnSerProValThrAlaThrLeuSerAspGluSpasgLyPheValaap 219
DB 12 TACACCCCTGCTCTCC-----AGTGATGATGACAGAGGCTTTGTGGAC 53
XX
CY 220 LeuIeu 221
DB 54 CTAAATT 59
XX
RESULT 6
AAA73939
ID AAA73939 standard; DNA; 54 BP.
XX
AC AAA73939;
XX
DT 06-DEC-2000 (first entry)
XX
DE GFP His(CAC)5 forward primer.
XX
KW Green fluorescent protein; GFP; reporter gene; codon utilisation;
KW translational efficiency; protein abundance; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200042215-A1.
XX
PD 20-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-AU000008.
XX

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```

PR 08-JAN-1999; 99AU-00008078.
XX
XX (UYOU ) UNIV QUEENSLAND.
PA (SDMX/) SUN X.
XX
XX Zhou J, Frazer IH;
XX
DR WPI, 2000-499118/44.
XX
PT Determining translational efficiency of codons in cells, comprising
PT introducing synthetic constructs with reporter genes fused in frame to
PT tandem repeats of the codon, and measuring expression.
XX
PS Example 1; Page 181, 190pp; English.
XX
CC The present sequence is a primer used to generate a synthetic gfp gene by
CC PCR amplification of a humanised gfp gene. A single artificial start
CC codon followed by a stretch of five identical codons was fused in frame
CC immediately upstream of a gfp coding sequence to form the synthetic gene.
CC The amplified fragment was cloned into the mammalian expression vector
CC pCDNA3, which contains SV40 ori and the CMV promoter, and was used in a
CC method for determining the translational efficiency of a codon in a cell.
CC The synthetic construct was introduced into COS-1 cells and expression of
CC the reporter protein (green fluorescent protein) was measured. A series
CC of 64 gfp reporter constructs was made in which the gfp gene is preceded
CC in frame by a tandem repeat of 5 identical codons. The series covers the
CC entire set of isocoding codon triplets. Codons with a higher
CC translational efficiency than their corresponding synonymous codons can
CC be identified. These codons may then be used to replace the less
CC preferred codons of a polynucleotide so that there is higher protein
CC expression within undifferentiated epithelial cells such as COS-1 cells
XX
SQ Sequence 54 BP; 14 A; 19 C; 15 G; 6 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.68e+04 Length: 54
Score: 47.00 Matches: 8
Percent Similarity: 70.59% Conservative: 4
Best Local Similarity: 47.06% Mismatches: 5
Query Match: 1.70% Indels: 0
DB: Gaps: 0
XX
US-08-864-955-2 (1-523) x AAA73939 (1-54)
XX
CY 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGluGlyLysAspLeuPheThr 172
DB 1 CGGGGTACATGACACACACACACACACAGGAGGCAAGAACTGTCTACT 51
XX
RESULT 7
AAA73940
ID AAA73940 standard; DNA; 54 BP.
XX
AC AAA73940;
XX
DT 06-DEC-2000 (first entry)
XX
DE GFP His(CAT)5 forward primer.
XX
KW Green fluorescent protein; GFP; reporter gene; codon utilisation;
KW translational efficiency; protein abundance; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200042215-A1.
XX
PD 20-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-AU000008.
XX
PR 08-JAN-1999; 99AU-00008078.
XX
PA (UYOU ) UNIV QUEENSLAND.
PA (SDMX/) SUN X.
XX

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```
XX Zhou J, Frazer IH;
XX WPI; 2000-499118/44.
XX
XX Determining translational efficiency of codons in cells, comprising
XX PT introducing synthetic constructs with reporter genes fused in frame to
XX tandem repeats of the codon, and measuring expression.
XX
XX Example 1; Page 182; 190pp; English.
XX
XX The present sequence is a primer used to generate a synthetic gfp gene by
XX PCR amplification of a humanised gfp gene. A single artificial start
XX codon followed by a stretch of five identical codons was fused in frame
XX immediately upstream of a gfp coding sequence to form the synthetic gene.
XX The amplified fragment was cloned into the mammalian expression vector
XX pCDNA3, which contains SV40 ori and the CMV promoter, and was used in a
XX method for determining the translational efficiency of a codon in a cell.
XX The synthetic construct was introduced into COS-1 cells and expression of
XX the reporter protein (green fluorescent protein) was measured. A series
XX of 64 gfp reporter constructs was made in which the gfp gene is preceded
XX in frame by a tandem repeat of 5 identical codons. The series covers the
XX entire set of 160 acceptable codon triplets. Codons with a higher
XX translational efficiency than their corresponding synonymous codons can
XX be identified. These codons may then be used to replace the less
XX preferred codons of a polynucleotide so that there is higher protein
XX expression within undifferentiated epithelial cells such as COS-1 cells
XX
XX Sequence 54 BP; 14 A; 14 C; 15 G; 11 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3.68e+04 Length: 54
XX Score: 47.00 Matches: 8
XX Percent Similarity: 70.59% Conservative: 4
XX Best Local Similarity: 47.06% Mismatches: 5
XX Query Match: 1.70% Indels: 0
XX DB: Gaps: 0
XX
XX US-08-864-955-2 (1-523) x AAA73940 (1-54)
XX
XX QY 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyLysAspLeuPheThr 172
XX DB 1 CGGGGTACCATGCATCATCATCATGACAGGCGAGGACATGTTCACT 51
XX
XX RESULT 8
XX ABNS8762/c
XX ID ABNS8762 standard; DNA; 60 BP.
XX
XX AC ABNS8762;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:31510.
XX
XX KM Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-1B001903.
XX
XX PR 28-JUL-2000; 2000US-0221607P.
XX
XX PR 02-MAY-2001; 2001US-0287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
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```
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of a
XX PT genome, useful for detecting tissue-, pathology-, and developmental-
XX PT specific genes.
XX
XX Example 1; SEQ ID NO 31510; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX transcriptome comprises messenger RNAs transcribed from multiple
XX oligonucleotide units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridising selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition; to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABNS9589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 60 BP; 15 A; 14 C; 18 G; 13 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.14e+04 Length: 60
XX Score: 46.00 Matches: 9
XX Percent Similarity: 62.50% Conservative: 1
XX Best Local Similarity: 56.25% Mismatches: 6
XX Query Match: 1.66% Indels: 0
XX DB: Gaps: 0
XX
XX US-08-864-955-2 (1-523) x ABNS8762 (1-60)
XX
XX QY 271 ValLeuIysArgProGluArgSerGlnGlnGlnSerProProGlySer 286
XX DB 55 ATRTTGCCAGGCGCTTGAAGAAGGAGCATVCTGTCCTCCGGAAGT 8
XX
XX RESULT 9
XX AAF89452
XX ID AAF89452 standard; DNA; 60 BP.
XX
XX AC AAF89452;
XX
XX DT 14-AUG-2001 (first entry)
XX
XX DE Human genetic marker PCR primer SEQ ID NO: 41.
XX
XX KM Genetic marker; genetic disease diagnosis; cystic fibrosis; haemophilia;
XX sickle cell disease; muscular dystrophy; Huntington's disease;
XX retinoblastoma; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200134839-A1.
XX
XX PD 17-MAY-2001.
XX
XX PF 03-NOV-2000; 2000WO-US030493.
XX
XX PR 12-NOV-1999; 99US-0165301P.
XX
XX PA (DUNL/) DUNLOP C L M.
```

PA (WEIS/) WEISEL J M.  
XX  
XX Dunlop CLM, Weisel JM;  
PI  
XX WPI: 2001-323096/34.  
DR  
XX  
XX Detecting multiple genetic markers in one assay, useful to simultaneously  
PT detect a number of genetic disorders, comprises generating extension  
PT products and separating them on the basis of melting behavior is.  
XX  
XX  
PS Claim 44; Page 35; 40pp; English.  
XX  
XX The present invention describes a method of identifying the presence of a  
CC plurality of genetic markers in a subject, involving generating extension  
CC products using PCR primers flanking the plurality of markers, separating  
CC the extension products depending on their melting temperatures, and  
CC analysing them to determine the presence or absence of each genetic  
CC marker. This can be used in the diagnosis of genetic diseases, including  
CC familial hypercholesterolaemia, cystic fibrosis, Tay-Sachs, thalassaemia,  
CC sickle cell disease, phenylketonuria, galactosaemia, fragile X syndrome,  
CC haemophilia A, myotonic dystrophy, medium chain acyl-CoA dehydrogenase,  
CC maturity onset diabetes, cystinuria, methylmalonic acidemia, urea cycle  
CC disorders, hereditary fructose intolerance, hereditary haemochromatosis,  
CC neonatal thrombocytopenia, Gaucher's disease, tyrosinaemia, Wilson's  
CC disease, acromiuria, hypolactasia, Baker's disease, argininaemia,  
CC adrenomatous polyposis coli, hereditary non-polyposis colorectal cancer,  
CC Huntington's disease, adult polycystic kidney disease, alpha-1-  
CC antitrypsin deficiency, Duchenne muscular dystrophy, Marfan's syndrome,  
CC neurofibromatosis, osteogenesis imperfecta, retinoblastoma, Friedreich's  
CC ataxia, haemoglobinopathies, Leber's hereditary optic neuropathy, MCAD,  
CC Canavan's disease, retinitis pigmentosa, Bloom syndrome, Fanconi anaemia  
CC or Neuman Pick disease. The present sequence is one of the PCR primers  
CC of the invention  
XX  
XX  
SQ Sequence 60 BP; 4 A; 39 C; 14 G; 3 T; 0 U; 0 Other;  
XX  
XX  
Alignment Scores:  
Pred. No.: 5.66e+04 Length: 60  
Score: 45.50 Matches: 10  
Percent Similarity: 60.00% Conservative: 2  
Best Local Similarity: 50.00% Mismatches: 3  
Query Match: 1.64% Indels: 5  
DB: Gaps: 1  
XX  
US-08-864-955-2 (1-523) x AAF89452 (1-60)  
QY 5 ProSePrProAlaProAGArgLeuLeuPheAlaCySeSerProProProAlaSerGInPro 24  
Db 7 CCGCGCCCGCGCGCC-----GCCCGCGCGCGCCCGCGCGCGAGCCAGCC 51  
RESULT 10  
AAD50221  
ID AAD50221 standard; DNA; 60 BP.  
XX  
XX AAD50221;  
AC  
XX 24-MAR-2003 (first entry)  
DT  
XX  
XX Human GALT 5 specific PCR primer #1.  
DE  
XX  
XX Human; cystic fibrosis; Tay-Sachs; familial hypercholesterolaemia; FH;  
KW fragile X syndrome; haemophilia A; diabetes; cystinuria; tyrosinaemia;  
KW urea cycle disorder; hereditary fructose intolerance; Baker's disease;  
KW Wilson's disease; alcaptonuria; adult polycystic kidney disease; MCAD;  
KW Huntington's disease; myotonic dystrophy; retinitis pigmentosa; cancer;  
KW Gaucher's disease; Canavan's disease; galactosaemia; thrombocytopenia;  
KW thalassaemia; sickle cell disease; phenylketonuria; Marfan's syndrome;  
KW haemoglobinopathy; Bloom syndrome; Neuman Pick's disease; PCR; primer;  
KW galactose-1-phosphate uridylyl transferase; GALT; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200290374-A1.  
PN

XX  
XX 14-NOV-2002.  
PD  
XX  
XX 06-MAY-2002; 2002MO-US014562.  
PF  
XX  
XX 08-MAY-2001; 2001US-00851501.  
PR  
XX  
XX (AMBR-) AMERY GENETICS CORP.  
PA  
XX  
XX Dunlop CLM, Weisel JM;  
PI  
XX  
XX WPI: 2003-103498/09.  
DR  
XX  
XX  
XX Identifying the presence or absence of a mutation or polymorphism in a  
PT subject, useful for diagnosing genetic diseases, comprises generating  
PT extension products and analyzing the melting behavior of the mixed DNA  
PT sample.  
XX  
XX  
PS Claim 56; Page 44; 49pp; English.  
XX  
XX The invention relates to a method for identifying the presence or absence  
CC of a mutation or polymorphism in a plurality of genes. The method is used  
CC for identifying the presence or absence of a mutation or polymorphism in a  
CC subject, or the presence or absence of several genetic markers in a  
CC subject for diagnosing genetic diseases, e.g. cystic fibrosis, Tay-Sachs,  
CC familial hypercholesterolaemia (FH), thalassaemia, sickle cell disease,  
CC phenylketonuria, galactosaemia, fragile X syndrome, haemophilia A,  
CC myotonic dystrophy, medium-chain acyl CoA dehydrogenase, maturity onset  
CC diabetes, cystinuria, methylmalonic acidemia, urea cycle disorders,  
CC hereditary fructose intolerance, hereditary haemochromatosis, neonatal  
CC thrombocytopenia, Gaucher's disease, tyrosinaemia, Wilson's disease,  
CC alcaptonuria, hypolactasia, Baker's disease, argininaemia adrenomatous  
CC polyposis coli (APC), adult polycystic kidney disease, Duchenne muscular  
CC dystrophy, alpha-1-antitrypsin deficiency, hereditary non-polyposis  
CC colorectal cancer, Huntington's disease, neurofibromatosis, Marfan's  
CC syndrome, osteogenesis imperfecta, retinoblastoma, Friedreich's ataxia,  
CC haemoglobinopathies, MCAD, Canavan's disease, Leber's hereditary optic  
CC neuropathy, retinitis pigmentosa, Bloom syndrome, Fanconi's anaemia, or  
CC Neuman Pick's disease. The present sequence is human galactose-1-  
CC phosphate uridylyl transferase (GALT) specific PCR primer used to  
CC illustrate the method of the invention  
XX  
XX  
SQ Sequence 60 BP; 4 A; 39 C; 14 G; 3 T; 0 U; 0 Other;  
XX  
XX  
Alignment Scores:  
Pred. No.: 5.66e+04 Length: 60  
Score: 45.50 Matches: 10  
Percent Similarity: 60.00% Conservative: 2  
Best Local Similarity: 50.00% Mismatches: 3  
Query Match: 1.64% Indels: 5  
DB: Gaps: 1  
XX  
US-08-864-955-2 (1-523) x AAD50221 (1-60)  
QY 5 ProSePrProAlaProAGArgLeuLeuPheAlaCySeSerProProProAlaSerGInPro 24  
Db 7 CCGCGCCCGCGCGCC-----GCCCGCGCGCGCCCGCGCGCGAGCCAGCC 51  
RESULT 11  
AAV04087/C  
ID AAV04087 standard; DNA; 40 BP.  
XX  
XX AAV04087;  
AC  
XX 22-JUN-1998 (first entry)  
DT  
XX  
XX Enkephalin gene cAMP response element.  
DE  
XX  
XX ApCSEB-2; cAMP response element binding protein-2; snail;  
KW transcription factor; memory loss; Alzheimer's disease; amnesia;  
KW ischaemia; head trauma; neuronal injury; Parkinson's disease; senility;  
KW therapy; Aplysia californica; enkephalin; CRE; ds.  
XX

```

OS Synthetic.
XX Key Location/Qualifiers
FH misc_feature 9..40
FT //tag= a
FT /function= "CRE"
XX
XX MO9746257-A1.
XX PN
XX PD 11-DEC-1997.
XX PF 03-JUN-1997; 97MO-US009438.
XX PR 03-JUN-1996; 96US-00656811.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI
XX PI Bartech D, Kandel ER, Ghirardi M;
XX WPI; 1998-051903/05.
XX
XX Enhancing long-term memory in subjects whose CAMP-responsive gene is
PT repressed - used to treat long-term memory defects, e.g. age-related
PT memory loss, Alzheimer's disease.
XX
XX Example 2; Page 47; 100pp; English.
XX
XX This oligonucleotide includes the CAMP response element (CRE) of the
CC enkephalin gene. The DNA binding capability of Aplysia CAMP-response
CC element binding protein-2 (APCREB-2) (see AAW41508) was examined by
CC electrophoretic mobility shifts using double stranded oligonucleotides
CC (see AAV04084-93) comprising symmetrical and asymmetrical CREs and CAP
CC motifs of C/EBP binding sites. Recombinant APCREB-2 bound in solution to
CC the asymmetrical CRE of the enkephalin gene, as well as to the
CC symmetrical CRE of the somatostatin gene (see AAV04084), but did not bind
CC to any of the CAP sites tested. The invention provides a method of
CC enhancing long-term memory in a subject whose CAMP-responsive gene
CC expression is repressed. It involves administering a compound, especially
CC an anti-CREB-2 antibody, that is capable of interfering with the binding
CC of CREB-2 to a protein or DNA associated with CAMP-responsive gene
CC expression.
XX
XX Sequence 40 BP; 4 A; 12 C; 18 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
Pred. No.: 3.61e+04 Length: 40
Score: 45.00 Matches: 7
Percent Similarity: 90.91% Conservative: 3
Best Local Similarity: 63.64% Mismatches: 1
Query Match: 1.63% Indels: 0
DB: 2 Gaps: 0
US-08-864-955-2 (1-523) x AAV04087 (1-40)
QY 2 GluLeuGlyProSerProAlaProArgArgLeu 12
DB 33 GACGACAGGCGCTTACGACGACGCGCGCGGATC 1
XX
XX RESULT 12
XX AAX27070/C
XX ID AAX27070 standard; DNA; 43 BP.
XX
XX AAX27070;
XX AC
XX XX 20-MAR-2003 (revised)
XX DT 21-MAY-1999 (first entry)
XX DE
XX DE PCR primer for pHOK-1-GM-CSF fusion protein coding sequence.
XX XX GM-CSF; granulocyte macrophage colony stimulating factor; vaccine;
XX KW membrane-bound fusion protein; non-antibody immunomodulator; infection;
XX KW membrane attachment domain; cancer; autoimmune disease; therapy;
XX PCR primer; ss.

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```

XX
XX OS Synthetic.
XX OS Mus sp.
XX XX MO9906544-A1.
XX PN
XX PD 11-FEB-1999.
XX PF 27-JUL-1998; 98MO-US015622.
XX PR 29-JUL-1997; 97US-00902516.
XX PA (IMMU-) IMMUNE RESPONSE CORP.
XX PI
XX PI Soo Hoo W;
XX WPI; 1999-153774/13.
XX
XX Vaccine having a membrane-bound fusion protein - comprising an
PT immunomodulator and heterologous membrane attachment domain useful for
PT modulation of immune response against a disease-associated antigen.
XX
XX Example 1; Page 50; 91pp; English.
XX
XX This sequence represents a PCR primer used in the construction of DNA
CC encoding the pHOK-1-GM-CSF fusion protein. The invention relates to a
CC vaccine comprising a cell having a membrane-bound fusion protein (FP)
CC consisting of a non-antibody immunomodulator (I) linked to a heterologous
CC membrane attachment domain. The vaccines are used to treat or prevent a
CC wide variety of cancers (e.g. of colon, breast or prostate, melanoma,
CC glioma), alone or as adjunct to other therapies; autoimmune diseases
CC (e.g. rheumatoid arthritis, psoriasis, multiple sclerosis, systemic lupus
CC erythematosus, type I diabetes, allergy) or viral, bacterial or parasitic
CC infections (e.g. human immune deficiency virus, Helicobacter pylori,
CC Porphyromonas gingivalis, or Candida albicans). A panel of cells (or cell
CC lines) each genetically modified to express different antigens can be
CC maintained as a repository, for treatment or prevention of the
CC appropriate tumour type, e.g. based on histological analysis. Membrane-
CC bound (I) provides a vaccine with increased receptor-cytokine avidity,
CC and thus stimulates a stronger immune response. (Updated on 20-MAR-2003
CC to correct PF field.)
XX
XX Sequence 43 BP; 7 A; 8 C; 13 G; 15 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
Pred. No.: 3.98e+04 Length: 43
Score: 45.00 Matches: 9
Percent Similarity: 76.92% Conservative: 1
Best Local Similarity: 69.23% Mismatches: 3
Query Match: 1.63% Indels: 0
DB: 2 Gaps: 0
US-08-864-955-2 (1-523) x AAX27070 (1-43)
QY 145 PheGluPheLeuGlyProValArgProValArgSerAArgGly 157
DB 39 TTGGAATGCAAAAACCAAGTCCAAAAGTCAGCCGGT 1
XX
XX RESULT 13
XX ABZ04528/C
XX ID ABZ04528 standard; DNA; 50 BP.
XX
XX ABZ04528;
XX AC
XX XX 09-JAN-2003 (first entry)
XX DT
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 4519.
XX XX T7; leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.

```

OS Homo sapiens.  
XX  
XX WO200257414-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 22-OCT-2001; 2001WO-US047856.  
XX  
XX 20-OCT-2000; 2000US-0241994P.  
XX  
XX 08-JUN-2001; 2001US-0296764P.  
XX  
XX (BIOC-) BIOCARDIA INC.  
XX  
XX Mollgumuch J, Fry K, Marcuk G, Altman P, Prentice J, Phillips J,  
PI Ly N, Woodward R, Quertermous T, Johnson F;  
XX WPI; 2002-636525/68.  
XX  
XX New system for leukocyte expression profiling, diagnosing a disease, or  
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
PT or congestive heart failure, comprises diagnostic oligonucleotides.  
XX  
XX Claim 1; Page 472; Opp; English.  
XX  
XX The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the gene corresponds to any of 8143 oligonucleotides  
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,  
CC predicting disease complications in an individual or monitoring response  
CC to treatment in an individual. The diseases include cardiac allograft  
CC rejection, kidney allograft rejection, liver allograft rejection,  
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
XX  
SQ Sequence 50 BP; 12 A; 14 C; 14 G; 10 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 4.87e+04 Length: 50  
Score: 45.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 77.78% Mismatches: 0  
Query Match: 1.63% Indels: 0  
DB: 6 Gaps: 0  
US-08-864-955-2 (1-523) x ABZ04528 (1-50)  
QY 233 ProSerCysMetAlaSerLeuTPThr 241  
DB 30 CCGAGCTGTGTGGCATCCCTGTGTCA 4  
RESULT 14  
AA178262/c  
ID AA178262 standard; DNA: 51 BP.  
XX  
XX AA178262;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:5203.  
XX  
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;  
XX protein therapy; vaccine; probe; diagnostic assay; detection;  
XX quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX

PF 30-NOV-2000; 2000WO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinketsu RA, Leach M;  
PI WPI; 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 2102; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 22 A; 12 C; 9 G; 8 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 5e+04 Length: 51  
Score: 45.00 Matches: 7  
Percent Similarity: 62.50% Conservative: 3  
Best Local Similarity: 43.75% Mismatches: 6  
Query Match: 1.63% Indels: 0  
DB: 4 Gaps: 0  
US-08-864-955-2 (1-523) x AA178262 (1-51)  
QY 235 CysMetAlaSerLeuTPThrAlaProLeuValMetArgThrIhrAsn 250  
DB 50 TGTGTGTTGCTTATGACACCTGCTGTGTCTGCACTGTTAAT 3  
RESULT 15  
AAA95764/c  
ID AAA95764 standard; DNA: 57 BP.  
XX  
XX AAA95764;  
XX  
XX 15-SEP-2003 (revised)  
XX  
XX 28-FEB-2001 (first entry)  
XX  
XX HIV envelope protein gp160 "Kennedy" peptide coding sequence.  
XX  
XX Recombinant gene; flagellin; fusion protein; immunogen; cholera toxin;  
XX antibody; Salmonella enterica subspecies enterica serovar muenchen; ss;  
XX vaccine; passive immunotherapy; contrareception; feed conversion; epitope;  
XX hormone imbalance; anticancer; anti-allergic; antiidiotypic antibody.  
XX  
XX Human immunodeficiency virus 1.  
XX  
XX US6130082-A.  
XX  
XX 10-OCT-2000.  
XX



KW mononucleotide microsatellite; gene therapy; diagnosis; tumour; human;  
 KM dinucleotide microsatellite; cytostatic; immunisation; ss.  
 OS Homo sapiens.  
 XX WO200204664-A2.  
 XX  
 XX 17-JAN-2002.  
 XX  
 XX 04-JUL-2001; 2001WO-DE002510.  
 XX  
 XX 07-JUL-2000; 2000DE-01032608.  
 XX  
 XX (DOEB/) KNEBEL DOEBERITZ M.  
 XX  
 XX Knebel Doebertz M, Bork P, Yuan YP, Gebert J, Woerner S;  
 PI Linnebacher M;  
 DR WPI; 2002-171723/22.  
 XX  
 XX Mutant genes isolated from tumors showing microsatellite instability,  
 PT useful for diagnosis, treatment and prevention of tumors, also related  
 PT peptides and antibodies.  
 PS  
 PS Claim 3; Fig 2; 31pp; German.  
 XX  
 XX This invention describes novel genes isolated from MSI+ (microsatellite  
 CC instability) tumour cells, containing coding mononucleotide or  
 CC dinucleotide microsatellites (CMNR and CDNR), differing by mutations in  
 CC CMNR or CDNR from the corresponding genes of non-MSI+ (tumour) cells, and  
 CC encoding 'neopeptide'-containing gene products. The products of the  
 CC invention have cytostatic activity, are capable of inducing a specific  
 CC immune response (humoral and cellular) and are useful for gene therapy.  
 CC The products of the invention are used for the molecular investigation  
 CC and diagnosis of MSI+ tumors (or their precursors) and are useful for  
 CC prophylactic or therapeutic immunisation against MSI+ tumors. This  
 CC sequence encodes the human FLT3LG wt CMNR region described in the  
 CC disclosure of the invention  
 XX  
 XX Sequence 49 BP; 3 A; 28 C; 6 G; 12 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 5.22e+04 Length: 49  
 Score: 44.50 Matches: 10  
 Percent Similarity: 58.82% Conservative: 0  
 Best Local Similarity: 58.82% Mismatches: 7  
 Query Match: 1.61% Indels: 1  
 DB: Gaps: 1  
 US-08-864-955-2 (1-523) x ABN75019 (1-49)  
 QY 5 ProSeProAlaProAkgArgLeuPheAlaCysSeProProProAla 21  
 DB 4 CCCTCCCTGCTGCC-----AGCCCCCCCCCAGCT 33  
 RESULT 18  
 AAL33848/c  
 ID AAL33848 standard; DNA; 50 BP.  
 AC AAL33848;  
 XX  
 XX 24-JAN-2002 (first entry)  
 XX  
 XX Human SNP oligonucleotide #7056.  
 DE  
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KM neuroprotective; antitubercial; gene therapy; vaccine; amylose; cancer;  
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KM multifactorial disease; autoimmune disease; infection;  
 KM nervous system disease; ss.

XX Homo sapiens.  
 OS  
 XX WO200147944-A2.  
 XX  
 XX 05-JUL-2001.  
 XX  
 XX 28-DEC-2000; 2000WO-US035498.  
 XX  
 XX 28-DEC-1999; 99US-0173419P.  
 XX  
 XX 27-DEC-2000; 2000US-00173419.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shinkets RA, Leach M;  
 PI  
 DR WPI; 2001-465210/50.  
 XX  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 PS  
 PS Claim 1; Page 3407; 4143pp; English.  
 XX  
 XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukin, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one  
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms  
 XX  
 XX Sequence 50 BP; 18 A; 12 C; 8 G; 12 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 5.9e+04 Length: 50  
 Score: 44.00 Matches: 11  
 Percent Similarity: 82.35% Conservative: 3  
 Best Local Similarity: 64.71% Mismatches: 3  
 Query Match: 1.59% Indels: 1  
 DB: Gaps: 0  
 US-08-864-955-2 (1-523) x AAL33848 (1-50)  
 QY 371 LysPheAlaAsnLeuIleLysGluPheValIleLeuAspCysArgTyrPro 387  
 DB 50 AAGTTCCAGGGCTCGATTGAGAGTTTA-GTCAATTATGTGCTATCCA 1  
 RESULT 19  
 AAL29098  
 ID AAL29098 standard; DNA; 50 BP.  
 AC AAL29098;  
 XX  
 XX 24-JAN-2002 (first entry)  
 XX  
 XX Human SNP oligonucleotide #2306.  
 DE  
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KM neuroprotective; antitubercial; gene therapy; vaccine; amylose; cancer;  
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;

KM	multifactorial disease; autoimmune disease; infection;
KM	nervous system disease; ss.
OS	Homo sapiens.
PN	W0200147944-A2.
PD	05-JUL-2001.
XX	
PF	28-DEC-2000; 2000MO-US035498.
XX	
PR	28-DEC-1999; 99US-0173419P.
PR	27-DEC-2000; 2000US-00173419.
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX	autoimmune diseases and infections.
PS	Claim 1; Page 2042; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC	protein coupled receptors and thioesterases. The present sequence is one
CC	such oligonucleotide. The oligonucleotides and the peptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of the proteins listed above.
CC	Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukemia), diseases of the nervous system and an infection of pathogenic
CC	organisms
XX	
SO	Sequence 50 BP; 8 A; 26 C; 11 G; 5 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	5.9e+04 Length: 50
Score:	44.00 Matches: 7
Percent Similarity:	100.00% Conservative: 2
Best Local Similarity:	77.78% Mismatches: 0
Query Match:	1.59% Indels: 0
DB:	4 Gaps: 0
US-08-864-955-2 (1-523) x AAL29098 (1-50)	
Oy	3 LenglyProSePrAlaPArGArg 11
DB	4 ATGCGCCATCAGACGAGCCCGGCGC 30
RESULT 20	
ABZ07506	
ID	ABZ07506 standard; DNA; 50 BP.
XX	
AC	ABZ07506;
XX	
DT	09-JAN-2003 (first entry)
XX	
DE	Human leukocyte gene expression profiling probe SEQ ID NO 7497.
XX	
KM	T7: leukocyte: gene expression profiling; allograft rejection;
KM	atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KM	rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
ss.	

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XX OS Homo sapiens.
XX PN W0200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PR 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.
XX PA Mohnigsmuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J,
XX PI Loh N, Woodward R, Quertermous T, Johnson F,
XX PI WPI; 2002-636525/68.
XX DR
XX PT New system for leukocyte expression profiling, diagnosing a disease, or
XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX PS
XX PS Claim 1; Page 569; Opp: English.
XX CC The invention relates to a system for detecting gene expression, which
XX CC comprises one or two isolated DNA molecules that detect expression of a
XX CC gene, where the gene corresponds to any of 8143 oligonucleotides
XX CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX CC for leukocyte expression profiling. It is particularly useful for
XX CC diagnosing a disease, monitoring (rate of) progression of a disease,
XX CC predicting therapeutic outcome, determining prognosis for a patient,
XX CC predicting disease complications in an individual or monitoring response
XX CC to treatment in an individual. The diseases include cardiac allograft
XX CC rejection, kidney allograft rejection, liver allograft rejection,
XX CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX SQ Sequence 50 BP; 7 A; 21 C; 4 G; 18 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.9e+04 Length: 50
XX Score: 44.00 Matches: 7
XX Percent Similarity: 69.23% Conservative: 2
XX Best Local Similarity: 53.85% Mismatches: 4
XX Query Match: 1.59% Indels: 0
XX Gaps: 0
XX
XX US-08-864-955-2 (1-523) x ABZ07506 (1-50)
XX
XX Cy 8 A1AProArggLeuLeuPheAlaCysSerProProPro 20
XX ||||| ||||| ||||| ||||| |||||
XX Db 10 GCCCCTAACAGAAATGTTCTCTCTCTCTCCACACCCT 48
XX
XX RESULT 21
XX ABZ07133 ID *ABZ07133 standard; DNA; 50 BP.
XX
XX AC ABZ07133;
XX
XX DT 09-JAN-2003 (first entry)
XX
XX Human leukocyte gene expression profiling probe SEQ ID NO 7124.
XX
XX KW T7: leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
XX OS Homo sapiens.
XX PN W0200257414-A2.
XX

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PI Ly N, Woodward R, Quartermous T, Johnson F;  
 XX WPI; 2002-635525/68.  
 XX  
 PT New system for leukocyte expression profiling, diagnosing a disease, or  
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX  
 PS Claim 1; Page 546; Opp; English.  
 XX  
 CC The invention relates to a system for detecting gene expression, which  
 CC comprises one or two isolated DNA molecules that detect expression of a  
 CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,  
 CC predicting disease complications in an individual or monitoring response  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 CC  
 SQ Sequence 50 BP; 18 A; 4 C; 21 G; 7 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 5.9e+04 Length: 50  
 Score: 44.00 Matches: 7  
 Percent Similarity: 69.23% Conservative: 2  
 Best Local Similarity: 53.85% Mismatches: 4  
 Query Match: 1.59% Indels: 0  
 Gaps: 0  
 DB: 6  
 US-08-864-955-2 (1-523) x ABZ06743 (1-50)  
 OY 8 AAlaProArgArgLeuLeuPheAlaCySerProProPro 20  
 Db 41 GCCCCTAACAGAGTCTCTCTCTGCTCCACACCCCT 3  
 RESULT 24  
 ID AAl29072 standard; DNA; 51 BP.  
 XX  
 AC AAl29072;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #2280.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX

DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Claim 1; Page 2035; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC protein, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one  
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Graves' disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms  
 XX  
 SQ Sequence 51 BP; 5 A; 28 C; 7 G; 11 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 6.06e+04 Length: 51  
 Score: 44.00 Matches: 10  
 Percent Similarity: 52.17% Conservative: 2  
 Best Local Similarity: 43.48% Mismatches: 3  
 Query Match: 1.59% Indels: 8  
 Gaps: 1  
 DB: 4  
 US-08-864-955-2 (1-523) x AAl29072 (1-51)  
 OY 3 LeuGlyProSerProAlaProArgArgLeuLeuPheAlaCySerProProProAlaSer 22  
 Db 3 CTGGAGCCACATCCGACTCC-----CCCTCCCGGCATCA 38  
 RESULT 25  
 ID AAl77671 standard; DNA; 51 BP.  
 XX  
 AC AAl77671;  
 XX  
 DT 09-NOV-2001 (first entry)  
 XX  
 DE Human silent SNP containing nucleic acid SEQ:4612.  
 XX  
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
 KW protein therapy; vaccine; probe; diagnostic assay; detection;  
 KW quantitation; restorative therapy; polymorphic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140521-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 30-NOV-2000; 2000WO-US032758.  
 XX  
 PR 30-NOV-1999; 99US-0168138P.  
 PR 29-NOV-2000; 2000US-00726173.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX

```

XX  WPI; 2001-356160/37.
XX  Polymorphic nucleic acid sequences, useful in genetic testing and
PT  therapy.
XX
XX  Claim 1; Page 1922; 2653bp; English.
XX
CC  AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC  sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC  AA53114 to AA53339 represent peptide sequences related to human polymorphic
CC  polynucleotide sequences. The sequences can be used in gene and protein
CC  therapy, and in vaccine production. (I) and the polypeptides encoded by
CC  them may be used in the prevention, diagnosis and treatment of diseases
CC  associated with inappropriate expression of polymorphic polypeptides. For
CC  example, (I) may be used to treat disorders by rectifying mutations or
CC  deletions in a patient's genome that affect the activity of polypeptides
CC  by expressing inactive proteins or to supplement the patient's own
CC  production of polypeptide. Additionally, (I) and its complementary
CC  sequences may also be used as DNA probes in diagnostic assays to detect
CC  and quantitate the presence of similar nucleic acids in samples, and
CC  therefore which patients may be in need of restorative therapy. The
CC  polypeptides encoded by (I) may be used as antigens in the production of
CC  antibodies specific for polymorphic polypeptides. The antibodies may also
CC  be used to down regulate expression and activity. The antibodies may also
CC  be used as diagnostic agents for detecting the presence of polymorphic
CC  polypeptides in samples
XX
SQ  Sequence 51 BP; 11 A; 16 C; 11 G; 13 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6 06e+04 Length: 51
Score: 44.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 1.59% Indels: 0
DB: Gaps: 0
US-08-864-955-2 (1-523) x AA17671 (1-51)
QY 7 ProAlaProAlaGArgLeuPheAlaCysSerPro 18
Db 6 CCACGTCGACAGAGATGGTGTACCTTGCACGCCT 41
RESULT 26
ACD94372 standard; cDNA; 52 BP.
XX
AC ACD94372;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #2784.
XX
KW Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.

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PA (BREN/) BRENTANI R. R.
XX
XX Simpson ATG, Neto ED, Brentani RR;
XX
XX WPI; 2003-182626/18.
XX
XX Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
XX Example 9; Page 415; 959pp; English.
XX
XX The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency; preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I); amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer. The method can also be used in the study of
CC tolerance, and so forth. To determine antibiotic resistance or non-
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 52 BP; 16 A; 15 C; 13 G; 8 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.22e+04 Length: 52
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 1.59% Indels: 0
DB: Gaps: 0
US-08-864-955-2 (1-523) x ACD94372 (1-52)
QY 278 SerGingIugIuserProPGIserThrIysArg 289
Db 14 TCTAAGTCAGAAATCCCGCCGACGAGACCACTAAGCA 49
RESULT 27
ADA88986 standard; DNA; 59 BP.
XX
AC ADA88986;
XX
DT 20-NOV-2003 (first entry)
XX
XX S. coelicolor cosmid SC3B6 gene disruption PCR primer.
XX

```

KW targeted nucleic acid disruption; actinomycete; Streptomyces coelicolor;  
 KW Streptomyces ambodaciensis; screening; phenotype; characteristic;  
 KW gene disruption; FLP recognition target; FRT; PCR primer; ss.  
 XX Synthetic.  
 OS Streptomyces coelicolor.  
 XX MO2002103010-A1.  
 XX 27-DEC-2002.  
 XX 14-JUN-2002; 2002WO-GB002798.  
 XX 14-JUN-2001; 2001GB-00014535.  
 XX 09-JAN-2002; 2002GB-00000477.  
 XX (PLAN-) PLANT BIOSCIENCE LTD.  
 XX Gust B, Chater KF, Kieser TE;  
 XX WPI; 2003-167518/16.  
 DR WPI; 2003-167518/16.  
 XX Generating a targeted nucleic acid disruption in an actinomycete,  
 PT comprises integrating nucleic acid of the first nucleic acid construct  
 PT from a transferred plasmid into a target actinomycete nucleic acid by  
 PT homologous recombination.  
 XX  
 PS Disclosure; Page 53; 105pp; English.  
 XX  
 CC The present invention describes a method for generating a targeted  
 CC nucleic acid disruption in an actinomycete, comprising providing a  
 CC nucleic acid construct, recombining the construct with a plasmid bearing  
 CC at least part of the actinomycete target nucleic acid of interest to form  
 CC a recombinant plasmid, and integrating nucleic acid of the construct from  
 CC the transferred plasmid into the target actinomycete nucleic acid by  
 CC homologous recombination. Also described: (1) producing a library of  
 CC actinomycete host cells having respective different gene disruption  
 CC disruptions repeating the method described above to generate different gene  
 CC actinomycete host cells having different respective gene disruptions  
 CC produced by the method of (1); (3) screening the library of (2) for  
 CC phenotypic characteristics or changes resulting from the gene disruptions  
 CC; (4) a first nucleic acid construct as described above, with the  
 CC optional exception of lacking targeting sequences; (5) a helper nucleic  
 CC acid construct; (6) an additional disruption construct; (7) a helper  
 CC plasmid; (8) a vector comprising the nucleic acid construct of (4), (5)  
 CC or (6), flanked by restriction sites for excising the nucleic acid  
 CC construct from the remainder of the vector; (9) a cell comprising the  
 CC vector of (8) or plasmid of (7); and (10) a kit comprising the first  
 CC nucleic acid construct and the helper nucleic acid construct, or the  
 CC additional disruption construct. The method is useful for generating a  
 CC targeted nucleic acid disruption in an actinomycete, e.g. Streptomyces  
 CC coelicolor or S. ambodaciensis. The method is also useful for screening a  
 CC library of actinomycete host cells for phenotypic characteristics or  
 CC changes resulting from the gene disruptions. The present sequence  
 CC represents a PCR primer which is used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 59 BP; 16 A; 20 C; 18 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.34e+04 Length: 59  
 Score: 44.00 Matches: 8  
 Percent Similarity: 76.92% Conservative: 2  
 Best Local Similarity: 61.54% Mismatches: 3  
 Query Match: 1.59% Indels: 0  
 DB: 7 Gaps: 0  
 US-08-864-955-2 (1-523) x ADA8686 (1-59)  
 OY 272 Leu1y5a1gProG1uaY5eRg1ngJ1uG1u5eRProPro 284  
 DB 1 GTCAAGCGCGCGGAAACGACGAGCGAGGAAACACCACC 39

RESULT 28  
 AEN35109  
 ID AEN35109 standard; DNA; 60 BP.  
 XX AEN35109;  
 AC AEN35109;  
 XX  
 DT 15-JUL-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:7857.  
 DE Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 OS Homo sapiens.  
 OS MO200210449-A2.  
 PN 07-FEB-2002.  
 PD  
 PF 20-JUL-2001; 2001WO-IB001903.  
 XX 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX (COMP-) COMPUGEN INC.  
 PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 DR  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 XX Example 1; SEQ ID NO 7857; 47pp; English.  
 PS  
 XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC oligonucleotide units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. AEN27233 to AEN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences  
 XX  
 SQ Sequence 60 BP; 17 A; 19 C; 10 G; 14 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 9  
 Percent Similarity: 68.75% Conservative: 2  
 Best Local Similarity: 56.25% Mismatches: 5  
 Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0  
 US-08-864-955-2 (1-523) x AEN35109 (1-60)

Query 248 ThrThrasnleuAspAsnaGcYsLysLeuPheAspSerProserneu 263  
 DB: 6 ACCGCGCTCCAGAGCAACAGCCAGCTTTTGACTCCACACTCTT 53  
 RESULT 29  
 ID ABN37833/c  
 AC ABN37833 standard; DNA; 60 BP.  
 XX  
 AC ABN37833;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:10581.  
 XX  
 DE Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1B001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PT Example 1; SEQ ID NO 10581; 47bp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition, to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 60 BP; 20 A; 12 C; 18 G; 10 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 8  
 Percent Similarity: 62.50% Conservativity: 2  
 Best Local Similarity: 50.00% Mismatches: 6

Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0  
 US-08-864-955-2 (1-523) x ABN37833 (1-60)  
 Query 4 GlyProSerProAlaProArgArgLeuPheAlaCysSerProPro 19  
 DB: 57 GGCTCATCCACATCTCCGTCAGCAGTTTCACATTGTTCACCTCT 10  
 RESULT 30  
 ID ABN42974/c  
 AC ABN42974 standard; DNA; 60 BP.  
 XX  
 AC ABN42974;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:15722.  
 XX  
 DE Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1B001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PT Example 1; SEQ ID NO 15722; 47bp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition, to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 60 BP; 14 A; 12 C; 18 G; 16 T; 0 U; 0 Other;  
 Alignment Scores:

Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 7  
 Percent Similarity: 71.43% Conservative: 3  
 Best Local Similarity: 50.00% Mismatches: 4  
 Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x ABN42974 (1-60)

OY 445 ArgGluArgAspArgLeuGlyAsnGluTyProIysLeuHis 458  
 DB 45 AGACAGCACCGAATGCTGGTCTTCGATCCGAAGATCCAC 4

RESULT 31  
 ID ABN59321/c  
 ID ABN59321 standard; DNA; 60 BP.

AC ABN59321;  
 DT 15-JUL-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:32069.  
 XX  
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 XX splice variant; transcriptome; oligonucleotide library; ss.  
 OS Homo sapiens.  
 XX MO200210449-A2.  
 PN 07-FEB-2002.  
 PD 20-JUL-2001; 2001WO-1B001903.  
 PF 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX (COMP-) COMPUGEN INC.  
 PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 DR New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX Example 1; SEQ ID NO 32069; 47bp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences

XX Sequence 60 BP; 15 A; 16 C; 11 G; 18 T; 0 U; 0 Other;  
 SQ Alignment Scores:  
 Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 9  
 Percent Similarity: 55.56% Conservative: 1  
 Best Local Similarity: 50.00% Mismatches: 8  
 Query Match: 1.59% Indels: 0  
 DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x ABN59321 (1-60)

OY 74 GlySerSerGlySerThrAspSerGlyPheCysLeuAspSerProGlyProLeu 91  
 DB 60 GGTTCCAGGAGGACCGCAAAATCTCATTTTGTAGAGGCTTTGAGACCACTA 7

RESULT 32  
 ID ABN42357/c  
 ID ABN42357 standard; DNA; 60 BP.

AC ABN42357;  
 DT 15-JUL-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:15105.  
 XX  
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 XX splice variant; transcriptome; oligonucleotide library; ss.  
 OS Homo sapiens.  
 XX MO200210449-A2.  
 PN 07-FEB-2002.  
 PD 20-JUL-2001; 2001WO-1B001903.  
 PF 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX (COMP-) COMPUGEN INC.  
 PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 DR New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX Example 1; SEQ ID NO 15105; 47bp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from

CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences

XX Sequence 60 BP; 13 A; 23 C; 11 G; 13 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score:	7.5e+04	60	9
Percent Similarity:	44.00		
Best Local Similarity:	71.43%		
Query Match:	64.29%	Mismatches:	4
	1.59%	Indels:	0
DB:	6	Gaps:	0

US-08-864-955-2 (1-523) x ABN42357 (1-60)

QY 155 SetargGlyCysLeuHisSerHisGlyLeuGlnGlyLys 168  
 DB 46 TCAAGGGGATGTGGAAACACCAAGGTGTGTGAGGGGAG 5

# RESULT 33

ID ABN58779/c  
 ID ABN58779 standard; DNA; 60 BP.

XX ABN58779;  
 AC  
 XX  
 DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:31527.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS WO200210449-A2.

PN 07-FEB-2002.

PD 20-JUL-2001; 2001WO-1B001903.

PP 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

PI WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.

XX Example 1; SEQ ID NO 31527; 47bp; English.

XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in

CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN5589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences

XX Sequence 60 BP; 15 A; 16 C; 11 G; 18 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score:	7.5e+04	60	9
Percent Similarity:	44.00		
Best Local Similarity:	55.56%		
Query Match:	50.00%	Mismatches:	8
	1.59%	Indels:	0
DB:	6	Gaps:	0

US-08-864-955-2 (1-523) x ABN58779 (1-60)

QY 74 GlySerSerGluSerThrAspSerGlyPheCysLeuAspSerProGlyProLeu 91  
 DB 60 GGTTCAGAGAGAGAGGACCAAAACTCATTTGTAGAGGCTTGGAGACCACTA 7

# RESULT 34

ID ABN58502/c  
 ID ABN58502 standard; DNA; 60 BP.

XX ABN58502;  
 AC  
 XX  
 DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:31250.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS WO200210449-A2.

PN 07-FEB-2002.

PD 20-JUL-2001; 2001WO-1B001903.

PP 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

PI WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.

XX Example 1; SEQ ID NO 31250; 47bp; English.

XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal

transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

US-08-864-955-2 (1-523) x ABN58502 (1-60)

Alignment Scores:

Pred. No.:	7.5e+04	Length:	60
Score:	44.00	Matches:	9
Percent Similarity:	55.56%	Conservative:	1
Best Local Similarity:	50.00%	Mismatches:	8
Query Match:	1.59%	Indels:	0
DB:	6	Gaps:	0

QY 74 GlySerSerGluSerThrAspSerGlyPheCysLeuaspSerProGlyProLeu 91  
DB 60 GGTCACAGAGAGAGCCAAAACCTCATTTGTAGAGGGCTTGAGGACCACTA 7

RESULT 35  
ID ABN35318/c  
ABN35318 standard; DNA; 60 BP.

AC ABN35318;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8066.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
XX 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.  
XX  
PT Example 1; SEQ ID NO 8066; 47bp; English.  
XX  
PS The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple CC transcription units that populate a genome. The library comprises several CC oligonucleotides, each capable of hybridising selectively to a set of CC messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The

oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

US-08-864-955-2 (1-523) x ABN35318 (1-60)

Alignment Scores:

Pred. No.:	7.5e+04	Length:	60
Score:	44.00	Matches:	9
Percent Similarity:	71.43%	Conservative:	1
Best Local Similarity:	64.29%	Mismatches:	4
Query Match:	1.59%	Indels:	0
DB:	6	Gaps:	0

QY 188 ArgAspSerSerGluProGlyAsnPhel1eProLeuPheThr 201  
DB 56 AGGAGACGCTCCGTTCCGAGACACTTCACTCCACCTCAGACC 15

RESULT 36  
ID ABN38507/c  
ABN38507 standard; DNA; 60 BP.

AC ABN38507;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:11255.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
XX 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.  
XX  
PT Example 1; SEQ ID NO 11255; 47bp; English.  
XX  
PS The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting RNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcripts. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 60 BP; 12 A; 18 C; 16 G; 14 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 9  
 Percent Similarity: 64.71% Conservative: 2  
 Best Local Similarity: 52.94% Mismatches: 6  
 Query Match: 1.59% Indels: 0  
 Gaps: 0

US-08-864-955-2 (1-523) x ABN38507 (1-60)  
 Qy 201 ThProGInSerProValThrAlaThrLeuSerAspGlnuSpaSpGlyPhe 217  
 Db 60 ACCCGCGATCCACAGTCACTGTAAGATCCAGTAGGAGGAGATGGCTTT 10

RESULT 37  
 ABN59505/c  
 ID ABN59505 standard; DNA; 60 BP.

AC ABN59505;  
 XX  
 DT 15-JUN-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:32253.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-IB001903.  
 XX  
 PR 28-JUN-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX

PA (COMP-) COMPUGEN INC.  
 XX  
 P1 Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S,  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 32253; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting RNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcripts. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 60 BP; 15 A; 16 C; 11 G; 18 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.5e+04 Length: 60  
 Score: 44.00 Matches: 9  
 Percent Similarity: 55.56% Conservative: 1  
 Best Local Similarity: 50.00% Mismatches: 8  
 Query Match: 1.59% Indels: 0  
 Gaps: 0

US-08-864-955-2 (1-523) x ABN59505 (1-60)  
 Qy 74 GlySerSerGluSerThrAspSerGlyPheCysLeuAspSerProGlyProLeu 91  
 Db 60 GATTCCAGAGGAGGAGCCAAACTCATTTGTGTAGAGGCTTGGAGGACCACTA 7

RESULT 38  
 AAD61489  
 ID AAD61489 standard; DNA; 39 BP.

AC AAD61489;  
 XX  
 DT 15-JAN-2004 (first entry)  
 DE Human MMP-29 mutant cDNA amplifying PCR primer #3.  
 XX  
 KW Human; metalloproteinase; MMP-29; immune disorder; reproductive disorder;  
 KW testicular disorder; gastrointestinal disorder; cardiovascular disorder;  
 KW ovarian disorder; hepatic disorder; pulmonary disorder; renal disorder;  
 KW metabolic disorder; neural disorder; inflammatory disease; sclerosis;  
 KW skeletal muscle disorder; amyotrophic lateral sclerosis; gene therapy;  
 KW immunomodulatory; antifertility; cytostatic; hepatotropic; pulmonary;  
 KW nephrotropic; cardiac; vascular; neuroprotective; nootropic; muscular;  
 KW PCR; primer; ss.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US2003109021-A1.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 26-APR-2002; 2002US-00133797.  
 XX  
 PR 26-APR-2001; 2001US-0286764P.  
 XX  
 PA (WUSS/) WU S.  
 PA (CHEN/) CHEN J.

PA (FEDE/) FEDER J N.  
PA (LEE/) LEE L.  
PA (KRYS/) KRYSKY S R.  
PI Mu S, Chen J, Feder JN, Lee L, Krystek SR;  
XX WPI: 2003-801269/75.  
XX  
XX  
XX New nucleic acid encoding a metalloprotease (MMP-29) useful for  
PT diagnosing a pathological condition or a susceptibility to a medical  
PT condition in a subject.  
XX  
XX  
XX Example 17; Page 115; 0pp; English.  
XX  
XX The present invention relates to novel metalloprotease (MMP-29) proteins  
CC and polynucleotides encoding such proteins. Sequences of the invention  
CC are used to diagnose a pathological condition or a susceptibility to a  
CC medical condition in a subject. They are useful for preventing, treating,  
CC or ameliorating medical conditions such as immune condition or disorders,  
CC reproductive conditions, female reproductive disorders, male reproductive  
CC disorders, ovarian disorders, testicular disorders, gastrointestinal  
CC disorders, cancer, hepatic disorders, pulmonary disorders, metabolic  
CC disorders, renal disorders, cardiovascular disorders, neural disorders,  
CC skeletal muscle disorders, inflammatory diseases, inflammatory diseases  
CC where proteases are either directly or indirectly involved in disease  
CC progression, sclerosis, amyotrophic lateral sclerosis, juvenile form of  
CC amyotrophic lateral sclerosis or a disorder associated with aberrations  
CC of chromosome 2q32. MMP-29 sequences are also useful in gene therapy. The  
CC present sequence is human MMP-29 mutant cDNA amplifying PCR primer. This  
CC sequence is used in the exemplification of the invention  
XX  
SQ Sequence 39 BP; 4 A; 18 C; 10 G; 7 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 5.11e+04 Length: 39  
XX Score: 43.00 Matches: 7  
XX Percent Similarity: 100.00% Conservative: 1  
XX Best Local Similarity: 87.50% Mismatches: 0  
XX Query Match: 1.55% Indels: 0  
XX DB: Gaps: 0  
XX  
XX US-08-864-955-2 (1-523) x AAD61489 (1-39)  
XX  
QY 15 AlaCySerProProAlaSer 22  
XX |||||  
DB 13 GCATGCTCGCGCTCATCTTCC 36  
XX  
XX RESULT 39  
XX AAL33854/c  
XX ID AAL33854 standard; DNA; 50 BP.  
XX  
XX AAL33854;  
XX  
XX 24-JAN-2002 (first entry)  
XX  
XX Human SNP oligonucleotide #7062.  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN WO200147944-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 28-DEC-2000; 2000WO-US035498.  
XX  
XX PF

XX  
XX 28-DEC-1999; 99US-0173419P.  
XX PR 27-DEC-2000; 2000US-00173419.  
XX  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach W;  
XX  
XX WPI: 2001-465210/50.  
XX  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
XX  
XX Claim 1; Page 3408; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
XX  
SQ Sequence 50 BP; 4 A; 17 C; 14 G; 15 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 7.11e+04 Length: 50  
XX Score: 43.00 Matches: 7  
XX Percent Similarity: 60.00% Conservative: 2  
XX Best Local Similarity: 46.67% Mismatches: 6  
XX Query Match: 1.55% Indels: 0  
XX DB: Gaps: 0  
XX  
XX US-08-864-955-2 (1-523) x AAL33854 (1-50)  
XX  
QY 113 GlyCySerProAlaLeuYsArgSerHisSerAspSerLeuAsp 127  
XX |||||  
DB 45 GGATGTAGCCACGTAGAGCCAAAGGCCACGAGAAACTGGAC 1  
XX  
XX RESULT 40  
XX AAA60434  
XX ID AAA60434 standard; DNA; 54 BP.  
XX  
XX AAA60434;  
XX  
XX 09-OCT-2000 (first entry)  
XX  
XX Plasmid pGFPuv construction PCR primer SEQ ID NO:5.  
XX  
XX Sensor protein, utilisation; binding protein; reporter protein;  
XX fusion protein; detection; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX OS  
XX PN WO200027872-A1.  
XX  
XX 18-MAY-2000.  
XX  
XX 10-NOV-1999; 99WO-JP006261.  
XX  
XX 11-NOV-1998; 98JP-00320102.  
XX  
XX (MITU ) MITSUBISHI CHEM CORP.  
XX  
XX PA

XX Yanagawa H, Doi N, Nemoto N;  
XX WPI; 2000-376488/32.  
XX  
XX New sensor protein having a binding sequence inserted into a reporter  
XX protein for detection and assay of protein/protein interactions.  
XX  
XX Example 1; Page 39; 45pp; Japanese.  
XX  
CC The present invention describes a sensor protein comprising a binding  
CC protein sequence inserted within the sequence of a reporter protein. Also  
CC described are: (1) polynucleotides encoding the sensor protein; (2)  
CC expression vectors containing the polynucleotides; (3) host cells  
CC transformed by the vectors; (4) the preparation of the sensor protein by  
CC culture of the transformants; (5) the detection and assay of a target  
CC protein, either independently or contained in live cells, tissues or a  
CC living body, by contact with the sensor protein; and (6) kits for this  
CC detection and assay. The sensor protein can be used for the detection and  
CC assay of in vivo secretory disturbances, imaging of intracellular  
CC activity, and examination of antigen/antibody reactions. The binding  
CC takes place without structural change in the sensor protein. The present  
CC sequence represents a PCR primer which is used in an example from the  
CC present invention  
XX  
SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.88e+04 Length: 54  
Score: 43.00 Matches: 6  
Percent Similarity: 83.33% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 1.55% Indels: 0  
DB: 3 Gaps: 0  
US-08-864-955-2 (1-523) x AAA60434 (1-54)  
QY 160 HisSerHisGlyLeuGlnGluGlyAspLeuPhe 171  
Db 19 CATCATCATGCTATGAGTAAAGGAGGAGAACTTTTC 54  
RESULT 41  
ABN40897/C  
ID ABN40897 standard; DNA; 60 BP.  
AC ABN40897;  
XX  
XX 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13645.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200210449-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 20-JUL-2001; 2001WO-IB001903.  
XX  
XX 28-JUL-2000; 2000US-0221607P.  
XX  
XX 02-MAY-2001; 2001US-0287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
XX WPI; 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
XX selectively hybridize to mRNAs transcribed from a transcription unit of a  
XX

PT genome; useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX Example 1; SEQ ID NO 13645; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialized mini-  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN7253 to ABN9589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 15 A; 19 C; 19 G; 7 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9.08e+04 Length: 60  
Score: 43.00 Matches: 8  
Percent Similarity: 64.71% Conservative: 3  
Best Local Similarity: 47.06% Mismatches: 6  
Query Match: 1.55% Indels: 0  
DB: 6 Gaps: 0  
US-08-864-955-2 (1-523) x ABN40897 (1-60)  
QY 19 PropGAlaSerGlnProValIValIyAlaLeuPheGlyAlaSerAlaAla 35  
Db 56 CCACCATCTGGGACGCTGAGCTGTCTGTACTGCTGTCTGTCTGTCTGCA 6  
RESULT 42  
ABN59521/C  
ID ABN59521 standard; DNA; 60 BP.  
AC ABN59521;  
XX  
XX 15-JUL-2002 (first entry)  
XX  
XX Human spliced transcript detection oligonucleotide SEQ ID NO:32269.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200210449-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 20-JUL-2001; 2001WO-IB001903.  
XX  
XX 28-JUL-2000; 2000US-0221607P.  
XX  
XX 02-MAY-2001; 2001US-0287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
XX

DR WPI: 2002-257383/30.  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 32269; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 60 BP; 14 A; 8 C; 26 G; 12 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.08e+04 Length: 60  
 Score: 43.00 Matches: 10  
 Percent Similarity: 61.90% Conservative: 3  
 Best Local Similarity: 47.62% Mismatches: 6  
 Query Match: 1.55% Indels: 2  
 DB: Gaps: 1  
 US-08-864-955-2 (1-523) x ABN59521 (1-60)  
 QY 3 LeuGlyProSerProAlaProArgLeuPheAlaCysSerProProAlaSer 22  
 Db 57 CTGGGACCTGCGCCCTTGTCC-----CTCACTACACAGCTGCTGTAAACACCCCTTCA 4  
 QY 23 Gln 23  
 Db 3 AAA 1  
 RESULT 43  
 ABN40259/c  
 ID ABN40259 standard; DNA; 60 BP.  
 AC ABN40259;  
 XX 15-JUL-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:13007.  
 XX  
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200210449-A2.  
 PN  
 XX 07-FEB-2002.  
 XX  
 XX 20-JUL-2001; 2001WO-IB001903.  
 PF

XX  
 FR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI: 2002-257383/30.  
 XX  
 CC New oligonucleotide libraries comprising oligonucleotides which  
 CC selectively hybridize to mRNAs transcribed from a transcription unit of a  
 CC genome, useful for detecting tissue-, pathology-, and developmental-  
 CC specific genes.  
 PT  
 PS Example 1; SEQ ID NO 13007; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 60 BP; 14 A; 8 C; 23 G; 15 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.08e+04 Length: 60  
 Score: 43.00 Matches: 7  
 Percent Similarity: 57.89% Conservative: 4  
 Best Local Similarity: 36.84% Mismatches: 8  
 Query Match: 1.55% Indels: 0  
 DB: Gaps: 0  
 US-08-864-955-2 (1-523) x ABN40259 (1-60)  
 QY 473 PHeMetIysCysGlnSerTyrcysGlnProProSerTyrcysGlnProMetHisGln 491  
 Db 58 TTTCGACGTCGTGAGCCATGTCATGCAATGCACGACGCTCTTCTTACACCATGAA 2  
 RESULT 44  
 ABN46250/c  
 ID ABN46250 standard; DNA; 60 BP.  
 AC ABN46250;  
 XX 15-JUL-2002 (first entry)  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:18998.  
 XX  
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200210449-A2.  
 PN

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XX 07-FEB-2002.
PD 20-JUL-2001; 2001WO-IB001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of a
XX genome, useful for detecting tissue-, pathology-, and developmental-
XX specific genes.
XX
XX Example 1; SEQ ID NO 18998; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialized mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition, to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ
Sequence 60 BP; 22 A; 13 C; 15 G; 10 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.08e+04 Length: 60
Score: 43.00 Matches: 6
Percent Similarity: 69.23% Conservative: 3
Best Local Similarity: 46.15% Mismatches: 4
Query Match: 1.55% Indels: 0
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x ABN46250 (1-60)
Qy 479 TyTCySGlupProPseRtyrArgPromeThiSisglu 491
Db 42 TTCTGTGAACACCTTCTTCTGTGAGCAGTCCACCA 4

RESULT 45
ABN35538/C
ID ABN35538 standard; DNA; 60 BP.
XX
XX ABN35538;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:8286.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.

```

```

XX OS Homo sapiens.
XX
XX PN WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of a
XX genome, useful for detecting tissue-, pathology-, and developmental-
XX specific genes.
XX
XX Example 1; SEQ ID NO 8286; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition, to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ
Sequence 60 BP; 15 A; 13 C; 16 G; 16 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.08e+04 Length: 60
Score: 43.00 Matches: 7
Percent Similarity: 69.23% Conservative: 2
Best Local Similarity: 53.85% Mismatches: 4
Query Match: 1.55% Indels: 0
DB: 6 Gaps: 0

US-08-864-955-2 (1-523) x ABN35538 (1-60)
Qy 343 GlyTyTLeuphneHsThValAlaGlylyneHsGlnaP 355
Db 53 GGCACATCTCTTACACACGTAGTGTAGTACATCTACTGAC 15

Search completed: September 9, 2004, 20:56:56
Job time : 437 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2004, 20:43:40 : Search time 519 Seconds

(without alignments)  
5070.301 Million cell updates/sec

Title: US-08-864-955-2

Perfect score: 2769

Sequence: 1 MEIGSPAPRRLLFACSPPP.....SRTWAGEKSKREMYSLTKXL 523

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Xgapop 10.0 , Xgapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delcp 6.0 , Delcxt 7.0

Searched: 3304383 segs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1905950

Minimum DB seq length: 10

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPFO.spool/US08864555/rnat.07092004.144931.24534/app.query.fasta\_1.711  
-DB=Published.Applications\_NA\_QFNT=fastap -SUFFIX=rmpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500  
-MINLEN=60  
-USR=US08864555 @cgn2\_1.1 354 @rnat.07092004.144931.24534 -NCPU=6 -ICPU=3  
-NO\_MMP -IARGGOUTRY -NEG\_SCORES=0 -WAIT -DSPELLOCK=100 -LONGIOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	95	3.4	60	10	US-09-908-975-12902	Sequence 12902, A
2	73	2.6	60	10	US-09-908-975-12941	Sequence 12941, A
3	49	1.8	60	10	US-09-908-975-12965	Sequence 12965, A
4	48	1.7	50	13	US-10-426-058-116	Sequence 116, App
5	48	1.7	50	15	US-10-280-117-116	Sequence 116, App
6	48	1.7	60	10	US-09-908-975-1473	Sequence 5473, App
7	47.5	1.7	56	16	US-10-300-683-170	Sequence 170, App
8	47.5	1.7	56	16	US-10-300-683-181	Sequence 381, App
9	47.5	1.7	56	16	US-10-300-683-187	Sequence 347, App
10	47	1.7	54	10	US-09-900-345A-150	Sequence 150, App
11	47	1.7	54	10	US-09-900-345A-151	Sequence 151, App
12	47	1.7	54	15	US-10-305-765-184	Sequence 184, App
13	47	1.7	54	15	US-10-305-765-185	Sequence 185, App
14	47	1.7	54	15	US-10-305-633-185	Sequence 185, App
15	47	1.7	54	15	US-10-305-633-184	Sequence 184, App
16	46	1.7	60	10	US-09-908-975-31510	Sequence 31510, A
17	45.5	1.6	60	9	US-09-851-501-41	Sequence 41, Appl
18	45.5	1.6	60	15	US-10-142-722-41	Sequence 41, Appl
19	45.5	1.6	60	16	US-10-300-683-41	Sequence 419, App
20	45	1.6	50	16	US-10-131-827-4519	Sequence 11, Appl
21	45	1.6	58	9	US-09-760-364-11	Sequence 6734, App
22	44	1.6	50	16	US-10-131-827-5734	Sequence 7124, App
23	44	1.6	50	16	US-10-131-827-7124	Sequence 7418, App
24	44	1.6	50	16	US-10-131-827-7418	Sequence 7497, App
25	44	1.6	50	16	US-10-131-827-7497	Sequence 7857, App
26	44	1.6	60	10	US-09-908-975-7857	Sequence 8066, App
27	44	1.6	60	10	US-09-908-975-8066	Sequence 10581, A
28	44	1.6	60	10	US-09-908-975-10581	Sequence 11253, A
29	44	1.6	60	10	US-09-908-975-11253	Sequence 15105, A
30	44	1.6	60	10	US-09-908-975-15105	Sequence 15722, A
31	44	1.6	60	10	US-09-908-975-15722	Sequence 31250, A
32	44	1.6	60	10	US-09-908-975-11250	Sequence 31527, A
33	44	1.6	60	10	US-09-908-975-11527	Sequence 3069, A
34	44	1.6	60	10	US-09-908-975-12069	Sequence 32253, A
35	44	1.6	60	10	US-09-908-975-32253	Sequence 26, Appl
36	43	1.6	39	15	US-10-133-797-46	Sequence 6147, App
37	43	1.6	60	10	US-09-908-975-6147	Sequence 8286, App
38	43	1.6	60	10	US-09-908-975-8286	Sequence 13007, A
39	43	1.6	60	10	US-09-908-975-13007	Sequence 13645, A
40	43	1.6	60	10	US-09-908-975-13645	Sequence 18998, A
41	43	1.6	60	10	US-09-908-975-18998	Sequence 3269, A
42	43	1.6	60	10	US-09-908-975-3269	Sequence 93, Appl
43	43	1.6	58	16	US-10-300-683-93	Sequence 251, App
44	42.5	1.5	58	16	US-10-300-683-251	
45	42.5	1.5	58	16	US-10-300-683-251	

## ALIGNMENTS

RESULT 1  
US-09-908-975-12902  
Sequence 12902, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Eli  
TITLE OF INVENTION: FAIGER, Simon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TITLE OF INVENTION: THAT PORTAL A TRANSCRIPTION  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12902

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/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-12902

Alignment Scores:
Pred. No.: 0.0495 Length: 60
Score: 95.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.43% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-12902 (1-60)

Cy 302 ThrsanProclutylsAlah:sglUthrLeuh:sglSerLeuSerLeuAlaSerSer 320
Db 2 ACTATCTCAGAGAGAGGCCCATGAGCTTTCATCAGCTTATCCCTGGATCTTCC 58

RESULT 2
US-09-908-975-12941
/ Sequence 12941, Application US/09908975
/ Publication No. US20030165843A1
/ GENERAL INFORMATION:
/ APPLICANT: SHOSHAN, Avi
/ APPLICANT: MASSEMAN, Alon
/ APPLICANT: MINTZ, Eli
/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGLER, Simchon
/ TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ PRIOR FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 12941
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-12941

Alignment Scores:
Pred. No.: 12.4 Length: 60
Score: 73.00 Matches: 12
Percent Similarity: 85.00% Conservative: 5
Best Local Similarity: 60.00% Mismatches: 3
Query Match: 2.64% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-12941 (1-60)

Cy 488 MethisHISGLuAspphlysgluAspleuLyshpheaRghrlysserArgThrTP 507
Db 1 ATGACCCAGAGAGGCTTCAGAGATGAGCTAAAGACCTTCGGCTCAAGACTCGAGCTGG 60

RESULT 3
US-09-908-975-12965
/ Sequence 12965, Application US/09908975
/ Publication No. US20030165843A1
/ GENERAL INFORMATION:
/ APPLICANT: SHOSHAN, Avi
/ APPLICANT: MASSEMAN, Alon
/ APPLICANT: MINTZ, Eli
/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGLER, Simchon
/ TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
/ FILE REFERENCE: 36688-0005
```

```
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 12965
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-12965

Alignment Scores:
Pred. No.: 5.12e+03 Length: 60
Score: 49.00 Matches: 8
Percent Similarity: 77.78% Conservative: 5
Best Local Similarity: 44.44% Mismatches: 4
Query Match: 1.77% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-12965 (1-60)

Cy 488 MethisHISGLuAspphlysgluAspleuLyshpheaRghrlysserArg 505
Db 2 ATGATCTCAGAGACACAGACTGAGTGTCTGAGTGTCTGAGACCCAGACCAA 55

RESULT 4
US-10-426-058-116/c
/ Sequence 116, Application US/10426058
/ Publication No. US2004005383A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Pamela A
/ APPLICANT: Cosme, Jose M
/ APPLICANT: Ward, Alison
/ APPLICANT: Brewerton, Suzanne C
/ APPLICANT: Hamilton, Bruce J
/ APPLICANT: Jhoti, Harren
/ APPLICANT: Jones, Michelle A
/ APPLICANT: Villiard, Laurent MM
/ APPLICANT: Williams, Mark G
/ TITLE OF INVENTION: Crystals of cytochrome P450 2C9, structures thereof and their use
/ FILE REFERENCE: 620-221
/ CURRENT APPLICATION NUMBER: US/10/426,058
/ PRIOR FILING DATE: 2003-04-30
/ PRIOR APPLICATION NUMBER: US/10/280,137
/ PRIOR FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: PCT/GB2002/004872
/ PRIOR FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US 60/330,585
/ PRIOR FILING DATE: 2001-10-25
/ PRIOR APPLICATION NUMBER: US 60/339,421
/ PRIOR FILING DATE: 2001-12-14
/ PRIOR APPLICATION NUMBER: US 60/341,267
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 60/396,588
/ PRIOR FILING DATE: 2002-07-18
/ NUMBER OF SEQ ID NOS: 238
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 116
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide
US-10-426-058-116

Alignment Scores:
Pred. No.: 5.01e+03 Length: 50
Score: 48.00 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 3
```

Query Match: 1.73% Indels: 0  
DB: 13 Gaps: 0

US-08-864-955-2 (1-523) x US-10-426-058-116 (1-50)

QY 12 LeuLeuheaLaCySerProProAlaSerGlnPro 24  
DB 41 CTGCTTCATTCCTCTCCACCAACCACTGAGTGCACG 3

RESULT 5

US-10-280-137-116/c  
Sequence 116, Application US/10280137  
Publication No. US20030170842A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Pamela A  
APPLICANT: Cosme, Jose M  
APPLICANT: Ward, Alison  
APPLICANT: Brewerton, Suzanne C  
APPLICANT: Hamilton, Bruce J  
APPLICANT: Jhotti, Harren  
APPLICANT: Jones, Michelle A  
APPLICANT: Villiard, Laurent MM  
APPLICANT: Williams, Mark G  
TITLE OF INVENTION: Crystals of cyclochrome P450 2C9, structures thereof and their use  
FILE REFERENCE: 620-221  
CURRENT APPLICATION NUMBER: US/10/280,137  
PRIOR APPLICATION NUMBER: PCT/GB2002/004872  
PRIOR FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US 60/330,585  
PRIOR FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: US 60/339,421  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/341,267  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: US 60/396,588  
PRIOR FILING DATE: 2002-07-18  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 116  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-10-280-137-116

Alignment Scores:  
Pred. No.: 5.01e+03 Length: 50  
Score: 48.00 Matches: 8  
Percent Similarity: 76.92% Conservative: 2  
Best Local Similarity: 61.54% Mismatches: 3  
Query Match: 1.73% Indels: 0  
DB: 15 Gaps: 0

US-08-864-955-2 (1-523) x US-10-280-137-116 (1-50)

QY 12 LeuLeuheaLaCySerProProAlaSerGlnPro 24  
DB 41 CTGCTTCATTCCTCTCCACCAACCACTGAGTGCACG 3

US-09-908-975-5473

Sequence 5473, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME

FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5473  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-5473

Alignment Scores:

Pred. No.: 6.58e+03 Length: 60  
Score: 48.00 Matches: 11  
Percent Similarity: 63.64% Conservative: 3  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 1.73% Indels: 6  
DB: 10 Gaps: 1

US-08-864-955-2 (1-523) x US-09-908-975-5473 (1-60)

QY 200 PheTrpProGlnSerProValThrAlaThrLeuSerAspGluAspAspGlyPheValAsp 219  
DB 12 TACACCCCTGCTCTCC-----AGTGATGATGACAGAGCGCTTGTGAC 53

QY 220 LeuLeu 221  
DB 54 CTAATT 59

RESULT 7

US-10-300-683-170  
Sequence 170, Application US/10300683  
Publication No. US20030235834A1  
GENERAL INFORMATION:  
APPLICANT: Dunlop, Charles L.M.  
TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS  
FILE REFERENCE: CHAUDUN.010A  
CURRENT APPLICATION NUMBER: US/10/300,683  
CURRENT FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: 60/333,531  
PRIOR FILING DATE: 2001-11-19  
NUMBER OF SEQ ID NOS: 554  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 170  
LENGTH: 56  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Diagnostic Oligonucleotide  
US-10-300-683-170

Alignment Scores:  
Pred. No.: 6.73e+03 Length: 56  
Score: 47.50 Matches: 11  
Percent Similarity: 57.14% Conservative: 1  
Best Local Similarity: 52.38% Mismatches: 4  
Query Match: 1.72% Indels: 5  
DB: 16 Gaps: 1

US-08-864-955-2 (1-523) x US-10-300-683-170 (1-56)

QY 5 ProSerProAlaProArgArgLeuPheAlaCySerProProProAlaSerGlnPro 24  
DB 7 CCGCGCCCGCGCC-----GCCCGCGCGCGCCCGCGCGCTTTAGAGCT 51  
QY 25 Val 25  
DB 52 GTC 54

```
RESULT 8
US-10-300-683-381
; Sequence 381, Application US/10300683
; Publication No. US20030235834A1
; GENERAL INFORMATION:
; APPLICANT: Dunlop, Charles L.M.
; TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
; FILE REFERENCE: CHARDUN.010A
; CURRENT APPLICATION NUMBER: US/10/300,683
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/333,531
; NUMBER OF SEQ ID NOS: 554
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 381
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-300-683-381

Alignment Scores:
Pred. No.: 6.73e+03 Length: 56
Score: 47.50 Matches: 11
Percent Similarity: 57.14% Conservative: 4
Best Local Similarity: 52.38% Mismatches: 1
Query Match: 1.72% Indels: 5
DB: 16 Gaps: 1

US-08-864-955-2 (1-523) x US-10-300-683-381 (1-56)
Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCGGGCCCCGGCGCC-----GCCCGCGCGCGCGCGCGCTTTGAGCCT 51

Qy 25 Val 25
Db 52 GTG 54

RESULT 9
US-10-300-683-547
; Sequence 547, Application US/10300683
; Publication No. US20030235834A1
; GENERAL INFORMATION:
; APPLICANT: Dunlop, Charles L.M.
; TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
; FILE REFERENCE: CHARDUN.010A
; CURRENT APPLICATION NUMBER: US/10/300,683
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/333,531
; NUMBER OF SEQ ID NOS: 554
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 547
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-300-683-547

Alignment Scores:
Pred. No.: 6.73e+03 Length: 56
Score: 47.50 Matches: 11
Percent Similarity: 57.14% Conservative: 1
Best Local Similarity: 52.38% Mismatches: 4
Query Match: 1.72% Indels: 5
DB: 16 Gaps: 1
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```
US-08-864-955-2 (1-523) x US-10-300-683-547 (1-56)
Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCGGGCCCCGGCGCC-----GCCCGCGCGCGCGCGCGCTTTGAGCCT 51

Qy 25 Val 25
Db 52 GTG 54

RESULT 10
US-09-900-345A-150
; Sequence 150, Application US/09900345A
; Publication No. US20030031999A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Ian Hector
; TITLE OF INVENTION: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
; FILE REFERENCE: 10338-50S
; CURRENT APPLICATION NUMBER: US/09/900,345A
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: AU P8078
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/AU00/00008
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His(CAC)5
US-09-900-345A-150

Alignment Scores:
Pred. No.: 7.22e+03 Length: 54
Score: 47.00 Matches: 8
Percent Similarity: 70.59% Conservative: 4
Best Local Similarity: 47.06% Mismatches: 5
Query Match: 1.70% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-900-345A-150 (1-54)
Qy 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGlyAspLeuPheThr 172
Db 1 CCGGGTACCATGCACACACACACACAGCAAGGCGAGAACTTTCCT 51

RESULT 11
US-09-900-345A-151
; Sequence 151, Application US/09900345A
; Publication No. US20030031999A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Ian Hector
; TITLE OF INVENTION: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
; FILE REFERENCE: 10338-50S
; CURRENT APPLICATION NUMBER: US/09/900,345A
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: AU P8078
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/AU00/00008
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
```





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; PRIOR APPLICATION NUMBER: 60/165,301
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-142-722-41

Alignment Scores:
Pred. No.: 1.23e+04 Length: 60
Score: 45.50 Matches: 10
Percent Similarity: 60.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 1.64% Indels: 5
DB: 15 Gaps: 1

US-08-864-955-2 (1-523) x US-10-142-722-41 (1-60)

QY 5 ProserProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
DB 7 CCGGGCCCCGGGGCC-----GCCCCGGGGCCCCCGCCGAGCCAGCC 51

RESULT 19
US-10-300-683-41
; Sequence 41, Application US/10300683
; Publication No. US20030235834A1
; GENERAL INFORMATION:
; APPLICANT: Dunlop, Charles L.M.
; APPLICANT: Weisel, James M.
; TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
; FILE REFERENCE: CHADDON 010A
; CURRENT APPLICATION NUMBER: US/10/300,683
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/333,531
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 554
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-300-683-41

Alignment Scores:
Pred. No.: 1.23e+04 Length: 60
Score: 45.50 Matches: 10
Percent Similarity: 60.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 1.64% Indels: 5
DB: 16 Gaps: 1

US-08-864-955-2 (1-523) x US-10-300-683-41 (1-60)

QY 5 ProserProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
DB 7 CCGGGCCCCGGGGCC-----GCCCCGGGGCCCCCGCCGAGCCAGCC 51

RESULT 20
US-10-131-827-4519/c
; Sequence 4519, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
```

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; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4519
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4519

Alignment Scores:
Pred. No.: 1.06e+04 Length: 50
Score: 45.00 Matches: 7
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 16 Gaps: 0

US-08-864-955-2 (1-523) x US-10-131-827-4519 (1-50)

QY 233 ProserCyMetAlaSerLeuTyrThr 241
DB 30 CCGAGCTGTGTGTCATCCCTGTGTC 4

RESULT 21
US-09-760-364-11
; Sequence 11, Application US/09760364
; Patent No. US20020152479A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Juergen Michael
; APPLICANT: Shiau, Andrew Kwan-Nan
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: CAR Modulators: Screening and Treatment of
; FILE REFERENCE: Hypercholesterolemia
; FILE REFERENCE: 018781-004110US
; CURRENT APPLICATION NUMBER: US/09/760,364
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/176,398
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:overlapping
US-09-760-364-11

Alignment Scores:
Pred. No.: 1.33e+04 Length: 58
Score: 45.00 Matches: 7
Percent Similarity: 71.43% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 4
Query Match: 1.63% Indels: 0
DB: 9 Gaps: 0

US-08-864-955-2 (1-523) x US-09-760-364-11 (1-58)

QY 481 GlnProProSerTyrArgProMetHisIsglnAspPheLys 494
DB 6 CAGCTCCAGCCTATCTGTTCATGCATCCGCGCTTCCAG 47

RESULT 22
US-10-131-827-6734/c
; Sequence 6734, Application US/10131827
```

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Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wobigemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6734
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-6734

Alignment Scores:
Pred. No.: 1.37e+04 Length: 50
Score: 44.00 Matches: 7
Percent Similarity: 69.23% Conservative: 2
Best Local Similarity: 53.85% Mismatches: 4
Query Match: 1.59% Indels: 0
DB: 16 Gaps: 0

US-08-864-955-2 (1-523) x US-10-131-827-6734 (1-50)

Qy 8 AlaProArgLeuPheAlaCysSerProPro 20
Db 41 GCCCTACAGATGTTCTTCTGCTTCCACACCT 3

RESULT 23
US-10-131-827-7124
Sequence 7124, Application US/10131827
GENERAL INFORMATION:
APPLICANT: Wobigemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7124
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-7124

Alignment Scores:
Pred. No.: 1.37e+04 Length: 50
Score: 44.00 Matches: 7
Percent Similarity: 69.23% Conservative: 2
Best Local Similarity: 53.85% Mismatches: 4
Query Match: 1.59% Indels: 0
DB: 16 Gaps: 0

US-08-864-955-2 (1-523) x US-10-131-827-7124 (1-50)
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Qy 8 AlaProArgLeuPheAlaCysSerProPro 20
Db 10 GCCCTACAGATGTTCTTCTGCTTCCACACCT 48

RESULT 24
US-10-131-827-7418/c
Sequence 7418, Application US/10131827
GENERAL INFORMATION:
APPLICANT: Wobigemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7418
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-7418

Alignment Scores:
Pred. No.: 1.37e+04 Length: 50
Score: 44.00 Matches: 7
Percent Similarity: 69.23% Conservative: 2
Best Local Similarity: 53.85% Mismatches: 4
Query Match: 1.59% Indels: 0
DB: 16 Gaps: 0

US-08-864-955-2 (1-523) x US-10-131-827-7418 (1-50)

Qy 8 AlaProArgLeuPheAlaCysSerProPro 20
Db 41 GCCCTACAGATGTTCTTCTGCTTCCACACCT 3

RESULT 25
US-10-131-827-7497
Sequence 7497, Application US/10131827
GENERAL INFORMATION:
APPLICANT: Wobigemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7497
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-7497

Alignment Scores:
Pred. No.: 1.37e+04 Length: 50
Score: 44.00 Matches: 7
```

Percent Similarity: 69.23% Conservative: 2  
Best Local Similarity: 53.85% Mismatches: 4  
Query Match: 1.59% Indels: 0  
DB: 16 Gaps: 0

US-08-864-955-2 (1-523) x US-10-131-827-7497 (1-50)

Cy 8 AlAProArgArgLeuLeuPheAlaCysSerProPro 20  
Db 10 GCGCTTACAGAGATGCTTCTTCTGCTTCCACACCT 48

RESULT 26

US-09-908-975-7857  
Sequence 7857, Application US/09908975  
Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

FILE REFERENCE: 36688-0005

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

SEQ ID NO 7857

LENGTH: 60

TYPE: DNA

ORGANISM: Homo sapiens

US-09-908-975-7857

US-08-864-955-2 (1-523) x US-09-908-975-7857 (1-60)

Cy 248 ThrThraAnleuAAspaAnArgCysLysleuPheAspSerProSerleu 263  
Db 6 ACCCGGTCACAGACACACAGCCAGCTTTTGTACTCCACACTCTT 53

RESULT 27

US-09-908-975-8066/c  
Sequence 8066, Application US/09908975  
Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

FILE REFERENCE: 36688-0005

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8066  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-8066

Alignment Scores:

Pred. No.: 1.79e+04 Length: 60  
Score: 44.00 Matches: 9  
Percent Similarity: 71.43% Conservative: 1  
Best Local Similarity: 64.29% Mismatches: 4  
Query Match: 1.59% Indels: 0  
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-8066 (1-60)

Cy 188 ArgAspSerSerGluProGlyAsnPhelleProLeuPheThr 201  
Db 56 AGGACAGCTCCGTTCCGAGACACTTCACTCCACTCAGACC 15

RESULT 28

US-09-908-975-10581/c  
Sequence 10581, Application US/09908975  
Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

FILE REFERENCE: 36688-0005

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

SEQ ID NO 10581

LENGTH: 60

TYPE: DNA

ORGANISM: Homo sapiens

US-09-908-975-10581

US-08-864-955-2 (1-523) x US-09-908-975-10581 (1-60)

Cy 4 GlyProSerProAlaProArgArgLeuPheAlaCysSerProPro 19  
Db 57 GCGTCATCAGCATCTCCGAGACAGTTTGTACTTGTCTACCTCT 10

RESULT 29

US-09-908-975-11255/c  
Sequence 11255, Application US/09908975  
Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

FILE REFERENCE: 36688-0005

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

```
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11255
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-11255

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 9
Percent Similarity: 64.71% Conservative: 2
Best Local Similarity: 52.94% Mismatches: 6
Query Match: 1.59% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-11255 (1-60)

Cy 201 ThrProGlnSerProValThrAlaThrLeuSerAspGluAspGlyPhe 217
Db 60 ACCCCGATTCACAGTCACCTGTCACATCCAGTAGCGAGAAATGGCTTT 10

RESULT 30
US-09-908-975-15105/c
Sequence 15105, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OR INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15105
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-15105

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 1.59% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-15105 (1-60)

Cy 155 SerArgGlyCysLeuHisSerHisGlyLeuGlnGluGlyLys 168
Db 46 TCAGGGGATGTGGGACAGCCACAGGTGTGTGAGGGGAG 5

RESULT 31
US-09-908-975-15722/c
Sequence 15722, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OR INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15722
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-15722

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 7
Percent Similarity: 71.43% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 4
Query Match: 1.59% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-15722 (1-60)

Cy 445 ArgGluArgAspArgLeuGlyAsnGlyTyrProIysLeuHis 458
Db 45 AGACGACGACCGAATGCTGGGTTCTTCGATCCGAAATCCAC 4

RESULT 32
US-09-908-975-31250/c
Sequence 31250, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OR INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31250
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-31250

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 9
Percent Similarity: 55.56% Conservative: 1
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 1.59% Indels: 0
DB: 10 Gaps: 0
```

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US-08-864-955-2 (1-523) x US-09-908-975-31250 (1-60)
QY
Db 74 G1ySerSerG1uSerThrAspSerG1yPheCysLeuAspSerProG1yProLeu 91
60 GGTTCGAAGAGAGGCCAAAACATCTTTGTAGAGGGCTTTGAGGACCACTA 7

RESULT 33
US-09-908-975-31527/c
; Sequence 31527, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31527
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-31527

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 9
Percent Similarity: 55.56% Conservative: 1
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 1.59% Indels: 0
DB: Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-31527 (1-60)
QY
Db 74 G1ySerSerG1uSerThrAspSerG1yPheCysLeuAspSerProG1yProLeu 91
60 GGTTCGAAGAGAGGCCAAAACATCTTTGTAGAGGGCTTTGAGGACCACTA 7

RESULT 34
US-09-908-975-32069/c
; Sequence 32069, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32069
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-32069

US-08-864-955-2 (1-523) x US-09-908-975-32253 (1-60)
QY
Db 74 G1ySerSerG1uSerThrAspSerG1yPheCysLeuAspSerProG1yProLeu 91
60 GGTTCGAAGAGAGGCCAAAACATCTTTGTAGAGGGCTTTGAGGACCACTA 7

RESULT 35
US-09-908-975-32253/c
; Sequence 32253, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32253
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-32253

Alignment Scores:
Pred. No.: 1.79e+04 Length: 60
Score: 44.00 Matches: 9
Percent Similarity: 55.56% Conservative: 1
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 1.59% Indels: 0
DB: Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-32253 (1-60)
QY
Db 74 G1ySerSerG1uSerThrAspSerG1yPheCysLeuAspSerProG1yProLeu 91
60 GGTTCGAAGAGAGGCCAAAACATCTTTGTAGAGGGCTTTGAGGACCACTA 7

RESULT 36
US-10-133-797-26
; Sequence 26, Application US/10133797
; Publication No. US20030109021A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shujian
; APPLICANT: Chen, Jian
; APPLICANT: Feder, John
; APPLICANT: Lee, Liara
; APPLICANT: Kravets, Stanley
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY
; FILE REFERENCE: D0141NP
; CURRENT APPLICATION NUMBER: US/10/133,797
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/286,764
; PRIOR FILING DATE: 2001-04-26
```

```

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-797-26

Alignment Scores:
Pred. No.: 1.21e+04      Length: 39
Score: 43.00             Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 1.55%       Indels: 0
DB: 15                    Gaps: 0

US-08-864-955-2 (1-523) x US-10-133-797-26 (1-39)

QY 15 AlacysseProProProAlaser 22
DB 13 GCATGCTCGCCGCTCCATCTTCC 36

RESULT 37
US-09-908-975-6147
; Sequence 6147, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6147
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-6147

Alignment Scores:
Pred. No.: 2.31e+04      Length: 60
Score: 43.00             Matches: 7
Percent Similarity: 68.75% Conservative: 4
Best Local Similarity: 43.75% Mismatches: 5
Query Match: 1.55%       Indels: 0
DB: 10                    Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-6147 (1-60)

QY 135 AspProspGluAenlySGluAsnGluAlaPheGluPheLysPro 150
DB 1 GATGAAGACAGACACACTAATAGCATCTTGATACAAAGACCA 48

RESULT 38
US-09-908-975-7477/c
; Sequence 7477, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
```

```

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7477
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-7477

Alignment Scores:
Pred. No.: 2.31e+04      Length: 60
Score: 43.00             Matches: 8
Percent Similarity: 53.33% Conservative: 0
Best Local Similarity: 53.33% Mismatches: 7
Query Match: 1.55%       Indels: 0
DB: 10                    Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-7477 (1-60)

QY 477 GlnSerTyrCysGluProPheSerTyrArgProMetHisGlu 491
DB 57 CAGCAGCAGTCATCCACCCCTTATCCAGGCCTCATCTAGA 13

RESULT 39
US-09-908-975-8286/c
; Sequence 8286, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8286
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-8286

Alignment Scores:
Pred. No.: 2.31e+04      Length: 60
Score: 43.00             Matches: 7
Percent Similarity: 69.23% Conservative: 2
Best Local Similarity: 53.85% Mismatches: 4
Query Match: 1.55%       Indels: 0
DB: 10                    Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-8286 (1-60)

QY 343 GlyTyrLeuPheHisThrValAlaGlyLysHisGlnAsp 355
DB 53 GCACATCTTACACACGACGATGATAGTAGACATCTACTGAC 15

RESULT 40
```

```

US-09-908-975-13007/c
; Sequence 13007, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13007
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-13007

Alignment Scores:
Pred. No.: 2.31e+04 Length: 60
Score: 43.00 Matches: 7
Percent Similarity: 57.89% Conservative: 4
Best Local Similarity: 36.84% Mismatches: 8
Query Match: 1.55% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-13007 (1-60)

QY 473 Phmetelcscysglnserlyrcysglnproproserlyrargpromethishisgln 491
DB 58 TTCTCCAGCGTGTGACCATGTCATGACCATGACCATGCTCTTCTTCACACATGAA 2

RESULT 41
US-09-908-975-13645/c
; Sequence 13645, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13645
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-13645

Alignment Scores:
Pred. No.: 2.31e+04 Length: 60
Score: 43.00 Matches: 8
Percent Similarity: 64.71% Conservative: 3
Best Local Similarity: 47.06% Mismatches: 6
Query Match: 1.55% Indels: 0

```

```

DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-13645 (1-60)

QY 19 ProProAlaSerGlnProValValLysAlaLeuPheGlyAlaSerAlaAla 35
DB 56 CCACCATCTGGCAGCGCTGAGCTGTCTGTACTGTCTGTCTGTCTGTCTGCA 6

RESULT 42
US-09-908-975-18998/c
; Sequence 18998, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18998
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18998

Alignment Scores:
Pred. No.: 2.31e+04 Length: 60
Score: 43.00 Matches: 6
Percent Similarity: 69.23% Conservative: 3
Best Local Similarity: 46.15% Mismatches: 4
Query Match: 1.55% Indels: 0
DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x US-09-908-975-18998 (1-60)

QY 479 Tyrcysglnproproserlyrargpromethishisgln 491
DB 42 TTCTGTGACCATGCTCTTCTTGTGTGACCATGTCACCA 4

RESULT 43
US-09-908-975-32269/c
; Sequence 32269, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32269
; LENGTH: 60
; TYPE: DNA

```

```
; ORGANISM: Homo sapiens
US-09-908-975-32269

Alignment Scores:
Pred. No.: 2.31e+04      Length: 60
Score: 43.00             Matches: 10
Percent Similarity: 61.90% Conservative: 3
Best Local Similarity: 47.62% Mismatches: 6
Query Match: 1.55%       Indels: 2
DB: 10                   Gaps: 1

US-08-864-955-2 (1-523) x US-09-908-975-32269 (1-60)

Qy 3 LeuGlyProSerProAlaProArgLeuPheAlaCysSerProProAlaSer 22
Db 57 CTGGACCTCCCTCTGTCC-----CTCCTCACAGCTGCTCGTAAACACCCCTTCA 4
Qy 23 Gln 23
Db 3 AAA 1

RESULT 44
US-10-300-683-93
; Sequence 93, Application US/10300683
; Publication No. US20030235834A1
; GENERAL INFORMATION:
; APPLICANT: Dunlop, Charles L.M.
; APPLICANT: Weisel, James M.
; TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
; FILE REFERENCE: CHARDUN 010A
; CURRENT APPLICATION NUMBER: US/10/300,683
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/333,531
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 554
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-300-683-93

Alignment Scores:
Pred. No.: 2.49e+04      Length: 58
Score: 42.50             Matches: 8
Percent Similarity: 52.38% Conservative: 3
Best Local Similarity: 38.10% Mismatches: 3
Query Match: 1.53%       Indels: 7
DB: 16                   Gaps: 1

US-08-864-955-2 (1-523) x US-10-300-683-93 (1-58)

Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCGGGCCCCGGGGCC-----GCCCGCGGGCCCCCGCGGAACCG 45
Qy 25 Val 25
Db 46 ATT 48

RESULT 45
US-10-300-683-251
; Sequence 251, Application US/10300683
; Publication No. US20030235834A1
; GENERAL INFORMATION:
; APPLICANT: Dunlop, Charles L.M.
; APPLICANT: Weisel, James M.
; TITLE OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
; FILE REFERENCE: CHARDUN 010A
; CURRENT APPLICATION NUMBER: US/10/300,683
; CURRENT FILING DATE: 2002-11-19
```

```
; PRIOR APPLICATION NUMBER: 60/333,531
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 554
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Diagnostic Oligonucleotide
US-10-300-683-251

Alignment Scores:
Pred. No.: 2.49e+04      Length: 58
Score: 42.50             Matches: 8
Percent Similarity: 52.38% Conservative: 3
Best Local Similarity: 38.10% Mismatches: 3
Query Match: 1.53%       Indels: 7
DB: 16                   Gaps: 1

US-08-864-955-2 (1-523) x US-10-300-683-251 (1-58)

Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24
Db 7 CCGGGCCCCGGGGCC-----GCCCGCGGGCCCCCGCGGAACCG 45
Qy 25 Val 25
Db 46 ATT 48

Search completed: September 9, 2004, 22:59:36
Job time : 522 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2004, 19:34:19 ; Search time 2612 Seconds  
(without alignments)  
5979.296 Million cell updates/sec

Title: US-08-864-955-2  
Perfect score: 2769  
Sequence: 1 MEGSPSPAPRRLLPACSPPP.....SRTWAGEKSKREMYRRLKTL 523

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 202368

Minimum DB seq length: 10  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q=/cgrt1/USPTO.spool/US08864955/runat 07092004.144931.24488/app.query.fasta.1.711  
-DB=EST -OPMT=fastlap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=45 -MODE=LOCAL  
-OUTFMT=ptc -NOR=exc -HEAPSIZE=500 -MINLEN=10 -MAXLEN=60  
-USRR=US08864955.@CGM.1.1.2607.@runat 07092004.144931.24488 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthum:\*  
16: em\_esthum:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_vit:\*  
23: em\_gss\_vit:\*  
24: em\_gss\_vit:\*  
25: em\_gss\_vit:\*  
26: em\_gss\_vit:\*  
27: em\_gss\_vit:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	1.8	58	13	BQ243808
2	49	1.8	53	28	BH231651
3	47	1.7	58	9	AT811130
4	46	1.7	52	9	AA503556
5	46	1.7	55	9	AT811260
6	46	1.7	60	28	CC045961
7	45	1.6	50	9	AU103642
8	45	1.6	52	28	BH900891
9	45	1.6	57	9	AA584628
10	45	1.6	58	9	AA718096
11	44	1.6	43	9	AM057505
12	44	1.6	52	9	AT904527
13	44	1.6	55	9	AA677297
14	44	1.6	57	10	BF791745
15	44	1.6	59	10	BF343430
16	44	1.6	60	28	AZ468975
17	44	1.6	60	28	CC020821
18	43.5	1.6	40	28	AZ793917
19	43.5	1.6	56	9	AT227071
20	43	1.6	49	9	AT445610
21	43	1.6	49	9	AT795548
22	43	1.6	50	9	AU102450
23	43	1.6	56	28	BH231699
24	43	1.6	57	28	BH232255
25	43	1.6	59	14	CF873115
26	43	1.6	60	28	AZ497698
27	42.5	1.5	52	12	BM393388
28	42.5	1.5	54	28	AZ616939
29	42.5	1.5	56	13	B0670806
30	42	1.5	41	10	BF383813
31	42	1.5	47	28	CC022113
32	42	1.5	52	9	AT687248
33	42	1.5	53	28	AZ575590
34	42	1.5	53	28	AZ966299
35	42	1.5	57	28	CC019445
36	42	1.5	57	28	CC023745
37	42	1.5	57	28	CC023871
38	42	1.5	57	28	CC023880
39	42	1.5	57	28	CC024177
40	42	1.5	57	28	CC023374
41	42	1.5	57	28	CC023449
42	42	1.5	57	28	CC030169
43	42	1.5	57	28	CC031476
44	42	1.5	57	28	CC034222
45	42	1.5	57	28	CC034238

#### ALIGNMENTS

RESULT 1  
LOCUS BQ243808 58 bp mRNA linear EST 03-MAY-2002  
DEFINITION TaB15008F07F TaB15 Triticum aestivum cDNA clone TaB15008F07F, mRNA  
ACCESSION BQ243808  
VERSION BQ243808.1 GI:20439684  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 58)  
 AUTHORS Cloutier, S.  
 TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Dr. Sylvie Cloutier  
 Cereal Research Centre, Agriculture and Agri-food Canada  
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9  
 Tel: (204) 983-2340  
 Fax: (204) 983-4604  
 Email: scloutier@agr.gc.ca

was cloned directionally, not all sequences generated with reverse  
 primer were from the 5' end (same with forward primer and 3' end).  
 Average insert size is >1.4 kb  
 Plate: 008 row: F column: 07  
 Seq primer: M13 Forward

#### FEATURES

Location/Qualifiers  
 1..58  
 /organism="Triticum aestivum"  
 /mol\_type="RNA"  
 /cultivar="Glenlea"  
 /db\_xref="taxon:4565"  
 /clone="TAE15008P07P"  
 /tissue\_type="developing seeds"  
 /dev\_stage="15 days after anthesis"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="TAE15"  
 /note="Vector: PCMV-SPORT6.0 (Invitrogen Technologies);  
 Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds  
 of cultivar Glenlea 15 days post-anthesis"

#### ORIGIN

##### Alignment Scores:

Pred. No.:	1.09e+05	Length:	58
Score:	51.00	Matches:	8
Percent Similarity:	56.25%	Conservative:	1
Best Local Similarity:	50.00%	Mismatches:	7
Query Match:	1.84%	Indels:	0
DB:	13	Gaps:	0

US-08-864-955-2 (1-523) x BQ243808 (1-58)

Qy 5 ProSePrAaPProAArgLeuPheAlaCysSerProPro 20  
 Db 10 CCCCCCCCCCCCCCATATCTATTGCGGCCCCCCCCCCCC 57

RESULT 2  
 BH231651 53 bp DNA linear GSS 08-NOV-2001  
 LOCUS 1006163G12.2EL.Y1.1006 - Rescemu Grid G Zea mays genomic, genomic  
 DEFINITION Survey sequence.

ACCESSION BH231651  
 VERSION BH231651.1 GI:16835996  
 KEYWORDS GSS.

#### SOURCE

ORGANISM Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 53)

REFERENCE 1 (bases 1 to 53)  
 AUTHORS Walbot, V.  
 TITLE Maize genomic sequences found using engineered Rescemu transposon  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1006163 row: 19  
 Class: transposon-tagged.

#### FEATURES

Location/Qualifiers  
 1..53  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="1006 - Rescemu Grid G"  
 /note="Organ: leaf; Vector: Rescemu (engineered from  
 pBluescript backbone); Site 1: BamHI, Site 2: BglII;  
 Rescemu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on Rescemu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'Rescemu', 'Grid G' was grown at Stanford in 2000. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

#### ORIGIN

##### Alignment Scores:

Pred. No.:	1.43e+05	Length:	53
Score:	49.00	Matches:	10
Percent Similarity:	73.33%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	4
Query Match:	1.77%	Indels:	0
DB:	28	Gaps:	0

US-08-864-955-2 (1-523) x BH231651 (1-53)

Qy 6 SerProAaPProAArgLeuPheAlaCysSerProPro 20  
 Db 49 TCTCCCGACCTCGCTTCGATTCGACGATCCGCGCACCT 5

RESULT 3  
 A1811130 58 bp mRNA linear EST 07-JUL-1999  
 LOCUS t106C06.X1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:221514.3  
 DEFINITION similar to FR:064371 Q64371 PR-VBETAL.1, mRNA sequence.  
 A1811130  
 A1811130.1 GI:5397696

#### SOURCE

ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 58)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapdb-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Jemson, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www-bio.lnl.gov/dbtrp/image/image.html

#### FEATURES

Trace considered overall poor quality  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..58  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"



Query Match:	1.66%	Indels:	0
DB:	9	Gaps:	0
US-08-864-955-2 (1-523) x A1811260 (1-55)			
QY	4	G1PProSerProAlaProaTgArIgfLeuDeuHeaIaCysSerProProPro	20
Db	53	GGGGCCCGAGCCTTCCCCCCCCGGGGCCTTGGTGTGGAGTATCCCCCCCCCCCC	3

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 60)	Walbot,V.	Maize genomic sequences found using engineered RescuenMu transposon		
		Unpublished (2001)		
	Contact: Walbot V			

Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence  
plate: 3591\_1\_181.1 row: 34  
class: transposon-tagged.

FEATURES	Location/Qualifiers
source	1. .60

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"

```

/clone.lib="j391 - RescueMu.Grid.P"  
/note="Organ: leaf, Vector: RescueMu (engineered from  
pBluescript backbone), Site.1: BamHI, Site.2: BglII;  
RescueMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescueMu, go to the web  
site 'www.zmd.ias.tate.edu and follow the links for  
'RescueMu'. Grid P was grown at Moloka'i in 2002. DNA was  
extracted from leaf strips, double digested using BamHI  
and BglII, and ligated to form circular plasmids. D10b  
cells were transformed and then screened on LB plates with  
ampicillin."

ORIGIN	
Alignment Scores:	
Pred. No.:	3,19e-05
Score:	46.00
Percent Similarity:	55.5%
Best Local Similarity:	50.0%
Query Match:	1.66%
DB:	28
length:	60
Matches:	9
Conservative:	1
Mismatches:	8
Indels:	0
Gaps:	0

US-08-864-955-2 (1-523) X CC045961 (1-60)

QY           7 ProAlaProArgLeuPheAlaCysserProProAlaSerGlnPro 24  
||| ||||||| ::| ||||||| |||

Db 57 CCGTGCCCCCGCCGCGAGTCTCTCGGAGTAGTCTCCCGCGGCATGTGCCCG 4

RESULT 7		
AU103642/c	50 bp	EST 30-AUG-2001
LOCUS		
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	
VERSION	HEP30480, mRNA sequence.	
ACCESION	AU103642.1 GI:1355163	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

## REFERENCE

AUTHOR

TITLE

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED

COMMENT Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

FEATURES  
source

```
/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="HEP03480"  
/clone_lib="Sugano Homo sapiens cDNA library"
```

## ORIGIN

Alignment Scores:	2.99e+05	Length:	5
Pred. No.:	45.00	Matches:	5
Score:	7.44%	Conservative:	2
Percent Similarity:	57.14%	Mismatches:	4
Best Local Similarity:	1.63%	Indels:	0
Query Match:	9	Gaps:	0
DB:			

US-08-864-955-2 (1-E23) x AUI03642 (1-50)

US-08-864-955-2 (1-523) X AU103642 (1-50)

```

Oy      87 SerProGlyProLeuAspSerLysGluAsnLeuGluAsnPro 100
          |||||
Db      45 AGCCCCGGGCCCCCTGATTCTGAGCACGGGCGGAGATCGCCT 4

```

RESULT 8  
BH900891/c  
\*\*\*\*\*  
C3 1m  
DATE 11-DEC-2003  
C66 03-SEP-2003

LOCUS	52 bp	DNA	linear	GS5 03-SEP-2001
BH900891				
KG06578-3prime				
Drosophila melanogaster				
P(SUPor-P)				
P element				
recovered				
from Drosophila melanogaster genomic				
genome				

VERSION BH900891.1 GI:22658052

NEWMORLD  
SOURCE

## ORGANISM

[illegible]

## REFERENCE

## AUTHORS

TITTLE

THE BENEVOLENT PROSPERITY OF THE



```

/clone="IMAGE:1195217"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NBMWG"
/notes="Organ: mammary gland; Vector: p773D-Pac
(Pharmacia) with a modified polylinker; Site: 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5,
TCTTACCAATCTGAGAGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

```

## ORIGIN

## Alignment Scores:

```

Pred. No.: 3.73e+05 Length: 58
Score: 45.00 Matches: 10
Percent Similarity: 72.22% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 1
Query Match: 1.63% Indels: 4
DB: 9 Gaps: 1

```

US-08-864-955-2 (1-523) x AA718096 (1-58)

Qy 87 SerProGlyProLeuApeSerGlyGlu-----AsnLeuGluAsnPro 100

Db 5 TCTCCGGCGCCATCGATCTTGAGAGCACGACAGATGGCCAGTCATGAGAACCA 58

RESULT 11  
AM057505/c 43 bp mRNA linear EST 29-SEP-1999  
LOCUS ca04h09.x1 C elegans fem3 Q23 S1 Caenorhabditis elegans cDNA 3'  
DEFINITION similar to gb:F44G3.2 (ELEGANS),WP:F44G3.2 CB16034 ARGININE KINASE  
ACCESSION AM057505 GI:5933144  
VERSION AM057505  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida;  
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 43)

REFERENCE  
AUTHORS Ward,S., Smith,H., Clifton,S., Marra,M., Hillier,L., Kucaba,T.,  
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Steptoe,M., Gibbons,M.,  
Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and  
Wilson,R.  
Unpublished (1999)  
TITLE UofArizona-Washu C. elegans EST project  
JOURNAL  
COMMENT Other ESTs: ca04h09.y1  
Contact: Samuel Ward, Ph.D.  
UofArizona-Washu C. elegans EST project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: esat@wason.wustl.edu  
Contact Harold Smith (hesou.aziona.edu) for further information  
relating to organism, libraries, or clone availability.  
Trace considered overall poor quality  
Seq primer: -40RP from Gibco  
High quality sequence stop: 1.

## FEATURES

```

Location/Qualifiers
1..43
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/lab_host="DH5alpha cells"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 2.93e+05 Length: 43
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 1.59% Indels: 0
DB: 9 Gaps: 0

```

US-08-864-955-2 (1-523) x AM057505 (1-43)

Qy 176 AsnSerAlaGlnLeuGlyMetLeuSerSerAsnGlu 187

Db 37 AATACCGTAGAGCTTGGATCCCTTCCAGCAATGAG 2

RESULT 12  
AI904527 52 bp mRNA linear EST 30-MAR-2000  
LOCUS PM-BT057-290199-317 BT057 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AI904527  
ACCESSION AI904527  
VERSION AI904527 GI:5494914  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 52)

REFERENCE  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,R.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01505-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/seq/gethtml.pl?cl=PM-BT057-317.html  
kt3=290199&tl=1)  
Seq primer: puc 18 forward.

## FEATURES

```

Location/Qualifiers
1..52
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"

```

/clone\_lib="BT057"  
 /note="Organ: breast; Vector: pUC18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

## Alignment Scores:

Pred. No.:	3,89e+05	Length:	52
Score:	44.00	Matches:	9
Percent Similarity:	83.33%	Conservative:	1
Best Local Similarity:	75.00%	Mismatches:	2
Query Match:	1.59%	Indels:	0
DB:	9	Gaps:	0

US-08-864-955-2 (1-523) x A1904527 (1-52)

QY 278 SerGlnGluSerProGlySerThrLysArg 289

Db 14 TCTAAGTACAGATCCCGCAGGACGACCTAAACGA 49

## RESULT 13

AA677297 55 bp mRNA linear EST 19-DEC-1997  
 zj61f05.s1 Soares fetal\_liver\_spleen INF15 S1 Homo sapiens cDNA  
 clone IMAGE:454785 3' similar to SW:TXN\_BOVIN P08858 NEUROKININ B  
 PRECURSOR ;, mRNA sequence.

## ACCESSION

AA677297 GI:2657819

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## 1..55

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:454785"

## /sex="male"

## /dev\_stage="20 week-post conception fetus"

## /lab\_host="DH10B (ampicillin resistant)"

## /clone\_lib="Soares fetal\_liver\_spleen INF15 S1"

## /note="Organ: liver and Spleen; Vector: pTZ19 (pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INF15 library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5',

## ACGTGAGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'];

## double-stranded cDNA was ligated to Eco RI adaptors

(pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.:	4,23e+05	Length:	55
Score:	44.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	1.59%	Indels:	0
DB:	9	Gaps:	0

US-08-864-955-2 (1-523) x AA677297 (1-55)

QY 298 ProlysgLysThrAsnProGlyLys 306

Db 55 CTTAAGATCAATCTCCGAGAA 29

## RESULT 14

BF791745 57 bp mRNA linear EST 12-JAN-2001

LOCUS 602251933F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4344105 5',

## DEFINITION

## mRNA sequence.

## ACCESSION

BF791745 GI:12096799

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## 1..57

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:4344105"

## /tissue\_type="adrenal cortex carcinoma, cell line"

## /lab\_host="DH10B (phage-resistant)"

## /clone\_lib="NIH\_MGC\_84"

## /note="Organ: adrenal gland; Vector: PCMV-SPORE; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by life technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	4,46e+05	Length:	57
Score:	44.00	Matches:	8
Percent Similarity:	66.67%	Conservative:	2
Best Local Similarity:	53.33%	Mismatches:	5
Query Match:	1.59%	Indels:	0
DB:	10	Gaps:	0

US-08-864-955-2 (1-523) x BF791745 (1-57)

QY 150 ProvAlaArgProValSerArgGlyCysLeuHisSerHisGlyIleu 164  
 Db 1 CCCACGGCTCCGGGACGCGTGGGTGCACCCACGCGTCCGACTA 45

RESULT 15  
 BF343430  
 LOCUS 59 bp mRNA linear EST 22-NOV-2000  
 DEFINITION 602014543F1 NCI\_CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4150259  
 5', mRNA sequence.  
 ACCESSION BF343430  
 VERSION BF343430.1 GI:11290704  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 59)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [rgabbs-remail.nih.gov](mailto:rgabbs-remail.nih.gov)  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LHM9413 row: e column: 12  
 High quality sequence stop: 59.  
 Location/Qualifiers  
 1..59  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_image="4150259"  
 /tissue\_type="gliblastoma with EGFR amplification"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Brn64"  
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NCI;  
 Site 2: Salt; Cloned unidirectionally; Primer: Oligo dt.  
 Average insert size 1.57 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.7e+05 Length: 59  
 Score: 44.00 Matches: 8  
 Percent Similarity: 66.67% Conservative: 2  
 Best Local Similarity: 53.33% Mismatches: 5  
 Query Match: 1.59% Indels: 0  
 DB: 10 Gaps: 0

US-08-864-955-2 (1-523) x BF343430 (1-59)

QY 150 ProvAlaArgProValSerArgGlyCysLeuHisSerHisGlyIleu 164  
 Db 3 CCCACGGCTCCGGGACGCGTGGGTGCACCCACGCGTCCGACTA 47

RESULT 16  
 AZ468975 60 bp DNA linear GSS 04-OCT-2000  
 LOCUS 602022D18F Mouse 10kb plasmid UNGCM library Mus musculus genomic  
 clone UNGCM0282D18 F, genomic survey sequence.  
 ACCESSION AZ468975  
 VERSION AZ468975.1 GI:10627100  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 60)

AUTHORS Dunn D., Aoyagi A., Barber M., Becorn T., Duval B., Hamil C.,  
 Islam H., Longacre S., Mahmoud M., Meenen E., Petersen T.,  
 Reilly M., Rose R., Rose R., Stokes R., Tinney A., von  
 Niederhausen A. and Wright D. Weis R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0282 row: D column: 18  
 Seq primer: CGTGTGAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 60.  
 Location/Qualifiers  
 1..60  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="UNGCM0282D18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UNGCM library"  
 /note="Vector: pMD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (GI:4732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.82e+05 Length: 60  
 Score: 44.00 Matches: 7  
 Percent Similarity: 76.92% Conservative: 3  
 Best Local Similarity: 53.85% Mismatches: 3  
 Query Match: 1.59% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x AZ468975 (1-60)

QY 331 AsnAspProArgAspLeuIleGlyAspPheSerIysGly 343  
 Db 59 AATGACCAAGACAGTATGATGACTTCTCTGTGGG 21

RESULT 17  
 CC020821 60 bp DNA linear GSS 01-APR-2003  
 LOCUS CC020821/c  
 DEFINITION 3591.1.21.1 D01.2EL.Y.1 3591 - Rescueu Grid P Zea mays genomic,  
 genomic survey sequence.  
 ACCESSION CC020821  
 VERSION CC020821.1 GI:29434894  
 KEYWORDS GSS.

SOURCE  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 60)

REFERENCE  
TITLE Maize genomic sequences found using engineered Rescuer transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 3591.1.21.1 row: 5  
Class: transposon-tagged.  
Location/Qualifiers  
1..60  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="3591 - Rescuer Grid P"  
/note="Organ: leaf; Vector: Rescuer (engineered from  
pBluescript backbone); Site 1: BamHI, Site 2: BglII;  
Rescuer is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescuer, go to the web  
site 'www.zmdb.lastate.edu' and follow the links for  
'RescuerMu.' Grid P was grown at Molokai in 2002. DNA was  
extracted from leaf strips, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.82e+05 Length: 60  
Score: 44.00 Matches: 9  
Percent Similarity: 55.56% Conservative: 1  
Best Local Similarity: 50.00% Mismatches: 8  
Query Match: 1.59% Indels: 0  
Gaps: 0  
DB: 28  
US-08-864-955-2 (1-523) x CC020821 (1-60)

OY 7 ProAlaProAlaPArgLeuPheAlaCySerProProAlaSerGlnPro 24  
Db 57 CCGGCCCGCCGCGGAGCCTCTTCGGAGTCTCCCGGCGATGTGCGCG 4

RESULT 18  
AZ793917 40 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0047L2AF Mouse 10kb plasmid UUGCM library Mus musculus genomic  
DEFINITION clone UUGC2M0047L2AF, genomic survey sequence.  
ACCESSION AZ793917  
VERSION AZ793917.1 GI:12939357  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 40)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niedermaier, A., and Wright, D., Weiss, R.  
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 1000 Std Error: 0.00  
Plate: 0047 row: 1 column: 24  
Seq primer: CTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 40.  
Location/Qualifiers  
1..40  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0047L24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_id="Mouse 10kb plasmid UUGCM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/notes/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Alignment Scores:  
Pred. No.: 2.91e+05 Length: 40  
Score: 43.50 Matches: 9  
Percent Similarity: 55.00% Conservative: 2  
Best Local Similarity: 45.00% Mismatches: 2  
Query Match: 1.57% Indels: 7  
Gaps: 1  
DB: 28  
US-08-864-955-2 (1-523) x AZ793917 (1-40)

OY 5 ProSerProAlaPArgArgLeuPheAlaCySerProProAlaSerGlnPro 24  
Db 1 CCTCTCTCTCTCTCC-----TCTCCCTCTCTCTCTCTCTCTCTCC 39

RESULT 19  
AI227071 56 bp mRNA linear EST 29-OCT-1998  
LOCUS u11ae09.y1 Sugano mouse kidney mR1a Mus musculus cDNA clone  
DEFINITION IMAGE1907752.5', mRNA sequence.  
ACCESSION AI227071  
VERSION AI227071.1 GI:3810124  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus



cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lemon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNI at:  
[www-bio.llnl.gov/bdrip/image/image.html](http://www-bio.llnl.gov/bdrip/image/image.html)

Trace considered overall poor quality  
 Seq primer: -40UP from Gdbco  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

## source

1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2221660"  
 /tissue\_type="tumor, 5 pooled (see description)"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Ov23"  
 /note="Organ: ovary; Vector: PCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.35 kb. Tumor types include: mixed  
 Mullerian tumor, papillary serous, clear cell, spindle  
 cell. All are primary tumors, metastasis positive. Life  
 Technologies catalog #: 11534-013"

## ORIGIN

## Alignment Scores:

Pred. No.: 4.37e+05 Length: 49  
 Score: 43.00 Matches: 7  
 Percent Similarity: 62.50% Conservative: 3  
 Best Local Similarity: 43.75% Mismatches: 6  
 Query Match: 1.55% Indels: 0  
 DB: 9 Gaps: 0

US-08-864-955-2 (1-523) x AU102450 (1-49)

QY 283 ProProGlySerThrIysArgArgIysSerMetSerGlyAlaSerPro 298

Db 1 CCCCCCGGCGACCCCGAGGAGGAAAAACAGGGGGGGGGCCCCC 48

RESULT 22

AU102450/c AU102450 50 bp mRNA linear EST 30-ANG-2001

LOCUS AU102450 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ADSE00304, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maryama, K.,

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

## ORIGIN

## Alignment Scores:

Pred. No.: 4.5e+05 Length: 50  
 Score: 43.00 Matches: 8  
 Percent Similarity: 57.14% Conservative: 0  
 Best Local Similarity: 57.14% Mismatches: 6  
 Query Match: 1.55% Indels: 0  
 DB: 9 Gaps: 0

US-08-864-955-2 (1-523) x AU102450 (1-50)

QY 7 ProAlaProArgArgLeuLeuPheAlaCysSerProProPro 20

Db 49 CCGCGCGGACCGGCTCACCGAGCGGTGCCACCGCGCGCA 8

RESULT 23

LOCUS BH231699/c BH231699 56 bp DNA linear GSS 08-NOV-2001

DEFINITION 1006163H01.2EL\_Y1 1006 - RescuedMu Grid G Zea mays genomic, genomic

survey sequence.

ACCESSION BH231699

VERSION BH231699.1 GI:16836088

KEYWORDS GSS

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 56)

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

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Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Maibot V.

Alignment Scores:

Pred. No.:	5.34e+05	Length:	56
Score:	43.00	Matches:	9
Percent Similarity:	76.92%	Conservative:	1
Best Local Similarity:	69.23%	Mismatches:	3
Query Match:	1.55%	Indels:	0
DB:	28	Gaps:	0

US-08-864-955-2 (1-523) x BH231699 (1-556)

QY 6 SerProAlaProArgArgLeuLeuPheAlaCysSerPro 18  
 DB 44 TCTCCGACCTCGTCCATTTCTCAAGCATCCGCTCC 6

RESULT 24

LOCUS B42255 57 bp DNA linear GSS 18-OCT-1997

DEFINITION HS-1055-B1-D05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=9 Row=H, genomic survey sequence.

ACCESSION B42255

VERSION B42255.1 GI:2546507

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., 1 (bases 1 to 57)

AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.

TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

JOURNAL Unpublished (1997)

COMMENT Contact: Mahairas GG, Zackrone KD, Hood L University of Washington Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7301 Email: kzackrone@u.washington.edu

Sequence Tagged Connector Plate: CT 777 row: H column: 9 Class: BAC ends

FEATURES

source

1..57 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="Genomic DNA"

/db\_xref="taxon:9606"

/clone="Plate=CT 777 Col=9 Row=H"

/sex="M"

/clone\_lib="CIT Human Genomic Sperm Library C"

/note="Organ: Sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.:	5.48e+05	Length:	57
Score:	43.00	Matches:	8
Percent Similarity:	64.29%	Conservative:	1
Best Local Similarity:	57.14%	Mismatches:	5
Query Match:	1.55%	Indels:	0
DB:	28	Gaps:	0

US-08-864-955-2 (1-523) x B42255 (1-57)

QY 298 ProLysGluSerThrAsnProGluValAlaHisGluThrIleu 311  
 DB 12 CCCGACGACGAGATCTCTCTGAAGCGCCACGAAAGTCTT 53

RESULT 25

LOCUS CF873115 59 bp mRNA linear EST 31-OCT-2003

DEFINITION trico04xa02.b11 T.reesei mycelial culture, Version 6 October 2003

ACCESSION Hypocrea jecorina CDNA clone trico04xa02, mRNA sequence.

VERSION CF873115

KEYWORDS EST.

SOURCE CF873115.1 GI:38127797

ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

REFERENCE Dienes,S.E., Dunkelweyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.

AUTHORS Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset

TITLE Unpublished (2003)

JOURNAL Contact: Ralph A. Dean

COMMENT Fungal Genomics Laboratory North Carolina State University Campus Box 7251, Raleigh, NC 27695, USA Tel: 919-513-0020 Fax: 919-513-0024 Email: ralph.dean@ncsu.edu

Seq primer: TR-P1 Primer.

FEATURES

source

1..59 Location/Qualifiers

/organism="Hypocrea jecorina"

/mol\_type="mRNA"

/strain="QM6a"

/db\_xref="taxon:51453"

/clone="trico04xa02"

/dev\_stage="mycelia"

/clone\_lib="T.reesei mycelial culture, Version 6 October 2003"

/note="Vector: PREPpY, Site:1, Not I/Sal I. Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Alignment Scores:

Pred. No.:	5.74e+05	Length:	59
Score:	43.00	Matches:	8
Percent Similarity:	50.00%	Conservative:	1
Best Local Similarity:	44.44%	Mismatches:	9
Query Match:	1.55%	Indels:	0
DB:	14	Gaps:	0

US-08-864-955-2 (1-523) x CF873115 (1-59)

QY 5 ProSerProAlaProArgArgLeuLeuPheAlaCysSerProProAlaSer 22  
 DB 1 CCCCTTCCTCCGCCCTCCGATCTTCCCAACCTACACGCGCGCTGTCTCC 54

RESULT 26

LOCUS A2497698 60 bp DNA linear GSS 05-OCT-2000

DEFINITION 1X0334H08 Mouse 10kb plasmid UUGCLW library Mus musculus genomic clone UUGCLW0334H08 R, genomic survey sequence.

ACCESSION A2497698

VERSION A2497698.1 GI:10674882

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ismail,H., Longacre,S., Mammond,M., Meenen,E., Pedersen,T., Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL



/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGC1M0448A04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_id="Mouse 10kb plasmid UGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1[473214]SP/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.: 5.57e+05 Length: 54  
 Score: 42.50 Matches: 11  
 Percent Similarity: 47.83% Conservative: 0  
 Best Local Similarity: 47.83% Mismatches: 3  
 Query Match: 1.53% Indels: 9  
 DB: 28 Gaps: 2

US-08-864-955-2 (1-523) X AZ616939 (1-54)

Qy 5 ProSerProAlaProAlaGArgLeuPheAlaCySerProProAlaSerGlnPro 24  
 Db 6 CCACTCCCTGCCCC-----TGCCCCCCCCCACC-----CCC 38  
 Qy 25 ValValIys 27  
 Db 39 GTTTTAA 47

RESULT 29  
 BU670806/c 56 bp mRNA linear EST 01-OCT-2002  
 LOCUS NISC.1r01e02.y1 NCI CGAP Pr49 Rattus norvegicus cDNA clone  
 DEFINITION IMAGE:5598026 5', mRNA sequence.  
 ACCESSION BU670806 GI:23398773  
 VERSION BU670806.1 GI:23398773  
 SOURCE EST.  
 ORGANISM Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 56)  
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 CDNA Library Preparation:  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 info@image.lnl.gov  
 Plate: LHAM12384 row: 1 column: 3

FEATURES  
 Seq primer: M13RP1 reverse primer (AB1).  
 Location/Qualifiers  
 1..56  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="IMAGE:5598026"  
 /sex="male"  
 /issue\_type="ventral prostate, pool of 3-, 5-, and 7-days post-castration"  
 /dev\_stage="adult", 11 week"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NCI CGAP Pr49"  
 /note="Organ: prostate; Vector: pCMV-Sport6.1; Site: 1: NCI; Site 2: EcorV; Cloned unidirectionally. Primer: Oligo dt. Pool of 3 primary libraries: NCI CGAP Pr30 (ventral prostate from 11 wk male, 3 days post-castration, average insert size 2 kb), NCI CGAP Pr40 (ventral prostate from 11 wk male, 5 days post-castration, average insert size 1.6 kb) and NCI CGAP Pr41 (ventral prostate from 11 wk male, 7 days post-castration, average insert size 2.5 kb). Constructed by Life Technologies/Invitrogen. Note: this is a NCI CGAP library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.88e+05 Length: 56  
 Score: 42.50 Matches: 9  
 Percent Similarity: 52.38% Conservative: 2  
 Best Local Similarity: 42.86% Mismatches: 5  
 Query Match: 1.53% Indels: 5  
 DB: 13 Gaps: 1

US-08-864-955-2 (1-523) X BU670806 (1-56)

Qy 5 ProSerProAlaProAlaGArgLeuPheAlaCySerProProAlaSerGlnPro 24  
 Db 52 CCGCGCCCCCGCCCCCG-----GCGCCCCCTCGCCCTCCTCCGCG 8  
 Qy 25 Val 25  
 Db 7 CTA 5

RESULT 30  
 BF383813 41 bp mRNA linear EST 27-NOV-2000  
 LOCUS 60204472BP1 NCI CGAP Pr49 Mus musculus cDNA clone IMAGE:4194102 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF383813  
 VERSION BF383813.1 GI:11365118  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 41)  
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LHAM9527 row: h column: 07  
 High quality sequence stop: 41.  
 Location/Qualifiers  
 1..41  
 source



Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0  
US-08-864-955-2 (1-523) x A1687248 (1-552)

CY 13 LeuphealacysseerProProPro 20  
DB 51 CTTTITTTTGTCTCTCCCCC 28

RESULT 33  
A2576590 53 bp DNA linear GSS 06-DEC-2000  
LOCUS A2576590  
DEFINITION AAT-T12C656 Genetrap T47D Human Breast Carcinoma Library Homo  
sapiens genomic 5', genomic survey sequence.  
ACCESSION A2576590  
VERSION A2576590.1 GI:11562901  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Henkel,G., Livanage,M., Pratt,E., Huang,D., Riley,M.,  
Bernardino,A., Durick,K. and Pollok,B.  
EXON-TRAP tags from a T47D Genomescreen(TM) Library  
Unpublished (2000)  
JOURNAL Contact: Greg Henkel  
COMMENT Gene Expression  
Aurora Biosciences Corp.  
11010 Torreyana Road, San Diego, CA 92121, USA  
Tel: 8584048436  
Fax: 8584046719  
Email: henkelg@aurorabio.com

FEATURES  
source  
1..53  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/tissue\_type="Carcinoma"  
/cell\_type="Epithelial"  
/cell\_line="T47D"  
/clone\_lib="Genetrap T47D Human Breast Carcinoma Library"  
/note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA  
from genetrap pools; shotgun clone in pAMP-1 and used to  
transform DHS-alpha competent bacteria."

ORIGIN  
Alignment Scores:  
Pred. No.: 6e+05 Length: 53  
Score: 42.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0  
US-08-864-955-2 (1-523) x A2576590 (1-53)

CY 88 ProGlyProLeuAlaSerLysGluAsn 96  
DB 16 CCAAGGCGCTTGGACAAAGAAAGAAAT 42

RESULT 34

A2966299 53 bp DNA linear GSS 27-APR-2001  
LOCUS A2966299  
DEFINITION 2M0236A16R Mouse 10kb plasmid U0G2M library Mus musculus genomic  
clone U0G2M0236A16 R, genomic survey sequence.  
ACCESSION A2966299  
VERSION A2966299.1 GI:13837526  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Dunn,P., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5506  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0236 Row: A Column: 16  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 53.  
Location/Qualifiers  
1..53  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U0G2M0236A16"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U0G2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gill473114|gb|AF129072.1), a copy-number  
infectible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Alignment Scores:  
Pred. No.: 6e+05 Length: 53  
Score: 42.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0  
US-08-864-955-2 (1-523) x A2966299 (1-53)

QY 15 AlAcYserProProAlaSerGln 23  
 Db 9 GCGTGGCTGCTCGCGCGGACTCAG 35

RESULT 35  
 CC019445/c 57 bp DNA linear GSS 01-APR-2003  
 LOCUS 3591\_1\_14\_1.H12.2EL\_Y\_1 3591 - RescueMu Grid P Zea mays genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC019445  
 VERSION CC019445.1 GI:29433518  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 57)

REFERENCE  
 AUTHORS Walbot, V.  
 TITLE Maize genomic sequences found using engineered RescueMu transposon  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 723 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 3591.1.14.1 row: 8  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..57  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /culturvar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="3591 - RescueMu Grid P"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 Bluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was  
 extracted from leaf strips, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 6.69e+05 Length: 57  
 Score: 42.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 9  
 Query Match: 1.52% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC019445 (1-57)

QY 7 ProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
 Db 54 CCGTGGCTGCTCGCGCGGACTCAGTGTGCGCG 1

RESULT 36  
 CC023745/c 57 bp DNA linear GSS 01-APR-2003  
 LOCUS 3591\_1\_14\_1.H01.2EL\_Y\_1 3591 - RescueMu Grid P Zea mays genomic,

DEFINITION 3591\_1\_36\_1.C06.2EL\_Y\_1 3591 - RescueMu Grid P Zea mays genomic,  
 genomic survey sequence.  
 ACCESSION CC023745  
 VERSION CC023745.1 GI:29438602  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 57)

REFERENCE  
 AUTHORS Walbot, V.  
 TITLE Maize genomic sequences found using engineered RescueMu transposon  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 723 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 3591.1.36.1 row: 3  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..57  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /culturvar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="3591 - RescueMu Grid P"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 Bluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was  
 extracted from leaf strips, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 6.69e+05 Length: 57  
 Score: 42.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 9  
 Query Match: 1.52% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC023745 (1-57)

QY 7 ProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
 Db 54 CCGTGGCTGCTCGCGCGGACTCAGTGTGCGCG 1

RESULT 37  
 CC023871/c 57 bp DNA linear GSS 01-APR-2003  
 LOCUS 3591\_1\_36\_1.H01.2EL\_Y\_1 3591 - RescueMu Grid P Zea mays genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC023871  
 VERSION CC023871.1 GI:29438728  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays



Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 3591\_138\_1 row: 23  
Class: transposon-tagged.  
Location/Qualifiers  
1..57

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/organism="Zea mays"  
/mol_type="genomic DNA"  
/culturivar="mixed background W23/A188/B73/K55"  
/db_xref="taxon:4577"  
/tissue_type="leaf"  
/dev_stage="adult"  
/lab_host="DH10B"  
/clone_lib="3591 - RescuedMu Grid P"  
/note="Organ: leaf; Vector: RescuedMu (engineered from  
pBluescript backbone); Site_1: BamHI; Site_2: BglII;  
RescuedMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuedMu, go to the web  
site 'www.zmmb.iastate.edu' and follow the links for  
'RescuedMu'. Grid P was grown at Molokai in 2002. DNA was  
extracted from leaf strips, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."
```

## ORIGIN

## Alignment Scores:

Pred. No.: 6.69e+05 Length: 57  
Score: 42.00 Matches: 9  
Percent Similarity: 50.00% Conservative: 0  
Best Local Similarity: 50.00% Mismatches: 9  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC024177 (1-57)

Qy 7 ProAlaProARgArgLeuPheAlaCySerProProAlaSerGlnPro 24  
Db 54 CCGTGGCCCCGGCGGCGAGCCTCTCGGCGTATCTCTCCGCGGATGTGGCGG 1

RESULT 40  
CC029374 57 bp DNA linear GSS 01-APR-2003  
LOCUS 3591\_1110\_1.B12.2EL.Y.1 3591 - RescuedMu Grid P Zea mays genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CC029374  
VERSION CC029374.1 GI:29444225  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 57)  
AUTHORS Walbot,V.  
TITLE Maize genomic sequences found using engineered RescuedMu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 3591\_1110\_1 column: 5  
Class: transposon-tagged.  
Location/Qualifiers  
1..57

## FEATURES

source  
1..57  
/organism="Zea mays"

## ORIGIN

Alignment Scores:  
Pred. No.: 6.69e+05 Length: 57  
Score: 42.00 Matches: 9  
Percent Similarity: 50.00% Conservative: 0  
Best Local Similarity: 50.00% Mismatches: 9  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC029374 (1-57)

Qy 7 ProAlaProARgArgLeuPheAlaCySerProProAlaSerGlnPro 24  
Db 54 CCGTGGCCCCGGCGGCGAGCCTCTCGGCGTATCTCTCCGCGGATGTGGCGG 1

RESULT 41  
CC029449 57 bp DNA linear GSS 01-APR-2003  
LOCUS 3591\_1110\_1.P04.2EL.Y.1 3591 - RescuedMu Grid P Zea mays genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CC029449  
VERSION CC029449.1 GI:29444300  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 57)  
AUTHORS Walbot,V.  
TITLE Maize genomic sequences found using engineered RescuedMu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 3591\_1110\_1 column: 5  
Class: transposon-tagged.  
Location/Qualifiers  
1..57

## FEATURES

source  
1..57  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/culturivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="3591 - RescuedMu Grid P"

/note="Organ: leaf; Vector: RescuMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescuMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
42.00	57	9	42.00
Percent Similarity:		Conservative:	50.00%
Best Local Similarity:		Mismatches:	50.00%
Query Match:	1.52%	Indels:	0
DB:	28	Gaps:	0

US-08-864-955-2 (1-523) x CC029449 (1-57)

Qy 7 ProlaPProAArgLeuPheAlaCySeSerProProAlaSerGinPro 24

Db 54 CCGTGGCCCCCGCGACGCTCTCGGCGTATGCTCTCCCGGCAATGTGGCGG 1

## RESULT 42

CC030169 57 bp DNA linear GSS 01-APR-2003

LOCUS CC030169/c 3591.1.115.1.C05.2EL\_Y.1 3591 - RescuMu Grid P Zea mays genomic.

DEFINITION genomic survey sequence.

ACCESSION CC030169

VERSION CC030169.1 GI:29445060

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 57)

Walbot, V.

Maize genomic sequences found using engineered RescuMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 3591\_1.115.1 column: 10

Class: transposon-tagged.

Location/Qualifiers

1..57

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="3591 - RescuMu Grid P"

/note="Organ: leaf; Vector: RescuMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for

## ORIGIN

'RescuMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
42.00	57	9	42.00
Percent Similarity:		Conservative:	50.00%
Best Local Similarity:		Mismatches:	50.00%
Query Match:	1.52%	Indels:	0
DB:	28	Gaps:	0

US-08-864-955-2 (1-523) x CC030169 (1-57)

Qy 7 ProlaPProAArgLeuPheAlaCySeSerProProAlaSerGinPro 24

Db 54 CCGTGGCCCCCGCGACGCTCTCGGCGTATGCTCTCCCGGCAATGTGGCGG 1

## RESULT 43

CC031476 57 bp DNA linear GSS 01-APR-2003

LOCUS CC031476/c 3591.1.125.1.B11.2EL\_Y.1 3591 - RescuMu Grid P Zea mays genomic.

DEFINITION genomic survey sequence.

ACCESSION CC031476

VERSION CC031476.1 GI:29446367

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 57)

Walbot, V.

Maize genomic sequences found using engineered RescuMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 3591\_1.125.1 row: 15

Class: transposon-tagged.

Location/Qualifiers

1..57

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="3591 - RescuMu Grid P"

/note="Organ: leaf; Vector: RescuMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescuMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

## Alignment Scores:

Pred. No.: 6.69e+05 Length: 57  
 Score: 42.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 9  
 Query Match: 1.52% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC034222 (1-57)

Qy 7 ProAlaProAArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24  
 Db 54 CCGTGCCTCCCGCCGCGAGCCTCTCGGCGTGTCTCTCCCGGCGCATGTGCGCG 1

## RESULT 44

LOCUS CC034222/c

DEFINITION 3591\_1\_67\_1.H02.2EL\_Y.1 3591 - RescuemU Grid P Zea mays genomic,  
 genomic survey sequence.

ACCESSION CC034222

VERSION CC034222.1 GI:29449113

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 57)

AUTHORS Walbot, V.

JOURNAL Maize genomic sequences found using engineered RescuemU transposon

COMMENT Unpublished (2001)

CONTACT Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 723 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.

Plate: 3591\_1\_67\_1 row: 36

Class: transposon-tagged.

Location/Qualifiers

source

1..57  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="3591 - RescuemU Grid P"  
 /note="Organ: leaf; Vector: RescuemU (engineered from  
 Bluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescuemU is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescuemU, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescuemU', 'Grid P was grown at Molokai in 2002. DNA was  
 extracted from leaf strips, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

## ORIGIN

## Alignment Scores:

Pred. No.: 6.69e+05 Length: 57  
 Score: 42.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 9  
 Query Match: 1.52% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC034222 (1-57)

Qy 7 ProAlaProAArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24  
 Db 54 CCGTGCCTCCCGCCGCGAGCCTCTCGGCGTGTCTCTCCCGGCGCATGTGCGCG 1

## RESULT 45

LOCUS CC034238/c

DEFINITION 3591\_1\_67\_1.H02.2EL\_Y.1 3591 - RescuemU Grid P Zea mays genomic,  
 genomic survey sequence.

ACCESSION CC034238

VERSION CC034238.1 GI:29449129

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 57)

AUTHORS Walbot, V.

JOURNAL Maize genomic sequences found using engineered RescuemU transposon

COMMENT Unpublished (2001)

CONTACT Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 723 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.

Plate: 3591\_1\_67\_1 row: 36

Class: transposon-tagged.

Location/Qualifiers

1..57  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="3591 - RescuemU Grid P"  
 /note="Organ: leaf; Vector: RescuemU (engineered from  
 Bluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescuemU is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescuemU, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescuemU', 'Grid P was grown at Molokai in 2002. DNA was  
 extracted from leaf strips, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

## ORIGIN

## Alignment Scores:

Pred. No.: 6.69e+05 Length: 57  
 Score: 42.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 9  
 Query Match: 1.52% Indels: 0  
 DB: 28 Gaps: 0

US-08-864-955-2 (1-523) x CC034238 (1-57)

Qy 7 ProAlaProAArgLeuLeuPheAlaCysSerProProAlaSerGlnPro 24  
 Db 54 CCGTGCCTCCCGCCGCGAGCCTCTCGGCGTGTCTCTCCCGGCGCATGTGCGCG 1

Mon Sep 20 10:36:38 2004

Search completed: September 9, 2004, 21:40:48  
Job time : 2517 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2004, 20:40:24 ; Search time 86 Seconds

(without alignments)  
3374.876 Million cell updates/sec

Title: US-08-864-955-2

Perfect score: 2769  
Sequence: 1 MEGSPAPRRLLFACSPFP.....SRTWAGKSKRMYSRLKYL 523

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 864424

Minimum DB seq length: 10  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.model -DSV=xlh  
-Q=/cgn2\_1/USPTO.spool/US08864955.runtac 07092004\_144931\_24504/app.query.fasta\_1.711  
-DB=Issued Patents.NA -OPMT=fastab -SUFTX=tni -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=45  
-MOE=LOCAL -OUTENT=plo -NORM=ext -HEAPSIZE=500 -MINLEN=10 -MAXLEN=60  
-USR=US08864955 @CGN 1.1 54 @runtac 07092004\_144931\_24504 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFBLOCK=100 -LONELOG  
-DEVTIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents.NA:\*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	3.0	49	2	US-08-677-298-9
2	48	1.7	53	2	US-08-670-175-3
3	47	1.7	54	4	US-09-479-645A-184
4	47	1.7	54	4	US-09-479-645A-185
5	42.5	1.5	34	4	US-09-636-215-831
6	42	1.5	34	4	US-09-685-166A-831
7	42	1.5	40	3	US-09-023-082A-9
8	42	1.5	40	3	US-09-248-998-9
9	42	1.5	48	6	5240847-31
10	42	1.5	53	2	US-08-483-636-43
11	42	1.5	53	2	US-08-483-632-43
12	42	1.5	53	2	US-08-483-632-43

13	42	1.5	53	3	US-09-275-850-266	Sequence 266, App
14	42	1.5	54	2	US-08-841-178-3	Sequence 3, Appl
15	41.5	1.5	48	4	US-09-119-507B-78	Sequence 78, Appl
16	41.5	1.5	48	4	US-09-119-507B-79	Sequence 79, Appl
17	41.5	1.5	48	4	US-08-897-556A-78	Sequence 78, Appl
18	41.5	1.5	48	4	US-08-897-556A-79	Sequence 79, Appl
19	41.5	1.5	48	4	US-09-547-693-78	Sequence 78, Appl
20	41.5	1.5	48	4	US-09-547-693-79	Sequence 79, Appl
21	41.5	1.5	60	4	US-09-128-354-15	Sequence 15, Appl
22	41.5	1.5	60	4	US-09-128-354-16	Sequence 16, Appl
23	41.5	1.5	42	1	US-08-375-116A-39	Sequence 39, Appl
24	41.5	1.5	48	4	US-08-840-713-28	Sequence 28, Appl
25	41.5	1.5	57	3	US-09-538-709-1170	Sequence 1170, Ap
26	41.5	1.5	60	3	US-09-076-761-9	Sequence 9, Appl
27	41.5	1.5	60	3	US-09-253-025-22	Sequence 22, Appl
28	40.5	1.5	60	4	US-09-734-188-22	Sequence 22, Appl
29	40.5	1.5	55	4	US-09-357-740-17	Sequence 17, Appl
30	40	1.4	24	2	US-08-859-998-962	Sequence 962, App
31	40	1.4	24	4	US-09-225-928-962	Sequence 962, App
32	40	1.4	24	4	US-09-225-201B-962	Sequence 962, App
33	40	1.4	36	4	US-09-043-959A-11	Sequence 11, Appl
34	40	1.4	37	4	US-09-027-287-12	Sequence 12, Appl
35	40	1.4	37	4	US-09-027-287-16	Sequence 16, Appl
36	40	1.4	37	4	US-09-252-656B-12	Sequence 12, Appl
37	40	1.4	37	4	US-09-252-656B-16	Sequence 16, Appl
38	40	1.4	37	4	US-09-523-323-12	Sequence 12, Appl
39	40	1.4	37	4	US-09-523-323-16	Sequence 16, Appl
40	40	1.4	38	1	US-08-44E-050-13	Sequence 13, Appl
41	40	1.4	38	1	US-08-204-691-13	Sequence 13, Appl
42	40	1.4	42	4	US-09-119-507B-86	Sequence 86, Appl
43	40	1.4	42	4	US-08-897-556A-86	Sequence 86, Appl
44	40	1.4	44	1	US-09-547-693-86	Sequence 86, Appl
45	40	1.4	44	1	US-08-463-090B-13	Sequence 13, Appl
			48	4	US-09-119-507B-88	Sequence 88, Appl

## ALIGNMENTS

RESULT 1  
US-08-677-298-9  
Sequence 9, Application US/08677298  
Patent No. 5863729  
GENERAL INFORMATION:  
APPLICANT: PAMICA-WORMS, Helen  
TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1  
TITLE OF INVENTION: KINASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/677,298  
FILING DATE: 09-JUL-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Caruthers, Jennie M.  
REGISTRATION NUMBER: 34,464  
REFERENCE/DOCKET NUMBER: 9-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49 base pairs  
TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer"
; HYPOTHETICAL: NO
; US-08-677-298-9

Alignment Scores:
Pred. No.: 0.461 Length: 49
Score: 83.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 3.00% Indels: 0
DB: 2 Gaps: 0

US-08-864-955-2 (1-523) x US-08-677-298-9 (1-49)
Qy 427 ValPheHisCysGluPheSerSerGluArgGlyProArgMetCysArg 442
Db 2 GTGTCACCTCCTGAATTCCTCTCGAGAGGGGCCCGGATGCGCCG 49

RESULT 2
; Sequence 3, Application US/08670175
; Patent No. 5854081
; GENERAL INFORMATION:
; APPLICANT: LINDEN, JOEL
; APPLICANT: TAYLOR, HEIDI
; APPLICANT: ROBEVA, ANNA
; APPLICANT: WOODARD, ROBIN
; APPLICANT: JIN, XIAOWEI
; TITLE OF INVENTION: STABLE EXPRESSION OF HUMAN ADENOSINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,175
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 494-176-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA PRIMER"
; US-08-670-175-3

Alignment Scores:
Pred. No.: 2.07e+03 Length: 53
Score: 48.00 Matches: 8
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 53.33% Mismatches: 4

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Query Match: 1.73% Indels: 0
DB: 2 Gaps: 0

US-08-864-955-2 (1-523) x US-08-670-175-3 (1-53)
Qy 489 HisHisGluAspPheLeuGluAspLeuLeuGlyPheArgThrHis 503
Db 53 CATCACCATGACTACACAGAGACGATGACACAGGCTTGAAGCGCT 9

RESULT 3
; Sequence 184, Application US/09479645A
; Patent No. 6489141
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; FILE REFERENCE: 210338.0001/1US
; CURRENT APPLICATION NUMBER: US/09/479,645A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: Patent in Ver. 2.0
; LENGTH: 54
; SEQ ID NO 184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His(CAC)5
; US-09-479-645A-184

Alignment Scores:
Pred. No.: 2.7e+03 Length: 54
Score: 47.00 Matches: 8
Percent Similarity: 70.59% Conservative: 4
Best Local Similarity: 47.06% Mismatches: 5
Query Match: 1.70% Indels: 0
DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-479-645A-184 (1-54)
Qy 156 ArgGlyCysLeuHisSerHisGlyLeuGlnGluGlyLysAspLeuPheThr 172
Db 1 CGGGGTACATGACACACACACACACACACAGGCGAGGAACTGTTCAC 51

RESULT 4
; Sequence 185, Application US/09479645A
; Patent No. 6489141
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; FILE REFERENCE: 210338.0001/1US
; CURRENT APPLICATION NUMBER: US/09/479,645A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 185

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US-08-864-955-2 (1-523) x US-09-636-215-831 (1-34)
Oy          90 ProLeaPseRlyGluAsnIeuGlusnPro 100
Db          1 CGCCTCGAGATTACGAAAATACAGCATCA 33

RESULT 7
US-09-685-166A-831
; Sequence 831, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Uiang, Yungui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C021
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-685-166A-831

Alignment Scores:
Pred. No.:      4,14e+03      Length:      34
Score:          42.00         Matches:       7
Percent Similarity: 90.91%    Conservative:   3
Best Local Similarity: 63.64% Mismatches:     1
Query Match:    1.52%        Indels:        0
DB:             Gaps:        0

US-08-864-955-2 (1-523) x US-09-685-166A-831 (1-34)
Oy          90 ProLeaPseRlyGluAsnIeuGlusnPro 100
Db          1 CGCCTCGAGATTACGAAAATACAGCATCA 33

ALIGNMENT SCORES:
Pred. No.:      4,14e+03      Length:      34
Score:          42.00         Matches:       7
Percent Similarity: 90.91%    Conservative:   3
Best Local Similarity: 63.64% Mismatches:     1
Query Match:    1.52%        Indels:        0
DB:             Gaps:        0

US-08-864-955-2(1-523) X US-09-685-166A-831 (1-34)
Pred. No.:      4,14e+03      Length:      34
Score:          42.00         Matches:       7
Percent Similarity: 90.91%    Conservative:   3
Best Local Similarity: 63.64% Mismatches:     1
Query Match:    1.52%        Indels:        0
DB:             Gaps:        0

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Oy 90 ProLeuAspSerIyGluAsnIleuGIuAenPro 100  
 Db 1 CCGCTGAGAGATAGAGAAATGAGACATCC 33  
 RESULT 8  
 US-09-023-082A-9/c  
 Sequence 9, Application US/09023082A  
 Patent No. 6077692  
 GENERAL INFORMATION:  
 APPLICANT: RUBEN, STEVEN M.  
 APPLICANT: JIMENEZ, PABLO  
 APPLICANT: DUAN, D. ROXANNE  
 APPLICANT: RAMPY, MARK A.  
 APPLICANT: MENDRICK, DONNA  
 APPLICANT: ZHANG, JUN  
 APPLICANT: NI, JIAN  
 APPLICANT: MOORE, PAUL A.  
 APPLICANT: COLEMAN, TIMOTHY A.  
 APPLICANT: GRUBER, JOACHIM R.  
 APPLICANT: DILON, PATRICK J.  
 APPLICANT: GENTZ, REINER L.  
 TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2  
 NUMBER OF SEQUENCES: 148  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
 STREET: 1100 NEW YORK AVE, NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/023,082A  
 FILING DATE: 13-FEB-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/01790  
 FILING DATE: 14-FEB-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/461,195  
 FILING DATE: 05-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/023,852  
 FILING DATE: 13-AUG-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/039,045  
 FILING DATE: 28-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/862,432  
 FILING DATE: 23-MAY-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/910,875  
 FILING DATE: 13-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/055,561  
 FILING DATE: 13-AUG-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.0360008/EKS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-09-023-082A-9  
 Alignment Scores:  
 Pred. No.: 5.4e+03 Length: 40  
 Score: 42.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4  
 Best Local Similarity: 50.00% Mismatches: 1  
 Query Match: 1.52% Indels: 0  
 DB: 3 Gaps: 0  
 US-08-864-955-2 (1-523) x US-09-023-082A-9 (1-40)  
 Oy 384 CysArgTyrProTyrGluTyrGluGly 393  
 Db 39 TGTCAGTATCCATTCCATGATGAGGCGGA 10  
 RESULT 9  
 US-09-248-998-9/c  
 Sequence 9, Application US/09248998  
 Patent No. 6539879  
 GENERAL INFORMATION:  
 APPLICANT: Jimenez, Pablo  
 APPLICANT: Rampy, Mark A.  
 APPLICANT: Mendrick, Donna  
 APPLICANT: Russell, Deborah  
 APPLICANT: Louie, Arthur  
 TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2  
 FILE REFERENCE: 1488.1060002  
 CURRENT APPLICATION NUMBER: US/09/248,998  
 CURRENT FILING DATE: 1999-02-12  
 EARLIER APPLICATION NUMBER: US 60/114,387  
 EARLIER FILING DATE: 30-DEC-1998  
 EARLIER APPLICATION NUMBER: US 60/074,585  
 EARLIER FILING DATE: 13-FEB-1998  
 NUMBER OF SEQ ID NOS: 148  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 9  
 LENGTH: 40  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-248-998-9  
 Alignment Scores:  
 Pred. No.: 5.4e+03 Length: 40  
 Score: 42.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4  
 Best Local Similarity: 50.00% Mismatches: 1  
 Query Match: 1.52% Indels: 0  
 DB: 4 Gaps: 0  
 US-08-864-955-2 (1-523) x US-09-248-998-9 (1-40)  
 Oy 384 CysArgTyrProTyrGluTyrGluGly 393  
 Db 39 TGTCAGTATCCATTCCATGATGAGGCGGA 10  
 RESULT 10  
 US-08-864-955-2 (1-523) x US-09-248-998-9 (1-40)  
 Patent No. 5240847  
 APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBOURG;  
 ZOPHEL, ANDREAS; KREYER, EDELTRAUD; MAURER-FOGY, INGRID;  
 NITCHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HUPPMANN, RUDOLF  
 TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE  
 (HMN-SOD)  
 NUMBER OF SEQUENCES: 34  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/167,261  
 FILING DATE: 11-MAR-1988  
 SEQ ID NO: 31  
 LENGTH: 48  
 5240847-31

BEST LOCAL STABILITY:

3 LeuglyproserpproAlaproargargleu 1

3 LeuglyproserprroAlaProargargLeuLeu 1  
QY

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Db
1 CTTGTCCTCCCTCCCGACCTCGAGATCCTC 33
|||||
RESULT 13
US-09-275-850-266
; Sequence 266, Application US/09275850A
; Patent No. 6261774
; GENERAL INFORMATION:
; APPLICANT: Patratlis, Nikos
; APPLICANT: Shtatland, Timur
; APPLICANT: Gold, Larry
; APPLICANT: Shtatland, Timur
; APPLICANT: Shtatland, Timur
; TITLE OF INVENTION: Truncation SELEX Method
; FILE REFERENCE: NEX 79
; CURRENT APPLICATION NUMBER: US/09/275,850A
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 53
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified Base
; LOCATION: (1)..(53)
; OTHER INFORMATION: All pyrimidines are 2'-F
US-09-275-850-266

Alignment Scores:
Pred. No.: 8.56e+03 Length: 53
Score: 42.00 Matches: 6
Percent Similarity: 91.67% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 1.52% Indels: 0
Gaps: 0
DB: 3

US-08-864-955-2 (1-523) x US-09-275-850-266 (1-53)
Qy
100 PromeTArGArGleuHleuSerLeuProGlnLysLeu 111
|||||
Db
12 CCGTMAAGACGGCUCUUAUUUGUCCGACGACGACUC 47
|||||
RESULT 14
US-08-861-178-3/C
; Sequence 3, Application US/08841178
; Patent No. 5880275
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; TITLE OF INVENTION: Synthetic Plant Genes and Method for Preparation
; FILE REFERENCE: 38-21(151197A
; CURRENT APPLICATION NUMBER: US/08/841,178
; CURRENT FILING DATE: 1997-04-29
; EARLIER APPLICATION NUMBER: US 08/433,111
; EARLIER FILING DATE: 1995-05-03
; EARLIER APPLICATION NUMBER: US 07/959,506
; EARLIER FILING DATE: 1992-10-09
; EARLIER APPLICATION NUMBER: US 07/476,661
; EARLIER FILING DATE: 1990-02-12
; EARLIER APPLICATION NUMBER: US 07/315,355
; EARLIER FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: mutagenesis
US-08-841-178-3
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Alignment Scores:
Pred. No.: 8.83e+03 Length: 54
Score: 42.00 Matches: 7
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 46.67% Mismatches: 5
Query Match: 1.52% Indels: 0
Gaps: 0
DB: 2

US-08-864-955-2 (1-523) x US-08-841-178-3 (1-54)
Qy
8 AlArProArGArGleuPheAlaCySerProProAlaSerGln 22
|||||
Db
49 TCTCTCTCTCGTGTACTTCAAGCTGCACCTCCCTCTCTGCT 5
|||||
RESULT 15
US-09-119-507B-78
; Sequence 78, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-78

Alignment Scores:
Pred. No.: 8.19e+03 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
Query Match: 1.50% Indels: 7
Gaps: 1
DB: 4

US-08-864-955-2 (1-523) x US-09-119-507B-78 (1-48)
Qy
5 ProSerProAlaProArGArGleuPheAlaCySerProProAlaSerGlnPro 24
|||||
Db
7 CCTTACCACTCCCA-----TCTCCCACTCCCTCCCTCCCA 45
|||||
RESULT 16
US-09-119-507B-79/C
; Sequence 79, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-79

Alignment Scores:
Pred. No.: 8.19e+03 Length: 48
Score: 41.50 Matches: 9
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 3
```

Query Match: 1.50% Indels: 7  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-119-507B-79 (1-48)

Qy 5 ProSePrOAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
DB 39 CCATCTCCCCCAGCT-----TCCCTCCACCATACACCCACCT 1

RESULT 17  
US-08-897-556A-78  
Sequence 78, Application US/08897556A  
Patent No. 6570062  
GENERAL INFORMATION:  
APPLICANT: KIELSZESKI, MARCIA J.  
TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
CORRESPONDENCE ADDRESSES: 106  
NUMBER OF SEQUENCES: 106  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,556A  
FILING DATE: 21-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: OHU-02908  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-08-897-556A-78

Alignment Scores:  
Pred. No.: 8.19e+03 Length: 48  
Score: 41.50 Matches: 9  
Percent Similarity: 50.00% Conservative: 1  
Best Local Similarity: 45.00% Mismatches: 3  
Query Match: 1.50% Indels: 7  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-08-897-556A-78 (1-48)

Qy 5 ProSePrOAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
DB 7 CCHTCCACCTCCA-----TCTCCCACTTCCCTCCACCA 45

RESULT 18  
US-08-897-556A-79/c  
Sequence 79, Application US/08897556A  
Patent No. 6570062  
GENERAL INFORMATION:  
APPLICANT: KIELSZESKI, MARCIA J.  
TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS

NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,556A  
FILING DATE: 21-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: OHU-02908  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-08-897-556A-79

Alignment Scores:  
Pred. No.: 8.19e+03 Length: 48  
Score: 41.50 Matches: 9  
Percent Similarity: 50.00% Conservative: 1  
Best Local Similarity: 45.00% Mismatches: 3  
Query Match: 1.50% Indels: 7  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-08-897-556A-79 (1-48)

Qy 5 ProSePrOAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
DB 39 CCATCTCCCCCAGCT-----TCCCTCCACCATACACCCACCT 1

RESULT 19  
US-09-547-693-78  
Sequence 78, Application US/09547693  
Patent No. 6639050  
GENERAL INFORMATION:  
APPLICANT: KIELSZESKI, Marcia  
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
TITLE OF INVENTION: Glycoproteins  
FILE REFERENCE: OHU-04088  
CURRENT APPLICATION NUMBER: US/09/547,693  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 78  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthetic

US-09-547-693-78

Alignment Scores:  
Pred. No.: 8.19e+03 Length: 48  
Score: 41.50 Matches: 9

Percent Similarity: 50.00% Conservative: 1  
Best Local Similarity: 45.00% Mismatches: 3  
Query Match: 1.50% Indels: 7  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-547-693-78 (1-48)

Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
Db 7 CCTTCACACCTCCA-----TCTCCCTCACCATCCTCCACCA 45

RESULT 20  
US-09-547-693-79/c  
Sequence 79, Application US/09547693  
Patent No. 6639050  
GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia  
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
FILE REFERENCE: OH0-04089  
CURRENT APPLICATION NUMBER: US/09/547,693  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 79  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthetic  
US-09-547-693-79

Alignment Scores:  
Pred. No.: 8.19e+03 Length: 48  
Score: 41.50 Matches: 9  
Percent Similarity: 50.00% Conservative: 1  
Best Local Similarity: 45.00% Mismatches: 3  
Query Match: 1.50% Indels: 7  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-547-693-79 (1-48)

Qy 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
Db 39 CCATCTCCCTCCACCT-----TCCCTCCACCATCCTCCACCACT 1

RESULT 21  
US-09-128-354-15

Sequence 15, Application US/09128354  
Patent No. 6337200  
GENERAL INFORMATION:

APPLICANT: Morin, Gregg B.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
FILE REFERENCE: 015389-003310US  
CURRENT APPLICATION NUMBER: US/09/128,354  
CURRENT FILING DATE: 1998-08-03

EARLIER APPLICATION NUMBER: US 08/851,843  
EARLIER FILING DATE: 1997-05-06  
EARLIER APPLICATION NUMBER: US 08/854,050  
EARLIER FILING DATE: 1997-05-09  
EARLIER APPLICATION NUMBER: US 08/911,312  
EARLIER FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: US 08/912,951  
EARLIER FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: US 08/915,503  
EARLIER FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
EARLIER FILING DATE: 1997-10-01  
EARLIER APPLICATION NUMBER: WO PCT/US97/17865  
EARLIER FILING DATE: 1997-10-01  
EARLIER APPLICATION NUMBER: US 08/974,549

EARLIER FILING DATE: 1997-11-19  
EARLIER APPLICATION NUMBER: US 08/974,584  
EARLIER FILING DATE: 1997-11-19  
EARLIER APPLICATION NUMBER: US 09/052,864  
EARLIER FILING DATE: 1998-03-31  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: RT3A/5 oligo  
US-09-128-354-15

Alignment Scores:  
Pred. No.: 1.18e+04 Length: 60  
Score: 41.50 Matches: 10  
Percent Similarity: 54.55% Conservative: 2  
Best Local Similarity: 45.45% Mismatches: 5  
Query Match: 1.50% Indels: 5  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-128-354-15 (1-60)

Qy 4 GlyProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGln 23  
Db 6 GCCCGGCGCCCGCCACACGC-----TAGCTGCTCCGCGACACAGAG 50

Qy 24 Proval 25  
Db 51 CCCCTG 56

RESULT 22

US-08-375-116A-39/c  
Sequence 39, Application US/08375116A  
Patent No. 5631146  
GENERAL INFORMATION:

APPLICANT: Huizenga, David E.  
TITLE OF INVENTION: DNA APTAMERS AND CATALYSTS THAT BIND  
TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE-5'-PHOSPHATES AND METHODS FOR

NUMBER OF SEQUENCES: 136  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,116A  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/266001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 961/7 542-5070  
TELEFAX: 617/ 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO. 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-08-375-116A-39

Alignment Scores:

Pred. No.:	7.41e+03	Length:	42
Score:	41.00	Matches:	6
Percent Similarity:	53.85%	Conservative:	1
Best Local Similarity:	46.15%	Mismatches:	6
Query Match:	1.48%	Indels:	0
DB:	1	Gaps:	0

US-08-864-955-2 (1-523) x US-08-375-116A-39 (1-42)

QY 477 GlnSerTrCysGluProPheSerTrpArgProMetHis 489  
Db 39 GAACAGGTGTGCTTCTCCCAATACTCCCAAGCAC 1

RESULT 23

US-08-840-713-28/c

Sequence 28, Application US/08840713

Patent No. 6498233

GENERAL INFORMATION:

APPLICANT: WELLS, Winfried, Dr.

APPLICANT: FOYMINAYA, Jesus

TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

STREET: 655 15th St., N.W., Suite 330 - G St. Lobby

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/840,713

FILING DATE: 25-APR-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kites, Monica Chin

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: 1614-7014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638 - 5000

TELEFAX: (202) 638 - 4810

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-840-713-28

Alignment Scores:

Pred. No.:	9.22e+03	Length:	48
Score:	41.00	Matches:	9
Percent Similarity:	75.00%	Conservative:	3
Best Local Similarity:	56.25%	Mismatches:	0
Query Match:	1.48%	Indels:	4
DB:	4	Gaps:	1

US-08-864-955-2 (1-523) x US-08-840-713-28 (1-48)

QY 269 ArgSerValLeuLysArgProGluArgSerGlnGluSerProPro 284  
Db 39 AGGACAGTCTCTCCGAGACCG-----GAGGACAGTCTCTCG 4

RESULT 24

US-09-538-709-1170

Sequence 1170, Application US/09538709

Patent No. 6468749

GENERAL INFORMATION:

APPLICANT: Ulanovsky, et al

TITLE OF INVENTION: SEQUENCE-DEPENDENT GENE SORTING TECHNIQUES

FILE REFERENCE: 540579-2006

CURRENT APPLICATION NUMBER: US/09/538,709

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1311

SOFTWARE: Patent In version 3.0

SEQ ID NO 1170

LENGTH: 49

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Adaptor

US-09-538-709-1170

Alignment Scores:

Pred. No.:	9.54e+03	Length:	49
Score:	41.00	Matches:	8
Percent Similarity:	71.43%	Conservative:	2
Best Local Similarity:	57.14%	Mismatches:	4
Query Match:	1.48%	Indels:	0
DB:	4	Gaps:	0

US-08-864-955-2 (1-523) x US-09-538-709-1170 (1-49)

QY 441 CysArgTrpValArgGluArgAspArgLeuGluArgLysGlyArg 454  
Db 4 TGCAGTACGTGTGATCCGCGCGGAGTACGCGCCGAAGCAC 45

RESULT 25

US-09-076-761-9/c

Sequence 9, Application US/09076761

Patent No. 6190669

GENERAL INFORMATION:

APPLICANT: NORRIGA, Fernando

APPLICANT: SATEIN, Marcelo B.

APPLICANT: LEVINE, Myron M.

TITLE OF INVENTION: ATTENUATED MUTANTS OF SALMONELLA

TITLE OF INVENTION: WHICH CONSTITUTIVELY EXPRESS THE

TITLE OF INVENTION: V1 ANTIGEN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/076,761

FILING DATE: 13-MAY-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: A-7140

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 57 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; US-09-076-761-9

Alignment Scores:
Pred. No.: 1.22e+04 length: 57
Score: 41.00 Matches: 7
Percent Similarity: 64.71% Conservative: 4
Best Local Similarity: 41.18% Mismatches: 6
Query Match: 1.48% Indels: 0
DB: 3 Gaps: 0

US-08-864-955-2 (1-523) x US-09-076-761-9 (1-57)

QY 271 ValLeuLYaRgPProGIuAArgSerGIuGIuSerProProGIaSerGIuThr 287
DB 54 ATCATTCGAGGCCAGAAATGATGAAACCTCATCCGGGCCGCGATCCACC 4

RESULT 26
US-09-253-025-22
; Sequence 22, Application US/09253025
; Patent No. 6200758
; GENERAL INFORMATION:
; APPLICANT: Richardson Ph.D., Mary Ann
; APPLICANT: Goldman, Assistant Counsel, Robin A.
; APPLICANT: New York State Office of Mental Health
; APPLICANT: Nathan S. Kline Institute for Psychiatric Research
; TITLE OF INVENTION: PAH
; FILE REFERENCE: Kline Inst.
; CURRENT APPLICATION NUMBER: US/09/253,025
; CURRENT FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-253-025-22

Alignment Scores:
Pred. No.: 1.33e+04 length: 60
Score: 41.00 Matches: 9
Percent Similarity: 45.00% Conservative: 0
Best Local Similarity: 45.00% Mismatches: 5
Query Match: 1.48% Indels: 1
DB: 3 Gaps: 1

US-08-864-955-2 (1-523) x US-09-253-025-22 (1-60)

QY 5 ProSerProAlaProArgLeuPheAlaCySerProProProAlaSerGIuPro 24
DB 7 CCGCGCCCGCCGCC-----GTCCCGCCCGCCCGCCGCCGCCACCA 48

RESULT 27
US-09-734-188-22
; Sequence 22, Application US/09734188
; Patent No. 6649345
; GENERAL INFORMATION:
; APPLICANT: Richardson Ph.D., Mary Ann
; APPLICANT: Goldman, Assistant Counsel, Robin A.
; APPLICANT: New York State Office of Mental Health
; APPLICANT: Nathan S. Kline Institute for Psychiatric Research
; TITLE OF INVENTION: PAH
; FILE REFERENCE: Kline Inst.
; CURRENT APPLICATION NUMBER: US/09/734,188
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/253,025
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 60
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-734-188-22

Alignment Scores:
Pred. No.: 1.33e+04 length: 60
Score: 41.00 Matches: 9
Percent Similarity: 45.00% Conservative: 0
Best Local Similarity: 45.00% Mismatches: 5
Query Match: 1.48% Indels: 6
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-734-188-22 (1-60)

QY 5 ProSerProAlaProArgLeuPheAlaCySerProProProAlaSerGIuPro 24
DB 53 CCATCCCGCAGCC-----CTCCCGCATTCACCGCGCC 21

QY 25 ValValIysAlaLeu 29
DB 20 ATCACAAGCGGATC 6

RESULT 29
US-08-859-998-962/C
; Sequence 962, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jekhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
```

;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 2200 Sand Hill Road, Suite 100  
;; CITY: Menlo Park  
;; STATE: CA  
;; COUNTRY: US  
;; ZIP: 94025  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/859,998  
;; FILING DATE: 21-MAY-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Field, Bret E.  
;; REGISTRATION NUMBER: 37,620  
;; REFERENCE/DOCKET NUMBER: 09096/002001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-322-5070  
;; TELEFAX: 415-854-0875  
;; INFORMATION FOR SEQ ID NO: 962:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 24 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; FEATURE:  
;; OTHER INFORMATION: oligonucleotide primer  
;;  
US-08-864-955-2 (1-523) x US-08-859-998-962 (1-24)  
;;  
Alignment Scores:  
Pred. No.: 3.75e+03 Length: 24  
Score: 40.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.44% Indels: 0  
DB: 2 Gaps: 0  
;;  
QY 499 LysPheArgThrLysSerArgThr 506  
DB 24 AAGTTCGACCAAGAGCCGAC 1  
;;  
RESULT 30  
US-09-225-928-962/c  
; Sequence 962, Application US/09225928  
; Patent No. 6352829  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,998  
; FILING DATE: 21-MAY-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/859,998  
; FILING DATE: 21-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Field, Bret E.  
; REGISTRATION NUMBER: 37,620  
; REFERENCE/DOCKET NUMBER: 09096/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-322-5070  
; TELEFAX: 415-854-0875  
; INFORMATION FOR SEQ ID NO: 962:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
; SEQUENCE DESCRIPTION: SEQ ID NO: 962:  
US-09-225-928-962  
;;

;;  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/225,928  
;; FILING DATE: 05-Jan-1999  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/859,998  
;; FILING DATE: 21-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Field, Bret E.  
;; REGISTRATION NUMBER: 37,620  
;; REFERENCE/DOCKET NUMBER: 09096/002001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-322-5070  
;; TELEFAX: 415-854-0875  
;; INFORMATION FOR SEQ ID NO: 962:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 24 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; FEATURE:  
;; OTHER INFORMATION: oligonucleotide primer  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 962:  
US-08-864-955-2 (1-523) x US-09-225-928-962 (1-24)  
;;  
Alignment Scores:  
Pred. No.: 3.75e+03 Length: 24  
Score: 40.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.44% Indels: 0  
DB: 4 Gaps: 0  
;;  
QY 499 LysPheArgThrLysSerArgThr 506  
DB 24 AAGTTCGACCAAGAGCCGAC 1  
;;  
RESULT 31  
US-09-225-201B-962/c  
; Sequence 962, Application US/09225201B  
; Patent No. 6489455  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/225,201B  
; FILING DATE: 05-Jan-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,998  
; FILING DATE: 21-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Field, Bret E.  
; REGISTRATION NUMBER: 37,620  
; REFERENCE/DOCKET NUMBER: 09096/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-322-5070  
; TELEFAX: 415-854-0875  
; INFORMATION FOR SEQ ID NO: 962:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
; SEQUENCE DESCRIPTION: SEQ ID NO: 962:  
US-09-225-928-962  
;;

```

? REGISTRATION NUMBER: 37,620
? REFERENCE/POCKET NUMBER: 09096/002001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-322-5070
? TELEFAX: 415-884-0875
? INFORMATION FOR SEQ ID NO: 962:
? SEQUENCE CHARACTERISTICS
? LENGTH: 24 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
? OTHER INFORMATION: oligonucleotide primer
? SEQUENCE DESCRIPTION: SEQ ID NO: 962:
? US-09-225-2013-962

```

Prasanna's Score:	3.75e+3	24
Pred. No.:	40.00	Matches:
Score:	100.00	Conservative:
Percent Similarity:	100.00	Mismatches:
Best Local Similarity:	1.44	Indels:
Query Match:	4	Gaps:
DB:	0	0

US-08-864-955-2 (1-523) X US-09-225-201B-962 (1-24)

Oy	499	LysPheArgThrLysSerArgThr	506
Db	24	AAgTCCGACCAAGAGCCGACC	1

RESULT 32  
 US-09-043-959A-11/c  
 : Sequence 11, Application US/09043959A  
 : Patent No. 6478248  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Krell, Siegfried  
 : Geber, Annegret  
 :  
 : TITLE OF INVENTION: Process and agent for detecting antibodies against  
 : Treponema pallidum  
 :  
 : NUMBER OF SEQUENCES: 17  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Krell, Siegfried  
 : STREET: 15 Immermannstr.  
 : CITY: Magdeburg  
 : STATE: Sachsen-Anhalt  
 : COUNTRY: Germany  
 : ZIP: 39108  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.50 inch, 1.4 Mb storage  
 :  
 : COMPUTER: IBM compatible  
 : OPERATING SYSTEM: Microsoft Windows Millennium Edition  
 : SOFTWARE: Microsoft Wordpad  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/043,959A  
 : FILING DATE: 30-Mar-1998  
 :  
 : CLASSIFICATION: not available  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/EP 96/04249  
 : FILING DATE: 30-SEP-1996  
 :  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Salter, Michaelson  
 : REGISTRATION NUMBER: <Unknown>  
 : REFERENCE/DOCKET NUMBER: 01089  
 :  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: +001 401 861 1953  
 : TELEFAX: <Unknown>  
 : TELEX: <Unknown>  
 :  
 : INFORMATION FOR SEQ ID NO. 11:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 36 bases  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single

```

1 TOPOLOGY: linear
2 MOLECULE TYPE: other nucleic acid
3 DESCRIPTION: synthetic oligonucleotide with partial homology to genomic T
4 HYPOETHERICAL: no
5 ANTI-SENSE: no
6 FEATURE:
7 NAME/KEY: 5Primer TDN23-35
8 LOCATION: TREPAN34K:398-421
9 IDENTIFICATION METHOD: partial similarity with known sequence
10 OTHER INFORMATION: 5Primer with an adapter for BamHI
11 PUBLICATION INFORMATION:
12 AUTHORS: Gerder, A
13          Krell, S
14          Moenz, J
15 TITLE: Recombinant Treponema pallidum antigens in syphilis serology
16 JOURNAL: Immunobiology
17 VOLUME: 196
18 ISSUE: 5
19 PAGES: 535-549
20 DATE: 1990-1997
21 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
22 US-09-043-959A-11

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Alignment Score:	7.2e+03	Length:	3
Pred. No.:	40.00	Matches:	6
Score:	66.6%	Conservative:	0
Percent Similarity:	66.6%	Mismatches:	3
Best Local Similarity:	1.44%	Indels:	0
Query Match:	4	Gaps:	0
DB:			

US-08-864-955-2 (1-523) X US-09-043-959A-11 (1-36)

QY 16 CysSerProProProAlaSerGlnPro 24  
 |||||  
 Db 32 TgCTCTCCACCGCCCCCGCAGATCCA 6

```

RESULT 33
US-09-027-287-12
; Sequence 12, Application US/09027287A
; Patent No. 6479254
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ulrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488, 0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-027-287-12

Alignment Scores:
Pred. No.: 7.63e+03 Length: 37
Score: 40.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 1.44% Indels: 0  
DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-027-287-12 (1-37)

QY 485 TyTArGPrOmEtHsHs 490  
DB 8 TACCGTCATGCACAC 25

RESULT 34

US-09-027-287-16  
Sequence 16, Application US/09027287A  
Patent No. 6479254  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Ullrich, Stephen  
TITLE OF INVENTION: Apoptosis Inducing Molecule II  
FILE REFERENCE: 1488.0650004  
CURRENT APPLICATION NUMBER: US/09/027,287A  
CURRENT FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: US 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: US 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: US 60/030,157  
EARLIER FILING DATE: 1996-10-31  
EARLIER APPLICATION NUMBER: US 60/013,923  
EARLIER FILING DATE: 1996-03-22  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-027-287-16

Alignment Scores:  
Pred. No.: 7.63e+03 Length: 37  
Score: 40.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.44% Indels: 0  
DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-027-287-16 (1-37)

QY 485 TyTArGPrOmEtHsHs 490  
DB 8 TACCGTCATGCACAC 25

RESULT 35

US-09-252-656B-12  
Sequence 12, Application US/09252656B  
Patent No. 6495520  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Zhang, Jun  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.0650006  
CURRENT APPLICATION NUMBER: US/09/252,656B  
CURRENT FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: US 60/075,409  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/027,287  
PRIOR FILING DATE: 1998-02-20

PRIOR APPLICATION NUMBER: US 09/003,886  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/013,923  
PRIOR FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-09-252-656B-12

Alignment Scores:  
Pred. No.: 7.63e+03 Length: 37  
Score: 40.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.44% Indels: 0  
DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-252-656B-12 (1-37)

QY 485 TyTArGPrOmEtHsHs 490  
DB 8 TACCGTCATGCACAC 25

RESULT 36

US-09-252-656B-16  
Sequence 16, Application US/09252656B  
Patent No. 6495520  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Zhang, Jun  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.0650006  
CURRENT APPLICATION NUMBER: US/09/252,656B  
CURRENT FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: US 60/075,409  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/027,287  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/013,923  
PRIOR FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-09-252-656B-16

Alignment Scores:  
Pred. No.: 7.63e+03 Length: 37  
Score: 40.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.44% Indels: 0  
DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-252-656B-16 (1-37)

QY 485 TyraGProMethisHis 490

DB 8 TACCGTCATGCACAC 25

RESULT 37

US-09-523-323-12

Sequence 12, Application US/09523323

Patent No. 6635743

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Yu, Guo-liang

APPLICANT: Ruben, Steven M.

APPLICANT: Ulrich, Stephen

APPLICANT: Zhai, Yifan

TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use

FILE REFERENCE: 1488.065000C

CURRENT APPLICATION NUMBER: US/09/523,323

CURRENT FILING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/168,380

EARLIER FILING DATE: 1999-12-02

EARLIER APPLICATION NUMBER: 60/148,326

EARLIER FILING DATE: 1999-08-11

EARLIER APPLICATION NUMBER: 60/142,657

EARLIER FILING DATE: 1999-07-06

EARLIER APPLICATION NUMBER: 60/137,457

EARLIER FILING DATE: 1999-06-04

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: 09/252,656

EARLIER FILING DATE: 1999-02-19

EARLIER APPLICATION NUMBER: 60/075,409

EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/027,287

EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/003,886

EARLIER FILING DATE: 1998-01-07

EARLIER APPLICATION NUMBER: 08/822,953

EARLIER FILING DATE: 1997-03-21

EARLIER APPLICATION NUMBER: 60/013,923

EARLIER FILING DATE: 1996-03-22

EARLIER APPLICATION NUMBER: 60/030,157

EARLIER FILING DATE: 1996-10-31

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 37

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: DNA Primer

US-09-523-323-12

Alignment Scores:

Pred. No.: 7.63e+03 Length: 37

Score: 40.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.44% Indels: 0

DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-523-323-12 (1-37)

QY 485 TyraGProMethisHis 490

DB 8 TACCGTCATGCACAC 25

RESULT 38

US-09-523-323-16

Sequence 16, Application US/09523323

Patent No. 6635743

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Yu, Guo-liang

APPLICANT: Ruben, Steven M.

APPLICANT: Ulrich, Stephen

APPLICANT: Zhai, Yifan

TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use

FILE REFERENCE: 1488.065000C

CURRENT APPLICATION NUMBER: US/09/523,323

CURRENT FILING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/168,380

EARLIER FILING DATE: 1999-12-02

EARLIER APPLICATION NUMBER: 60/148,326

EARLIER FILING DATE: 1999-08-11

EARLIER APPLICATION NUMBER: 60/142,657

EARLIER FILING DATE: 1999-07-06

EARLIER APPLICATION NUMBER: 60/137,457

EARLIER FILING DATE: 1999-06-04

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: 09/252,656

EARLIER FILING DATE: 1999-02-19

EARLIER APPLICATION NUMBER: 60/075,409

EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/027,287

EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/003,886

EARLIER FILING DATE: 1998-01-07

EARLIER APPLICATION NUMBER: 08/822,953

EARLIER FILING DATE: 1997-03-21

EARLIER APPLICATION NUMBER: 60/013,923

EARLIER FILING DATE: 1996-03-22

EARLIER APPLICATION NUMBER: 60/030,157

EARLIER FILING DATE: 1996-10-31

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 37

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: DNA Primer

US-09-523-323-16

Alignment Scores:

Pred. No.: 7.63e+03 Length: 37

Score: 40.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.44% Indels: 0

DB: 4 Gaps: 0

US-08-864-955-2 (1-523) x US-09-523-323-16 (1-37)

QY 485 TyraGProMethisHis 490

DB 8 TACCGTCATGCACAC 25

RESULT 39

US-08-445-050-13/c

Sequence 13, Application US/08445050

Patent No. 5763739

GENERAL INFORMATION:

APPLICANT: Blaeckberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lennart

APPLICANT: Herneil, Olle

APPLICANT: Lundberg, Lennart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5763739e1 Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,050  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-445-050-13

Alignment Scores:  
Pred. No.: 7.97e+03 Length: 38  
Score: 40.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 1.44% Indels: 0  
DB: 1 Gaps: 0

US-08-864-955-2 (1-523) x US-08-445-050-13 (1-38)

CY 451 GlyAsnGluTyrProLysLeuHisTyr 459  
DB 38 GGCGTGGAGTACCCCATGCTGCATAT 12

RESULT 40  
US-08-204-691-13/c  
Sequence 13, Application US/08204691  
Patent No. 5827683  
GENERAL INFORMATION:  
APPLICANT: Blackberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Hennell, Oile  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5827683e1 Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-204-691-13

Alignment Scores:  
Pred. No.: 7.97e+03 Length: 38  
Score: 40.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 1.44% Indels: 0  
DB: 1 Gaps: 0

US-08-864-955-2 (1-523) x US-08-204-691-13 (1-38)

CY 451 GlyAsnGluTyrProLysLeuHisTyr 459  
DB 38 GGCGTGGAGTACCCCATGCTGCATAT 12

RESULT 41  
US-09-119-507B-86  
Sequence 86, Application US/09119507B  
Patent No. 6548642  
GENERAL INFORMATION:  
APPLICANT: Kuliszewski, Marcia J.  
TITLE OF INVENTION: No. 6548642e1 Synthetic Genes for Plant Gums  
FILE REFERENCE: OHU-03417  
CURRENT APPLICATION NUMBER: US/09/119,507B  
CURRENT FILING DATE: 1998-07-20  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 86  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-119-507B-86

Alignment Scores:  
Pred. No.: 9.39e+03 Length: 42  
Score: 40.00 Matches: 8  
Percent Similarity: 50.00% Conservative: 2

Best Local Similarity: 40.00% Mismatches: 2  
Query Match: 1.44% Indels: 8  
DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-119-507B-86 (1-42)

Qy 5 ProSerProAlaProArgArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
Db 7 CCTTCACCCCTCTCCA-----CCTCCACCATCTCCGTACCA 42

RESULT 42

US-08-897-556A-86  
Sequence 86, Application US/08897556A  
Patent No. 6570062

GENERAL INFORMATION:

APPLICANT: KIELSZEWSKI, MARCIA J.

TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS

NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/897,556A

FILING DATE: 21-JUL-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: OHU-02908

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

US-08-897-556A-86

Alignment Scores:

Pred. No.: 9.39e+03 Length: 42

Score: 40.00 Matches: 8

Percent Similarity: 50.00% Conservative: 2

Best Local Similarity: 40.00% Mismatches: 2

Query Match: 1.44% Indels: 8

DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-08-897-556A-86 (1-42)

Qy 5 ProSerProAlaProArgArgLeuPheAlaCysSerProProAlaSerGlnPro 24

Db 7 CCTTCACCCCTCTCCA-----CCTCCACCATCTCCGTACCA 42

RESULT 43

US-09-547-693-86

Sequence 86, Application US/09547693

Patent No. 6639650

GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia

TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich

TITLE OF INVENTION: GLYCOPROTEINS  
FILE REFERENCE: OHU-04089  
CURRENT APPLICATION NUMBER: US/09/547,693  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: Patent in version 3.0  
SEQ ID NO: 86  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthetic  
US-09-547-693-86

Alignment Scores:

Pred. No.: 9.39e+03 Length: 42

Score: 40.00 Matches: 8

Percent Similarity: 50.00% Conservative: 2

Best Local Similarity: 40.00% Mismatches: 2

Query Match: 1.44% Indels: 8

DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-547-693-86 (1-42)

Qy 5 ProSerProAlaProArgArgLeuPheAlaCysSerProProAlaSerGlnPro 24

Db 7 CCTTCACCCCTCTCCA-----CCTCCACCATCTCCGTACCA 42

RESULT 44

US-08-463-090B-13/C

Sequence 13, Application US/08463090B

Patent No. 580105

GENERAL INFORMATION:

APPLICANT: Cottarel, Guillaume

APPLICANT: Dreaeta, Guilio

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley, Hoag & Elliot, LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,090B

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV032.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-7000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

US-08-463-090B-13

Alignment Scores:

Pred. No.: 1.01e+04 Length: 44  
 Score: 40.00 Matches: 7  
 Percent Similarity: 58.33% Conservative: 0  
 Best Local Similarity: 58.33% Mismatches: 5  
 Query Match: 1.44% Indels: 0  
 DB: 1 Gaps: 0

US-08-864-955-2 (1-523) x US-08-463-090B-13 (1-44)

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 DB 44 TAYCCNANRNTNNTNNTNSAVGNGNTAYAR 9

RESULT 45

US-09-119-507B-88  
 / Sequence 88, Application US/09119507B  
 / Patent No. 6548642  
 / GENERAL INFORMATION:  
 / APPLICANT: Kieliszewski, Marcia J.  
 / TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums  
 / FILE REFERENCE: OHU-03417  
 / CURRENT APPLICATION NUMBER: US/09/119,507B  
 / CURRENT FILING DATE: 1998-07-20  
 / NUMBER OF SEQ ID NOS: 118  
 / SOFTWARE: Patentln Ver. 2.0  
 / SEQ ID NO 88  
 / LENGTH: 48  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-119-507B-88

Alignment Scores:  
 Pred. No.: 1.17e+04 Length: 48  
 Score: 40.00 Matches: 9  
 Percent Similarity: 50.00% Conservative: 1  
 Best Local Similarity: 45.00% Mismatches: 4  
 Query Match: 1.44% Indels: 6  
 DB: 4 Gaps: 1

US-08-864-955-2 (1-523) x US-09-119-507B-88 (1-48)

QY 5 ProSerProAlaProArgLeuPheAlaCysSerProProAlaSerGlnPro 24  
 DB 1 CCAACCACTCTCACCCCA-----TCTCACCCTCACCATCTCCACCG 42

Search completed: September 9, 2004, 22:50:36  
 Job time : 88 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 10:10:34 ; Search time 5 Seconds  
(without alignments)  
3.272 Million cell updates/sec

Title: US-08-864-955-1  
Perfect score: 2419  
Sequence: 1 CGAAGCGCGCGCTTGCTG.....GCTGCCAATAGCAAGAGC 2419

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 169 seqs, 3382 residues

Total number of hits satisfying chosen parameters: 338

Minimum DB seq length: 10  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 169 summaries

Database: rmpb1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	71	2.9	71	US-10-388-360-84	Sequence 84, Appl
2	71	2.9	71	US-10-773-951-4	Sequence 4, Appl
3	60	2.5	60	US-09-908-975-12902	Sequence 12902, A
4	28	1.2	28	US-10-773-951-38	Sequence 38, Appl
5	21	0.9	21	US-10-388-360-83	Sequence 83, Appl
6	21	0.9	21	US-10-773-951-39	Sequence 39, Appl
7	20	0.8	20	US-10-388-360-82	Sequence 82, Appl
8	20	0.8	20	US-10-773-951-37	Sequence 37, Appl
9	19.4	0.8	21	US-10-444-795B-464	Sequence 464, Appl
10	19.2	0.8	25	US-10-098-263B-98758	Sequence 98758, A
11	19	0.8	19	US-10-444-795B-311	Sequence 311, Appl
12	19	0.8	19	US-10-444-795B-312	Sequence 312, Appl
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18	19	0.8	19	US-10-444-795B-318	Sequence 318, Appl
19	19	0.8	19	US-10-444-795B-319	Sequence 319, Appl
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C 152 14.4 0.6 19 1 US-10-665-951-1515 Sequence 1515, Ap  
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C 154 14 0.6 15 1 US-10-236-392-441 Sequence 498, App  
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C 168 14 0.6 18 1 US-10-287-949A-5402 Sequence 5402, Ap  
C 169 14 0.6 18 1 US-09-878-582-14 Sequence 14, Appl  
C 169 14 0.6 18 1 US-10-336-213B-14 Sequence 14, Appl

## ALIGNMENTS

APPLICANT: GENOMIC HEALTH  
APPLICANT: Baker, Joffie B.  
APPLICANT: Cronin, Maureen T.  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Shak, Steve  
APPLICANT: Walker, Michael Graham  
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSED TUMOR TISSUES  
FILE REFERENCE: 39740-000IUS  
CURRENT APPLICATION NUMBER: US/10/388,360  
CURRENT FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 60/412,049  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: US 60/364,890  
PRIOR FILING DATE: 2002-03-13  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84  
LENGTH: 71  
TYPE: DNA  
US-10-388-360-84  
ORGANISM: Homo sapiens

Query Match 2.9%; Score 71; DB 1; Length 71;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2203 TCTTGCTGGCTACGCTCTTCTGCTTACGCTCCGCTCATATCAGACTGTG 2262  
1 TCTTGCTGGCTACGCTCTTCTGCTTACGCTCCGCTCATATCAGACTGTG 60  
CCACATGCAG 2273  
61 CCACATGCAG 71

US-10-773-951-4  
Sequence 4, Application US/10773951  
Publication No. US20040157255A1  
GENERAL INFORMATION:  
APPLICANT: Agus, David  
APPLICANT: Shak, Steven  
APPLICANT: Cronin, Maureen  
APPLICANT: Baker, Joffie  
TITLE OF INVENTION: Gene Expression Markers for Response to  
FILE REFERENCE: 39740/0009  
CURRENT APPLICATION NUMBER: US/10/773,951  
CURRENT FILING DATE: 2004-02-06  
PRIOR APPLICATION NUMBER: 60/445,968  
PRIOR FILING DATE: 2003-02-06  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 71  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Amplicon  
US-10-773-951-4

Query Match 2.9%; Score 71; DB 1; Length 71;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CCACATGCAG 2273  
61 CCACATGCAG 71

RESULT 1  
US-10-388-360-84  
Sequence 84, Application US/10388360  
Publication No. US2003022528A1  
GENERAL INFORMATION:

RESULT 3

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US-09-908-975-12902
; Sequence 12902, Application US/09908975
; Publication No. US20030155843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Ilat
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12902
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12902

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Query Match      2.5%; Score 60; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 AACTAATCCAGAGAGGCCCATGAGACTCTTCATGCTGCTTTATCCCTGSCATCTCCCC 60

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RESULT 4

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US-10-773-951-38
; Sequence 38, Application US/10773951
; Publication No. US20040157255A1
; GENERAL INFORMATION:
; APPLICANT: Agus, David
; APPLICANT: Shak, Steven
; APPLICANT: Cronin, Maureen
; APPLICANT: Baker, Joffie
; TITLE OF INVENTION: Gene Expression Markers for Response to
; FILE REFERENCE: 39740/0009
; CURRENT APPLICATION NUMBER: US/10/773,951
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/445,968
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe
US-10-773-951-38

```

```

Query Match      1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2224 TGTCCCTGTAGAGCTCTCTCCGTCCATCA 2251
DB      1 TGTCCCTGTAGAGCTCTCTCCGTCCATCA 28

```

RESULT 5

```

US-10-388-360-83/C
; Sequence 83, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffie B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-83

```

```

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2253 CAGAACTGTGCCACATGCAG 2273
DB      21 CAGAACTGTGCCACATGCAG 1

```

RESULT 6

```

US-10-773-951-39/C
; Sequence 39, Application US/10773951
; Publication No. US20040157255A1
; GENERAL INFORMATION:
; APPLICANT: Agus, David
; APPLICANT: Shak, Steven
; APPLICANT: Cronin, Maureen
; APPLICANT: Baker, Joffie
; TITLE OF INVENTION: Gene Expression Markers for Response to
; FILE REFERENCE: 39740/0009
; CURRENT APPLICATION NUMBER: US/10/773,951
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/445,968
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse primer
US-10-773-951-39

```

```

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2253 CAGAACTGTGCCACATGCAG 2273
DB      21 CAGAACTGTGCCACATGCAG 1

```

```

RESULT 7
US-10-388-360-82
; Sequence 82, Application US/10388360

```

```
Publication No. US2003022528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Jeffrey B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Snak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-82

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2203 TCTTGCTGCTACGCTCTT 2222
Db      1 TCTTGCTGCTACGCTCTT 20

RESULT 8
US-10-773-951-37
; Sequence 37, Application US/10773951
; Publication No. US2004015725A1
; GENERAL INFORMATION:
; APPLICANT: Agus, David
; APPLICANT: Snak, Steven
; APPLICANT: Cronin, Maureen
; APPLICANT: Baker, Jeffrey
; TITLE OF INVENTION: Gene Expression Markers for Response to
; FILE REFERENCE: 39740/0009
; CURRENT APPLICATION NUMBER: US/10/773,951
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/445,968
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: forward primer
US-10-773-951-37

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2203 TCTTGCTGCTACGCTCTT 2222
Db      1 TCTTGCTGCTACGCTCTT 20

RESULT 9
US-10-444-795B-464
; Sequence 464, Application US/10444795B
; Publication No. US2004007757A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - 25 A.2
US-10-444-795B-464

Query Match          0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      816 GAGGAGCCATCTGATTCCT 836
Db      1 GAGGAGCCAUUCGUAUUCUTT 21

RESULT 10
US-10-098-263B-98758/c
; Sequence 98758, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitteran, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131065
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 98758
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-98758

Query Match          0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1511 GGAACATCAGATTTAAATACA 1534
Db      24 GGAACATCAGATGTATACACA 1

RESULT 11
US-10-444-795B-311
; Sequence 311, Application US/10444795B
; Publication No. US2004007757A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-311

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 17;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      615 GGGCTGGGCGAGGATGAT 633
DB      1 GGGCTGGGCGAGGATGAT 19

RESULT 12
US-10-444-795B-312
; Sequence 312, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghofer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-312

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 17;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      636 GCAACCACTGGAGGTGAG 654
DB      1 GCAACCACTGGAGGTGAG 19

RESULT 13
US-10-444-795B-313
; Sequence 313, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghofer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-313

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 17;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      755 ATCTATGAGAGATATCA 773
DB      1 ATCTATGAGAGATATCA 19

```

```

RESULT 14
US-10-444-795B-314
; Sequence 314, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghofer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-314

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      756 TCCTATGAGAGATATCAT 774
DB      1 TCCTATGAGAGATATCAT 19

RESULT 15
US-10-444-795B-315
; Sequence 315, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghofer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-315

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 17;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      786 AAAGCTGTGGGATGATGAT 804
DB      1 AAAGCTGTGGGATGATGAT 19

RESULT 16
US-10-444-795B-316
; Sequence 316, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghofer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE

```

FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 316  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-316

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 17;  
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 825 TTCTGATCTCTTGACCAT 843  
Db 1 UUCUGAUCUCUGACCAU 19

RESULT 17  
US-10-444-795B-317  
Sequence 317, Application US/10444795B  
Publication No. US2004007574A1  
GENERAL INFORMATION:  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Lewis, Stephen Patrick  
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 317  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-317

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 17;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 903 GAAGCAGTAAAGACTGTA 921  
Db 1 GAAGCAGUAAGACCGUA 19

RESULT 18  
US-10-444-795B-318  
Sequence 318, Application US/10444795B  
Publication No. US2004007574A1  
GENERAL INFORMATION:  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Lewis, Stephen Patrick  
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 318  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA

US-10-444-795B-318

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 17;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1079 CAGCCACTTGTCTGATGA 1097  
Db 1 CAGCCACUUCUCUGACUGA 19

RESULT 19  
US-10-444-795B-319  
Sequence 319, Application US/10444795B  
Publication No. US2004007574A1  
GENERAL INFORMATION:  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Lewis, Stephen Patrick  
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 319  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-319

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 17;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1207 AACCTGACAACCGATGCA 1225  
Db 1 AACCUAGACACCGAUGCA 19

RESULT 20  
US-10-444-795B-320  
Sequence 320, Application US/10444795B  
Publication No. US2004007574A1  
GENERAL INFORMATION:  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Lewis, Stephen Patrick  
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 320  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-320

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 17;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1215 CAACCGATGCAAGCTGTT 1233  
Db 1 CAACCGACCAAGCUGUU 19

```
RESULT 21
US-10-444-795B-321
; Sequence 321, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-321

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1217 ACCGATGCAAGCTGTTGA 1235
DB      1 ACCGAGCAAGCTGUUGA 19
|||||:|||||:|||||:|

RESULT 22
US-10-444-795B-322
; Sequence 322, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-322

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1262 CTCGCTCAGCTGTGAGAG 1280
DB      1 CCGCGUCAGUGUGAAGAG 19
|||||:|||||:|||||:|

RESULT 23
US-10-444-795B-323
; Sequence 323, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
```

```
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-323

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1287 ACCTTCACAGAGAGTCT 1305
DB      1 ACUCUCACAGAGAGUCU 19
|||||:|||||:|||||:|

RESULT 24
US-10-444-795B-324
; Sequence 324, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-324

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 17;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1359 GTCACCTATCCAGAGAG 1377
DB      1 GUCACUUAUCCAGAGAG 19
|||||:|||||:|||||:|

RESULT 25
US-10-444-795B-325
; Sequence 325, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-325
```

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 17;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1376 AGGCCCATGAGCTTCTCA 1394  
|||||:|||||:|:|  
Db 1 AGGCCCATGAGACUCUCA 19

RESULT 26  
US-10-444-795B-326  
; Sequence 326, Application US/10444795B  
; Publication No. US2004007574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 326  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-326

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 17;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1459 AGGACCTTATGAGAGACT 1477  
|||||:|||||:|:|  
Db 1 AGGACCTTATGAGAGACT 19

RESULT 27  
US-10-444-795B-327  
; Sequence 327, Application US/10444795B  
; Publication No. US2004007574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 327  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-327

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 17;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1460 GGGACCTTATGAGAGACT 1478  
|||||:|||||:|:|  
Db 1 GGGACCTTATGAGAGACT 19

RESULT 28  
US-10-444-795B-328

; Sequence 328, Application US/10444795B  
; Publication No. US2004007574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 328  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-328

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 17;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1474 GACTTCTCAAGGTTATC 1492  
|||||:|||||:|:|  
Db 1 GACTTCTCAAGGTTATC 19

RESULT 29  
US-10-444-795B-329  
; Sequence 329, Application US/10444795B  
; Publication No. US2004007574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 329  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-795B-329

Query Match 0.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 17;  
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1593 GTTGTATCATGACTGT 1611  
|||||:|||||:|:|  
Db 1 GTTGTATCATGACTGT 19

RESULT 30  
US-10-444-795B-330  
; Sequence 330, Application US/10444795B  
; Publication No. US2004007574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-330

```

```

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1608 CTGCGATACCCCATATGAA 1626
      1 CTGCGAUAACCAUAUGAA 19

```

```

RESULT 31
US-10-444-795B-331
; Sequence 331, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 19
; TYPE: RNA
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-331

```

```

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1698 GAAGCCCATGTACTACT 1716
      1 GAAGCCCAUUGUACCUACU 19

```

```

RESULT 32
US-10-444-795B-332
; Sequence 332, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-332

```

```

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;

```

```

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1700 AGCCCATGTACTACTGA 1718
      1 AGCCCAUUGUACCUACUGA 19

```

```

RESULT 33
US-10-444-795B-333
; Sequence 333, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-333

```

```

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 17;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1701 GCCCATGTACTACTGAT 1719
      1 GCCCAUUGUACCUACUGAU 19

```

```

RESULT 34
US-10-444-795B-334
; Sequence 334, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 19
; TYPE: RNA
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-334

```

```

Query Match          0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 17;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1719 TGGCAAGCGTGCTACTTT 1737
      1 TGGCAAGCGTGCTACTTT 19

```

```

RESULT 35
US-10-444-795B-335
; Sequence 335, Application US/10444795B
; Publication No. US2004007574A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-335
```

```
Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 17;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1724 AGCGTCATGTTGTTGTT 1742
Db 1 AGCGUGUUAUGUGUGU 19
```

```
RESULT 36
US-10-444-795B-336
; Sequence 336, Application US/10/444,795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-336
```

```
Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1778 TGTGCGGCTGTGTGAGAGA 1796
Db 1 UGUGCGCGUAGUGAGAGA 19
```

```
RESULT 37
US-10-444-795B-337
; Sequence 337, Application US/10/444,795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 337
```

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-337
```

```
Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 17;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1797 GAGAGTCGCTGGGTAAT 1815
Db 1 GAGAGUUGCCUGGUAU 19
```

```
RESULT 38
US-10-444-795B-338
; Sequence 338, Application US/10/444,795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-338
```

```
Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 17;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1799 GAGATCGCTGGGTAATGA 1817
Db 1 GAGATCGCTGGGTAATGA 19
```

```
RESULT 39
US-10-444-795B-339
; Sequence 339, Application US/10/444,795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-795B-339
```

```
Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1801 GATCGCCTGGTATGAT 1819
      |||:|||||:|||||:
Db      1 GATCGCCTGGTATGAT 19

RESULT 40
US-10-444-795B-465
; Sequence 465, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - 25 A.2
US-10-444-795B-465

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 17;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      816 GAGGAGCCATTCTGATTCT 834
      |||:|||||:|||||:
Db      1 GAGGAGCCATTCTGATTCT 19

RESULT 41
US-10-444-795B-466/C
; Sequence 466, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - 25 A.2
US-10-444-795B-466

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      816 GAGGAGCCATTCTGATTCT 834
      |||:|||||:|||||:
Db      1 GAGGAGCCATTCTGATTCT 1

RESULT 42
US-10-444-795B-467
; Sequence 467, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
```

```
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 467
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - 25 A.2
; NAME/KEY: misc_feature
; LOCATION: 20, 21
; OTHER INFORMATION: n = A,T,C,G or U
US-10-444-795B-467

Query Match      0.8%; Score 19; DB 1; Length 21;
Best Local Similarity 68.4%; Pred. No. 17;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      816 GAGGAGCCATTCTGATTCT 834
      |||:|||||:|||||:
Db      1 GAGGAGCCATTCTGATTCT 19

RESULT 43
US-10-444-795B-468/C
; Sequence 468, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - 25 A.2
; NAME/KEY: misc_feature
; LOCATION: 1, 2
; OTHER INFORMATION: n = A,T,C,G or U
US-10-444-795B-468

Query Match      0.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      816 GAGGAGCCATTCTGATTCT 834
      |||:|||||:|||||:
Db      21 GAGGAGCCATTCTGATTCT 3

RESULT 44
US-10-098-263B-99873/C
; Sequence 99873, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Maltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
```

```
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 99873
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-99873
```

```
Query Match          0.8%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1290 TTCTCAAGAGAGGAGTCTCCACT 1311
Db      25  TTCTCAAGAGAGGAGTATCTCTCT 4
```

```
RESULT 45
US-10-422-466-26/c
/ Sequence 26, Application US/10422466
/ Publication No. US20040006036A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Ji-Fan
/ APPLICANT: Bowersox, Scott
/ TITLE OF INVENTION: Silencing transcription by methylation
/ FILE REFERENCE: 112029.00005
/ CURRENT APPLICATION NUMBER: US/10/422,466
/ PRIOR FILING DATE: 2003-04-22
/ PRIOR APPLICATION NUMBER: 09/643,128
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: 60/196,749
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/214,148
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (2)
/ OTHER INFORMATION: m5c at base 2
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-26
```

```
Query Match          0.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      181 CTTACAGCTGCTGTTGCCGCGC 200
Db      21  CTTACAGCTGCTGTTGCCGACG 2
```

```
RESULT 46
US-10-422-466-18/c
/ Sequence 18, Application US/10422466
/ Publication No. US20040006036A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Ji-Fan
/ APPLICANT: Bowersox, Scott
/ TITLE OF INVENTION: Silencing transcription by methylation
/ FILE REFERENCE: 112029.00005
/ CURRENT APPLICATION NUMBER: US/10/422,466
/ PRIOR FILING DATE: 2003-04-22
/ PRIOR APPLICATION NUMBER: 09/643,128
/ PRIOR FILING DATE: 2000-08-21
```

```
/ PRIOR APPLICATION NUMBER: 60/196,749
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/214,148
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (2)..(13)
/ OTHER INFORMATION: m5c at bases 2 and 13
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-18
```

```
Query Match          0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      322 CCTGACCGCGAGTCTGT 339
Db      21  CCTGACCGCGAGTCTGT 4
```

```
RESULT 47
US-10-422-466-16/c
/ Sequence 16, Application US/10422466
/ Publication No. US20040006036A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Ji-Fan
/ APPLICANT: Bowersox, Scott
/ TITLE OF INVENTION: Silencing transcription by methylation
/ FILE REFERENCE: 112029.00005
/ CURRENT APPLICATION NUMBER: US/10/422,466
/ PRIOR FILING DATE: 2003-04-22
/ PRIOR APPLICATION NUMBER: 09/643,128
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: 60/196,749
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/214,148
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (3)..(21)
/ OTHER INFORMATION: m5c at bases 3 and 21
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-16
```

```
Query Match          0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      263 GCGCTTGAGAGTCTCCGCA 280
Db      18  GCGCTTGAGAGTCTCCGCA 1
```

```
RESULT 48
US-10-422-466-20/c
/ Sequence 20, Application US/10422466
/ Publication No. US20040006036A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Ji-Fan
```

```

APPLICANT: Bowersox, Scott
TITLE OF INVENTION: Silencing transcription by methylation
FILE REFERENCE: 112029.00005
CURRENT APPLICATION NUMBER: US/10/422,466
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: 09/643,128
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 60/196,749
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/214,148
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified_base
LOCATION: (3)..(21)
OTHER INFORMATION: msc at bases 3 and 21
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-20

```

```

Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      263 GCGCGTGGAGGTCGCCGA 260
DB      18 GCGCGTGGAGGTCGCCGA 1

```

```

RESULT 49
US-10-422-466-19/c
Sequence 19, Application US/10422466
Publication No. US20040006036A1
GENERAL INFORMATION:
APPLICANT: Hu, Ji-Fan
APPLICANT: Bowersox, Scott
TITLE OF INVENTION: Silencing transcription by methylation
FILE REFERENCE: 112029.00005
CURRENT APPLICATION NUMBER: US/10/422,466
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: 09/643,128
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 60/196,749
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/214,148
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)..(16)
OTHER INFORMATION: msc at bases 2 and 16
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-19

```

```

Query Match      0.7%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      430 AGCGGAGCTCTCGAGGC 448
DB      19 AGCGGAGCTCTCGAGGC 1

```

```

RESULT 50
US-10-422-466-17/c
Sequence 17, Application US/10422466
Publication No. US20040006036A1
GENERAL INFORMATION:
APPLICANT: Hu, Ji-Fan
APPLICANT: Bowersox, Scott
TITLE OF INVENTION: Silencing transcription by methylation
FILE REFERENCE: 112029.00005
CURRENT APPLICATION NUMBER: US/10/422,466
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: 09/643,128
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 60/196,749
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/214,148
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)..(13)
OTHER INFORMATION: msc at bases 2 and 13
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-17

```

```

Query Match      0.7%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      323 CTGAACCGGAGTCTGT 339
DB      20 CTGAACCGGAGTCTGT 4

```

```

RESULT 51
US-10-422-466-21/c
Sequence 21, Application US/10422466
Publication No. US20040006036A1
GENERAL INFORMATION:
APPLICANT: Hu, Ji-Fan
APPLICANT: Bowersox, Scott
TITLE OF INVENTION: Silencing transcription by methylation
FILE REFERENCE: 112029.00005
CURRENT APPLICATION NUMBER: US/10/422,466
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: 09/643,128
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 60/196,749
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/214,148
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: msc at base 2
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-21

```

```

Query Match      0.7%; Score 17; DB 1; Length 20;

```

Best Local Similarity 100.0%; Pred. No. 35;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 CATGAAGTGGGCGGA 475  
Db 20 CATGAAGTGGGCGGA 4

RESULT 52  
US-10-289-762-1735

; Sequence 1735, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1735  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-1735

Query Match 0.7%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1386 GACTCTTCATCAGCTT 1402  
Db 1 GACTCTTCATCAGCTT 17

RESULT 53  
US-10-422-466-22/c

; Sequence 22, Application US/10422466  
; Publication No. US20040006036A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Ji-Fan  
; TITLE OF INVENTION: Silencing transcription by methylation  
; FILE REFERENCE: 112029.00005  
; CURRENT APPLICATION NUMBER: US/10/422,466  
; CURRENT FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: 09/643,128  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 60/196,749  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/214,148  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; NAME/KEY: modified base  
; LOCATION: (2)..(16)  
; OTHER INFORMATION: m5c at bases 2 and 16  
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor  
US-10-422-466-22

Query Match 0.7%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 AGCCCGTGTGAAGCG 543  
|||||

Db 21 AGCCCGTGTGAAGCG 5

RESULT 54  
US-10-422-466-23/c

; Sequence 23, Application US/10422466  
; Publication No. US20040006036A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Ji-Fan  
; TITLE OF INVENTION: Silencing transcription by methylation  
; FILE REFERENCE: 112029.00005  
; CURRENT APPLICATION NUMBER: US/10/422,466  
; CURRENT FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: 09/643,128  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 60/196,749  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/214,148  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; NAME/KEY: modified base  
; LOCATION: (2)..(15)  
; OTHER INFORMATION: m5c at bases 2 and 15  
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor  
US-10-422-466-23

Query Match 0.7%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 GAAGCGCTATTGCG 553  
Db 21 GAAGCGCTATTGCG 5

RESULT 55  
US-10-148-355A-12

; Sequence 12, Application US/10148355A  
; Publication No. US20030207831A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cosvert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RSP-0082  
; CURRENT APPLICATION NUMBER: US/10/148,355A  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/467,642  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-148-355A-12

Query Match 0.7%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 283 CCGCGCGCGCGCGCGCTT 302  
|||||

Db 1 CCCTCCCGCGCGCGCTT 20

## RESULT 56

US-10-349-143-10169  
; Sequence 10169, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marla  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 10169  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURES:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..21  
; OTHER INFORMATION: downstream amplification primer 99-10267 for SEQ 2304, in complem  
US-10-349-143-10169

Query Match 0.7%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 37;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1037 CAGGAAATTCATTCCTT 1056

Db 1 CAGGAAATTCATTCCTT 20

## RESULT 57

US-10-444-795B-469  
; Sequence 469, Application US/10444795B  
; Publication No. US20040077574A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Lewis, Stephen Patrick  
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
; FILE REFERENCE: 200125.449  
; CURRENT APPLICATION NUMBER: US/10/444,795B  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 842  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 469  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Small interfering RNA - cdc25B.2  
US-10-444-795B-469

Query Match 0.7%; Score 16.8; DB 1; Length 21;

Best Local Similarity 75.0%; Pred. No. 37;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1858 GGGGATACAGAGATCTT 1877

Db 2 GGGGATACAGAGATCTT 21

## RESULT 58

US-08-424-550B-95  
; Sequence 95, Application US/08424550B  
; Publication No. US20020119447A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-WATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEKHOF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAMMAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 4.35435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-424-550B-95

Query Match 0.7%; Score 16.8; DB 1; Length 22;

Best Local Similarity 90.0%; Pred. No. 37;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTGACATGACATCTTC 853

Db 3 TCTGACATGACATCTTC 22

## RESULT 59

US-10-655-847-105  
; Sequence 105, Application US/10655847  
; Publication No. US20040063129A1  
; GENERAL INFORMATION:  
; APPLICANT: William M. Pfeiler  
; APPLICANT: Susan M. Gaarde  
; APPLICANT: Andrew T. Wale  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
; FILE REFERENCE: RTS-0189  
; CURRENT APPLICATION NUMBER: US/10/655,847  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US/10/160,807

; PRIOR FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 296  
; SEQ ID NO 105  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-655-847-105

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 240 CCCGTGCTGTGCTGCT 257  
Db 2 CCAGTGCCTGTGCTGCT 19

RESULT 60  
US-10-655-847-246/c  
; Sequence 246, Application US/10655847  
; Publication No. US20040063129A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Andrew T. Matt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
; FILE REFERENCE: RTS-0189  
; CURRENT APPLICATION NUMBER: US/10/655,847  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US/10/160,807  
; PRIOR FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 296  
; SEQ ID NO 246  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-655-847-246

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 240 CCCGTGCTGTGCTGCT 257  
Db 19 CCAGTGCCTGTGCTGCT 2

RESULT 61  
US-10-160-807-105  
; Sequence 105, Application US/10160807  
; Publication No. US20030224514A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Andrew T. Matt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
; FILE REFERENCE: RTS-0189  
; CURRENT APPLICATION NUMBER: US/10/160,807  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 296  
; SEQ ID NO 105  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-160-807-105

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 43;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 240 CCCGTGCTGTGCTGCT 257  
Db 2 CCAGTGCCTGTGCTGCT 19

RESULT 62  
US-10-160-807-246/c  
; Sequence 246, Application US/10160807  
; Publication No. US20030224514A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Andrew T. Matt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION  
; FILE REFERENCE: RTS-0189  
; CURRENT APPLICATION NUMBER: US/10/160,807  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 296  
; SEQ ID NO 246  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-160-807-246

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 240 CCCGTGCTGTGCTGCT 257  
Db 19 CCAGTGCCTGTGCTGCT 2

RESULT 63  
US-10-712-363-10  
; Sequence 10, Application US/10712363  
; Publication No. US20040072335A1  
; GENERAL INFORMATION:  
; APPLICANT: Dawson, Elliot P.  
; TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS  
; FILE REFERENCE: 13744-2  
; CURRENT APPLICATION NUMBER: US/10/712,363  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: US 60/306,675  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 10/360,790  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: PCT/US03/21468  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic primer  
US-10-712-363-10

Query Match 0.7%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 987 CTCTGCCAGCTCGAAT 1004  
Db 3 CTCTGCCAGCTCGAAT 20

RESULT 64  
US-10-422-466-24/c

```
/ Sequence 24, Application US/10422466
/ Publication No. US2004006036A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Ji-Fan
/ APPLICANT: Bowersox, Scott
/ TITLE OF INVENTION: Silencing transcription by methylation
/ FILE REFERENCE: 112029.00005
/ CURRENT APPLICATION NUMBER: US/10/422,466
/ PRIOR FILING DATE: 2003-04-22
/ PRIOR APPLICATION NUMBER: 09/643,128
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: 60/156,749
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/214,148
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (2)..(17)
/ OTHER INFORMATION: m5c at bases 2 and 17
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-24

Query Match          0.7%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      591 GACCGTCACTATGACCA 608
DB      21 GACCGTCACTATGACCA 4

RESULT 65
US-10-702-496-29
/ Sequence 29, Application US/10702496
/ Publication No. US20040121383A1
/ GENERAL INFORMATION:
/ APPLICANT: Myech
/ APPLICANT: Liu, Wei
/ APPLICANT: Wu, Leeying
/ TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
/ FILE REFERENCE: AM101071
/ CURRENT APPLICATION NUMBER: US/10/702,496
/ CURRENT FILING DATE: 2003-11-07
/ PRIOR APPLICATION NUMBER: 60/429,381
/ PRIOR FILING DATE: 2002-11-27
/ NUMBER OF SEQ ID NOS: 306
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 29
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-10-702-496-29

Query Match          0.7%; Score 16.4; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1920 CATGCACGACGAGACTT 1937
DB      4 CAUGACCAAGAGGACTU 21

RESULT 66
US-09-951-401-6/c
/ Sequence 6, Application US/09951401
/ Sequence 6, Application US/09951401
```

```
/ Patent No. US20020115104A1
/ GENERAL INFORMATION:
/ APPLICANT: Bartel, Paul L.
/ APPLICANT: Tavtigian, Sean V.
/ TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
/ FILE REFERENCE: MMSC2
/ CURRENT APPLICATION NUMBER: US/09/951,401
/ CURRENT FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: US 09/306,998
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: US 60/084,740
/ PRIOR FILING DATE: 1998-05-08
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-951-401-6

Query Match          0.7%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1317 TACAAAGAGAGGAG 1332
DB      16 TACAAAGAGAGGAG 1

RESULT 67
US-09-922-101-6/c
/ Sequence 6, Application US/09922101
/ Patent No. US20020146711A1
/ GENERAL INFORMATION:
/ APPLICANT: Bartel, Paul L.
/ APPLICANT: Tavtigian, Sean V.
/ TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
/ FILE REFERENCE: MMSC2
/ CURRENT APPLICATION NUMBER: US/09/922,101
/ CURRENT FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: 09/306,998
/ PRIOR FILING DATE: 1999-05-07
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-101-6

Query Match          0.7%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1317 TACAAAGAGAGGAG 1332
DB      16 TACAAAGAGAGGAG 1

RESULT 68
US-09-951-402-6/c
/ Sequence 6, Application US/09951402
/ Patent No. US20020168752A1
/ GENERAL INFORMATION:
/ APPLICANT: Bartel, Paul L.
/ APPLICANT: Tavtigian, Sean V.
/ TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
/ FILE REFERENCE: MMSC2
/ CURRENT APPLICATION NUMBER: US/09/951,402
/ CURRENT FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: US 09/306,998
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: US 60/084,740
```

;; PRIOR FILING DATE: 1998-05-08  
;; NUMBER OF SEQ ID NOS: 72  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 6  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-951-402-6

Query Match 0.7%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1317 TACAAGAGAGAGAG 1332  
DB 16 TACAAGAGAGAGAG 1

RESULT 69  
US-09-910-059-110  
; Sequence 110, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; TITLE OF INVENTION: Their Therapeutic use in an Adept System  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910, 059  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 110  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer for preproHCPB  
US-09-910-059-110

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 53;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACGAGTCGAGGTCGTG 621  
DB 1 GGACGTCGTGACAGATCTG 19

RESULT 70  
US-10-205-309-150/c  
; Sequence 150, Application US/10205309  
; Publication No. US20030190635A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Alzheimer's Disease Using  
; TITLE OF INVENTION: Interfering RNA  
; FILE REFERENCE: 900/033  
; CURRENT APPLICATION NUMBER: US/10/205,309  
; CURRENT FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 674  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 150

;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r  
US-10-205-309-150

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 53;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AGTAAGAAAACCTTGAA 754  
DB 19 AGAAAGAAAACATTGAA 1

RESULT 71  
US-10-205-309-475  
; Sequence 475, Application US/10205309  
; Publication No. US20030190635A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Alzheimer's Disease Using  
; TITLE OF INVENTION: Interfering RNA  
; FILE REFERENCE: 900/033  
; CURRENT APPLICATION NUMBER: US/10/205,309  
; CURRENT FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 674  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 475  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-205-309-475

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 53;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 736 AGTAAGAAAACCTTGAA 754  
DB 1 AGAAAGAAAACAUUGAA 19

RESULT 72  
US-10-349-143-6665/c  
; Sequence 6665, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marla  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.0200C21  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 6665  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:

```
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-16401 for SEQ 2721,
US-10-349-143-6665

Query Match
Best Local Similarity 89.5%; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2095 CAGAGAACTTAAGCAAG 2113
Db 19 CAGAGAACTTAAGCAAG 1

RESULT 73
US-10-289-762-6335
; Sequence 6335, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifaths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6335
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6335

Query Match
Best Local Similarity 89.5%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2297 TCTGAGCCACTGTGGAG 2315
Db 2 TCTGAGCCACTGTGGAG 20

RESULT 74
US-10-732-485-10
; Sequence 10, Application US/10732485
; Publication No. US20040126799A1
; GENERAL INFORMATION:
; APPLICANT: Genodysee
; APPLICANT: ESCARY, Jean-Louis
; TITLE OF INVENTION: New polynucleotides and polypeptides of the IFNa-7 gene
; FILE REFERENCE: 60711.000026
; CURRENT APPLICATION NUMBER: US/10/732,485
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: FR01/07588
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/EP02/07456
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-732-485-10

Query Match
Best Local Similarity 89.5%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1497 TCATACAGTTCGTGGAAA 1515
Db 2 TCATACAGTTCGTGGAAA 20

; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-16401 for SEQ 2721,
US-10-349-143-6665

Query Match
Best Local Similarity 89.5%; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2095 CAGAGAACTTAAGCAAG 2113
Db 19 CAGAGAACTTAAGCAAG 1

RESULT 75
US-10-671-395-1216
; Sequence 1216, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOVAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1216
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1216

Query Match
Best Local Similarity 89.5%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1274 TGAAGAGACCAAGCTTC 1292
Db 1 TGAAGAGACCAAGCTTC 19

RESULT 76
US-10-671-395-1306
; Sequence 1306, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOVAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1306
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1306

Query Match
Best Local Similarity 89.5%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1274 TGAAGAGACCAAGCTTC 1292
Db 1 TGAAGAGACCAAGCTTC 19

RESULT 77
US-09-901-106-17/C
; Sequence 17, Application US/09901106
; Patent No. US20020151067A1
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
```

```

; TITLE OF INVENTION: DNA Expression Systems Based on
;                               Altmaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/901,106
; FILING DATE: 10-Jul-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
;
; TELEX: 248345
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..21
; OTHER INFORMATION: /label= primer
; /note= "SP2 downstream sequencing primer"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-901-106-17
Query Match      0.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      356 CGGCGCCCGGTGGCGCGC 374
Db      21 CGGCGCCCGGTGGCGCGC 3

RESULT 78
US-09-778-510-14
; Sequence 14, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0

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```

; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer from Homo sapien
US-09-778-510-14
Query Match      0.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      492 CCTGCTCTGCGCTGCAGC 510
Db      1 CCTGCTGTGGCCCTGCTGC 19

RESULT 79
US-10-302-041-14
; Sequence 14, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer from Homo sapien
US-10-302-041-14
Query Match      0.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      492 CCTGCTCTGCGCTGCAGC 510
Db      1 CCTGCTGTGGCCCTGCTGC 19

RESULT 80
US-10-156-306-5802
; Sequence 5802, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 803
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5802
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5802
Query Match      0.6%; Score 15.4; DB 1; Length 17;

```

Best Local Similarity 86.2%; Pred. No. 61;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 431 GCGGAGCTCTGCAGG 447  
Db 1 GCGGAGCTCTGCAGG 17

## RESULT 81

US-10-209-676-31/c  
; Sequence 31, Application US/10209676  
; Publication No. US2003014831A1  
; GENERAL INFORMATION:  
; APPLICANT: Stratmann, Michael P.  
; TITLE OF INVENTION: APPLICATIONS OF PARALLEL GENOMIC ANALYSIS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/209,676  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/427,834  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-209-676-31

Query Match 0.6%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1112 TGAACCTTCTGATGGA 1128  
Db 18 TGAACCTTCTGATGGA 2

RESULT 82  
US-10-440-998-17  
; Sequence 17, Application US/10440998  
; Publication No. US20030215919A1  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/10/440,998  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/686,055  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 08/951,648  
; PRIOR FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-10-440-998-17

Query Match 0.6%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCA 2415  
Db 1 TGCTGGCCCAATAGCA 17

RESULT 83

US-09-902-176A-47/c  
; Sequence 47, Application US/09902176A  
; Publication No. US2003009943A1  
; GENERAL INFORMATION:  
; APPLICANT: Schreiber, Stefan  
; APPLICANT: Mascheretti, Silvia  
; APPLICANT: Hampe, Jochem  
; TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for  
; TITLE OF INVENTION: the TNF Receptor II and Method for Detecting  
; FILE REFERENCE: 25481-P001US  
; CURRENT APPLICATION NUMBER: US/09/902,176A  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: EP 00114786.7  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer  
US-09-902-176A-47

Query Match 0.6%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 493 CTGCTTCTGCCTGCAG 509  
Db 17 CTGCTTCTGCCTGCAG 1

RESULT 84  
US-10-116-963-3/c  
; Sequence 3, Application US/10116963  
; Publication No. US20030045492A1  
; GENERAL INFORMATION:  
; APPLICANT: UAB Research Foundation  
; APPLICANT: Tang, De-chu C.  
; APPLICANT: Marks, Donald H.  
; APPLICANT: Curiel, David T.  
; APPLICANT: Shi, Zhongkai  
; APPLICANT: Van Kampen, Kent Ridpy  
; TITLE OF INVENTION: VACCINATION BY TOPICAL APPLICATION OF RECOMBINANT VECTORS  
; FILE REFERENCE: 858610-2003.3  
; CURRENT APPLICATION NUMBER: US/10/116,963  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/563,826  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/132,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: 09/533,149  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: 60/055,520  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/075,113  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: 09/402,527  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US98/16739  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer used to amplify DNA  
US-10-116-963-3

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 60;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGGTATGATATACCCCA 1825  
 |||||  
 DB 18 GGGTATGATATACCCCA 2

RESULT 85  
 US-10-052-323-3/c  
 ; Sequence 3, Application US/10052323  
 ; Publication No. US20030125278A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: UAB Research Foundation  
 ; APPLICANT: Tang, De-chu C.  
 ; APPLICANT: Marks, Donald H.  
 ; APPLICANT: Curriel, David T.  
 ; APPLICANT: Shi, Zhongkai  
 ; APPLICANT: Van Kampen, Kent Rigby  
 ; TITLE OF INVENTION: Immunization of Animals by Topical Application of a Salmonella-ba  
 ; FILE REFERENCE: 858610-2003.2  
 ; CURRENT FILING DATE: US/10/052,323  
 ; PRIOR APPLICATION NUMBER: 2002-09-27  
 ; PRIOR FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: 09/563,826  
 ; PRIOR FILING DATE: 1999-05-03  
 ; PRIOR APPLICATION NUMBER: 60/112,216  
 ; PRIOR FILING DATE: 2000-03-23  
 ; PRIOR APPLICATION NUMBER: 09/533,149  
 ; PRIOR FILING DATE: 1997-08-13  
 ; PRIOR APPLICATION NUMBER: 60/055,520  
 ; PRIOR FILING DATE: 1998-02-11  
 ; PRIOR APPLICATION NUMBER: 09/402,527  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US98/16739  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer used to amplify DNA  
 US-10-052-323-3

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 60;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGGTATGATATACCCCA 1825  
 |||||  
 DB 18 GGGTATGATATACCCCA 2

RESULT 86  
 US-10-170-832-19/c  
 ; Sequence 19, Application US/10170832  
 ; Publication No. US2003017092A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chauv, Pascal  
 ; APPLICANT: Vanhoume, Valérie  
 ; APPLICANT: Strobart, Vincent  
 ; APPLICANT: Boon-Falleur, Thierry  
 ; APPLICANT: Van der Bruggen, Pierre  
 ; APPLICANT: Thielemans, Kris  
 ; APPLICANT: Cortals, Jürgen  
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 ; FILE REFERENCE: L0461/7052  
 ; CURRENT APPLICATION NUMBER: US/10/170,832  
 ; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US/09/166,448  
 ; PRIOR FILING DATE: 1998-10-05  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 19  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-170-832-19

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 60;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGCCGCCCATGG 463  
 |||||  
 DB 20 GCCGGCCGCCCATGG 4

RESULT 87  
 US-10-394-575-24/c  
 ; Sequence 24, Application US/10394575  
 ; Publication No. US20030236393A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TRUCKSIS, MICHELE  
 ; TITLE OF INVENTION: VIRULENCE GENES OF M. MARINUM AND M. TUBERCULOSIS  
 ; FILE REFERENCE: VET-2  
 ; CURRENT APPLICATION NUMBER: US/10/394,575  
 ; CURRENT FILING DATE: 2003-03-24  
 ; PRIOR APPLICATION NUMBER: 60/367,206  
 ; PRIOR FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/366,262  
 ; PRIOR FILING DATE: 2002-03-22  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 24  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US-10-394-575-24

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 60;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1989 GAAGAGCAAGAGGAGA 2005  
 |||||  
 DB 19 GAAGAGCAAGAGGAGA 3

RESULT 88  
 US-10-210-556-48/c  
 ; Sequence 48, Application US/10210556  
 ; Publication No. US20040023904A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lex M. Cowsett  
 ; APPLICANT: Susan M. Freiler  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION  
 ; FILE REFERENCE: PTS-0015  
 ; CURRENT APPLICATION NUMBER: US/10/210,556  
 ; CURRENT FILING DATE: 2002-07-31  
 ; NUMBER OF SEQ ID NOS: 227  
 ; SEQ ID NO 48  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-210-556-48

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1135 CTGAAGATGAGGAGA 1151  
DB 20 CTGAAGAGAGGAGGA 4

RESULT 89  
US-10-210-556-171  
Sequence 171, Application US/10210556  
Publication No. US20040023904A1  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowser  
APPLICANT: Susan M. Freier  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION  
FILE REFERENCE: PFS-0015  
CURRENT APPLICATION NUMBER: US/10/210,556  
CURRENT FILING DATE: 2002-07-31  
NUMBER OF SEQ ID NOS: 227  
SEQ ID NO 171  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-210-556-171

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1135 CTGAAGATGAGGAGA 1151  
DB 1 CTGAAGAGAGGAGGA 17

RESULT 90  
US-10-304-116-90  
Sequence 90, Application US/10304116  
Publication No. US20040101857A1  
GENERAL INFORMATION:  
APPLICANT: Donna T. Ward  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: MODULATION OF CYTOKINE-INDUCIBLE KINASE EXPRESSION  
FILE REFERENCE: RTS-0397  
CURRENT APPLICATION NUMBER: US/10/304,116  
CURRENT FILING DATE: 2002-11-23  
NUMBER OF SEQ ID NOS: 138  
SEQ ID NO 90  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-304-116-90

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 259 GCTGCGCCTGAGGAT 275  
DB 3 GCTGAGCCTGAGGAT 19

RESULT 91  
US-10-651-833-2/c  
Sequence 2, Application US/10651833  
Publication No. US20040110200A1  
GENERAL INFORMATION:  
APPLICANT: Peoples, Risa

APPLICANT: Van Atta, Renee B.  
TITLE OF INVENTION: POLYMORPHISM DETECTION AMONG HOMOLOGOUS SEQUENCES  
FILE REFERENCE: NX3  
CURRENT APPLICATION NUMBER: US/10/651,833  
CURRENT FILING DATE: 2003-08-29  
PRIOR APPLICATION NUMBER: US 60/407,598  
PRIOR FILING DATE: 2002-08-29  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
NAME/KEY: misc feature  
LOCATION: (19)..(19)  
OTHER INFORMATION: "r" represents a non-nucleosidic cross-linking agent  
US-10-651-833-2

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 988 TCTGCCAGCTCGAAT 1004  
DB 18 TCTGCCAGCTCGACT 2

RESULT 92  
US-09-752-983-123  
Sequence 123, Application US/09752983  
Patent No. US20010016575A1  
GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
APPLICANT: Graham, Brett P. Monia  
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDX2  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 271  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PC  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/752,983  
FILING DATE: 02-Jan-2001  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/280,805  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane Massey  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0346  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-810-1515  
TELEFAX: 609-810-1454  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes

US-09-752-983-123

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1005 GCTTCCTCAATGAAAGAG 1024  
Db 1 GCTTTCATCAAGGAGG 20

RESULT 93

US-09-870-002-20/c  
Sequence 20, Application US/09870002  
Publication No. US20030013670A1

GENERAL INFORMATION:

APPLICANT: Montu, B.P., Cowser, L.M. and Manoharan, M.  
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: WORDPERFECT 6.1 FOR WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/870,002

FILING DATE: 30-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/575,554

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0463

TELECOMMUNICATION INFORMATION:

TELEPHONE: (856) 810-1515

TELEFAX: (856) 810-1454

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 20

US-09-870-002-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 400 GGCGGTGCGCGGAGGCGAG 419  
Db 20 GGCGGCGCGCGGAGGCGAG 1

RESULT 94

US-09-824-322B-421

Sequence 421, Application US/09824322B

Publication No. US20030022848A1

GENERAL INFORMATION:

APPLICANT: Baker, Brenda

APPLICANT: Bennett, C. Frank

APPLICANT: Butler, Madeline M.

APPLICANT: Shanahan, William R.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALP  
TITLE OF INVENTION: ALP(A) EXPRESSION

FILE REFERENCE: ISPH-0501

CURRENT APPLICATION NUMBER: US/09/824,322B

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US 09/313,932

PRIOR FILING DATE: 1999-05-18

PRIOR APPLICATION NUMBER: US 09/166,186

PRIOR FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 503

SEQ ID NO 421

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-824-322B-421

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1783 CGGTATGTGAGAGAGAGA 1802  
Db 1 CAGTATGTGAGAGAGAGA 20

RESULT 95

US-09-932-367A-41

Sequence 41, Application US/09932367A

Publication No. US20030027152A1

GENERAL INFORMATION:

APPLICANT: RHODES, Simon J.

APPLICANT: BRIDWELL, Jeanne L.

APPLICANT: MEIER, Bradley C.

APPLICANT: PARKER, Gretchen E.

APPLICANT: PRICE, Jeffrey R.

APPLICANT: SHOWALTER, Aaron D.

APPLICANT: SLOOP, Kyle W.

TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN

FILE REFERENCE: LHX3/P-LIM/LIM-3 FACTOR

CURRENT APPLICATION NUMBER: US/09/932,367A

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: PCT/US00/04424

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/121,110

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PCR primer

US-09-932-367A-41

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 469 GGCCGAGCCCGCAGCGCG 488  
Db 1 GGCAAGAGCCCGCAGCGCG 20

RESULT 96

US-09-932-367A-44

Sequence 44, Application US/09932367A

Publication No. US20030027152A1

GENERAL INFORMATION:

APPLICANT: RHODES, Simon J.

APPLICANT: BRIDWELL, Jeanne L.  
APPLICANT: MEIER, Bradley C.  
APPLICANT: PARKER, Gretchen E.  
APPLICANT: PRICE, Jeffrey R.  
APPLICANT: SHOWALTER, Aaron D.  
APPLICANT: SLOOP, Kyle W.  
TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN  
FILE REFERENCE: 053884-5003  
CURRENT APPLICATION NUMBER: US/09/932,367A  
CURRENT FILING DATE: 2001-08-17  
PCT/US00/04424  
PRIORITY FILING DATE: 2000-02-22  
PRIORITY APPLICATION NUMBER: US 60/121,110  
PRIORITY FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 44  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PCR primer  
US-09-932-367A-44

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 469 GGCGGAGCGCGGCGCGCG 488  
DB 1 GGCGAGCGCGCGCGCGCG 20

RESULT 97  
US-09-784-674-231  
Sequence 231, Application US/09784674  
Publication No. US20030054346A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
Wolber, Paul K.  
Deleensart, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 2080  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 231:  
US-09-784-674-231

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 775 TCCCTACCTCAAAAGCTGT 794  
DB 1 TCCCACTCAAGATGT 20

RESULT 98  
US-09-784-674-232  
Sequence 232, Application US/09784674  
Publication No. US20030054346A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
Wolber, Paul K.  
Deleensart, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 2080  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 232:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 232:  
US-09-784-674-232

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 776 CCTACTCAAGCTGTG 795  
DB 1 CCCCACTCAAGATCTTG 20

## RESULT 99

US-10-643-130-20/c  
; Sequence 20, Application US/10643130  
; Publication No. US20040072766A1

## GENERAL INFORMATION:

APPLICANT: Monia, B.P., Cosseret, L.M. and Manoharan, M.  
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata  
STREET: 66 East Main Street  
City: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.1 for WINDOWS

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/643,130  
FILING DATE: 18-Aug-2003  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/575,554  
FILING DATE: 22-May-2000  
APPLICATION NUMBER: 09/128,494  
FILING DATE: August 3, 1998  
APPLICATION NUMBER: 08/411,734  
FILING DATE: April 3, 1995  
APPLICATION NUMBER: PCT/US93/09346  
FILING DATE: October 1, 1993  
APPLICATION NUMBER: 07/958,134  
FILING DATE: October 5, 1992  
APPLICATION NUMBER: 08/007,996  
FILING DATE: January 21, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0463  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (856) 810-1515  
TELEFAX: (856) 810-1454

## SEQUENCE CHARACTERISTICS:

LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear

ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 20

US-10-643-130-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTGGCGGAGGAG 419  
DB 20 GCGCGCGCGCGGAGGAG 1

RESULT 100  
US-10-103-076-7  
; Sequence 7, Application US/10103076  
; Publication No. US20030181351A1

## GENERAL INFORMATION:

APPLICANT: Lee, Emily Hsiao-Yuan  
APPLICANT: Tsai, Kuen-Jer  
TITLE OF INVENTION: SPATIAL LEARNING AND MEMORY  
FILE REFERENCE: 08919-078001  
CURRENT APPLICATION NUMBER: US/10/103,076  
CURRENT FILING DATE: 2002-03-21  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
US-10-103-076-7

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1843 CTGTATGCTGGAAGGCGG 1862  
DB 1 CTGTGTGCTGAAGGCGG 20

## RESULT 101

US-10-005-344-123  
; Sequence 123, Application US/10005344  
; Publication No. US20030203862A1

## GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia  
APPLICANT: Pamela Nero  
APPLICANT: Mark J. Graham  
APPLICANT: Brett P. Monia  
APPLICANT: Erich Koller  
APPLICANT: Mingyi Chang  
APPLICANT: Mano Manoharan  
TITLE OF INVENTION: Antisense Modulation of mdm2 expression.  
FILE REFERENCE: ISPH-0622  
CURRENT APPLICATION NUMBER: US/10/005,344  
CURRENT FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: US 09/048,810  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: US 09/280,805  
PRIOR FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 379  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 123  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-005-344-123

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1005 GCTTCTCAATGAAGAG 1024  
DB 1 GCTTCAATCAAGGAAGG 20

## RESULT 102

US-10-148-355A-15  
; Sequence 15, Application US/10148355A  
; Publication No. US20030207831A1

```

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2
; FILE REFERENCE: RTSP-0082
; CURRENT APPLICATION NUMBER: US/10/148,355A
; PRIOR FILING DATE: 2002-09-30
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-148-355A-15

Query Match
Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 199 CGCCCGCCCGCCCGCTGACC 218
Db 1 CGCCCGCCCGCCCGCTGACC 20

RESULT 103
US-10-174-456-50/c
; Sequence 50, Application US/10174456
; Publication No. US20030235910A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 49 EXPRESSION
; FILE REFERENCE: RTS-0374
; CURRENT APPLICATION NUMBER: US/10/174,456
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 139
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-456-50

Query Match
Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1586 TTAAGAGTTGTTATCATC 1605
Db 20 TTACAGAGCTTGATATCATC 1

RESULT 104
US-10-174-456-117
; Sequence 117, Application US/10174456
; Publication No. US20030235910A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 49 EXPRESSION
; FILE REFERENCE: RTS-0374
; CURRENT APPLICATION NUMBER: US/10/174,456
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 139
; SEQ ID NO 117
; LENGTH: 20
; TYPE: DNA
```

```

; ORGANISM: H. sapiens
; FEATURE:
US-10-174-456-117

Query Match
Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1586 TTAAGAGTTGTTATCATC 1605
Db 1 TTACAGAGCTTGATATCATC 20

RESULT 105
US-10-177-554-23/c
; Sequence 23, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-23

Query Match
Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1942 GAAGACCTGAAGAAGTCCG 1961
Db 20 GAGGACCTGAAGAAGTACCG 1
```

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RESULT 106
US-10-177-554-165
; Sequence 165, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 165
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-177-554-165

Query Match
Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1942 GAAGACCTGAAGAAGTCCG 1961
Db 1 GAGGACCTGAAGAAGTACCG 20

RESULT 107
US-10-349-143-6860
; Sequence 6860, Application US/10349143
```

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marla

TITLE OF INVENTION: Ballelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CPI

CURRENT APPLICATION NUMBER: US/10/349,143

PRIOR FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO: 6860

LENGTH: 20

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: primer\_bind

LOCATION: 1...20

OTHER INFORMATION: upstream amplification primer 99-19860 for SEQ 2926.

US-10-349-143-6860

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2385 TTACACAGAAATGCTGCTGG 2404

DB 1 TGACACAGAAATGAGCTGG 20

RESULT 108

US-10-447-136-151/c

Sequence 151, Application US/10447136

Publication No. US20040009948A1

GENERAL INFORMATION:

APPLICANT: WRIGHT, Jim A.

APPLICANT: YOUNG, Aiping H.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and

FILE REFERENCE: 032396-023

CURRENT APPLICATION NUMBER: US/10/447,136

PRIOR FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040

PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959

PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01

NUMBER OF SEQ ID NOS: 220

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO: 151

LENGTH: 20

TYPE: DNA

ORGANISM: Human

US-10-447-136-151

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAAGAAGAGGTGAAGACT 1687

DB 20 GGAAGCAGGGTTGAAGACT 1

RESULT 109

US-10-211-179-39

Sequence 39, Application US/10211179

Publication No. US20040023906A1

GENERAL INFORMATION:

APPLICANT: Kenneth M. Dobie

APPLICANT: Nicholas M. Dean

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTRYSYL PHOSPHATASE ACTIVATOR EXP

FILE REFERENCE: PLS-0011

CURRENT APPLICATION NUMBER: US/10/211,179

PRIOR FILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US/10/211,179

PRIOR FILING DATE: 2002-08-01

NUMBER OF SEQ ID NOS: 119

SEQ ID NO: 39

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-211-179-39

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 944 ATGACTCCAGGAGGTAAA 963

DB 1 ATGACTCCAGGAGGTAAA 20

RESULT 110

US-10-688-706-201/c

Sequence 201, Application US/10688706

Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Broesch, Kay

TITLE OF INVENTION: ANTISENSE MODULATION OF GPR EXPRESSION

FILE REFERENCE: 01393/1

CURRENT APPLICATION NUMBER: US/10/688,706

PRIOR FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: Patentln version 3.2

SEQ ID NO: 201

LENGTH: 20

TYPE: DNA

ORGANISM: artificial

OTHER INFORMATION: human GPR antisense

US-10-688-706-201

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 64;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2338 CTCACGATCTCATGAGGG 2357

DB 20 CTCACGATCTCATGAGGG 1

RESULT 111

US-10-652-795-421

Sequence 421, Application US/10652795

Publication No. US20040142346A1

GENERAL INFORMATION:

APPLICANT: Baker, Brenda

APPLICANT: Butlett, C. Frank

APPLICANT: Bennett, C. Frank

APPLICANT: Shanahan, William M.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALP

OTHER INFORMATION: ALPHA EXPRESSION

```
FILE REFERENCE: ISPH-0501
CURRENT APPLICATION NUMBER: US/10/652,795
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/824,322B
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 09/313,932
PRIOR FILING DATE: 1999-05-18
PRIOR APPLICATION NUMBER: US 09/166,186
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 503
SEQ ID NO 421
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-652-795-421

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1783 CGGTATGTGAGAGAGAGA 1802
DB      1 CAGTATGTGAGAGAGAGA 20

RESULT 112
US-10-647-918-421
Sequence 421, Application US/10647918
Publication No. US20040152652A1
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
FILE REFERENCE: ISPH-0501
CURRENT APPLICATION NUMBER: US/10/647,918
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US/09/824,322B
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 09/313,932
PRIOR FILING DATE: 1999-05-18
PRIOR APPLICATION NUMBER: US 09/166,186
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 503
SEQ ID NO 421
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-647-918-421

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1783 CGGTATGTGAGAGAGAGA 1802
DB      1 CAGTATGTGAGAGAGAGA 20

RESULT 113
US-10-349-143-8522
Sequence 8522, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Matra
APPLICANT: Chumakov, Ilya
```

```
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 8522
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: downstream amplification primer 99-16140 for SEQ 657, in complete
US-10-349-143-8522

Query Match      0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      864 CCCAGATGAACA 878
DB      3 CCCAGATGAACA 17

RESULT 114
US-09-752-983-11/c
Sequence 11, Application US/09752983
Patent No. US20010016575A1
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDW2
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESS: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
FILING DATE: 02-Jan-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
```

TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-09-752-983-11

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGTACTACTGATGG 1721  
DB 19 TGTACTACTGATGG 5

RESULT 115  
US-09-851-771A-11/c  
Sequence 11, Application US/09851771A  
Patent No. US2002015151A1

GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J. Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF HUMAN MDM2 EXPRESSION

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 66 East Main Street

CITY: Marlton

STATE: NJ

COUNTRY: U.S.A.

ZIP: 08053

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION NUMBER: US/09/851,771A

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/048,810

FILING DATE: 1998-03-26

ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0302

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-779-2400

TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-851-771A-11

Query Match 0.6%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGTACTACTGATGG 1721

DB 19 TGTACTACTGATGG 5

RESULT 116  
US-10-244-367-45/c  
Sequence 45, Application US/10244367  
Publication No. US20030113773A1  
GENERAL INFORMATION:

APPLICANT: Mikoshiba, Katsuhiko

APPLICANT: Aruga, Jun

APPLICANT: Nagai, Takeharu

APPLICANT: Katsunori, Nakata

TITLE OF INVENTION: Neurogenesis Inducing Gene

FILE REFERENCE: HIRAKI-03814

CURRENT APPLICATION NUMBER: US/10/244,367

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US/09/342,325

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: JP98/86979

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: JP98/121456

PRIOR FILING DATE: 1998-04-30

PRIOR APPLICATION NUMBER: 09/172,045

PRIOR FILING DATE: 1998-09-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-244-367-45

Query Match 0.6%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1106 GCTTGCGACCTTC 1120

DB 17 GCTTGCGACCTTC 3

RESULT 117  
US-10-005-344-11/c  
Sequence 11, Application US/10005344  
Publication No. US20030203862A1

GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia

APPLICANT: Pamela Nero

APPLICANT: Mark J. Graham

APPLICANT: Brett P. Monia

APPLICANT: Erich Koller

APPLICANT: Mingyi Chhang

APPLICANT: Mano Manoharan

TITLE OF INVENTION: Antisense Modulation of mdm2 expression.

FILE REFERENCE: ISPH-0622

CURRENT APPLICATION NUMBER: US/10/005,344

CURRENT FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: US 09/048,810

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: US 09/280,805

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 379

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-005-344-11

Query Match 0.6%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGTACTACTGATGG 1721

DB 19 TGTACTACTGATGG 5

```
RESULT 118
US-10-407-449-5
; Sequence 5, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Beares, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-407-449-5

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GGGGGGGGGGGGGG 404
Db 4 GGGGGGGGGGGGGG 18

RESULT 119
US-10-407-449-9
; Sequence 9, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Beares, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/10/407,449
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-407-449-9

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GGGGGGGGGGGGGG 404
Db 4 GGGGGGGGGGGGGG 18
```

```
RESULT 120
US-10-467-008-22
; Sequence 22, Application US/10467008
; Publication No. US20040116366A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT E
; FILE REFERENCE: ISPH-0746
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/US02/02805
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 09/780,045
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-467-008-22

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 CCCGCCGCCGCCGCCG 297
Db 2 CCCGCCGCCGCCGCCG 16
```

```
RESULT 121
US-10-660-897-9
; Sequence 9, Application US/10660897
; Publication No. US20040115706A1
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 532232000800
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/660,897
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: quadruplex forming sequence
US-10-660-897-9

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GGGGGGGGGGGGGG 404
Db 4 GGGGGGGGGGGGGG 18
```

```
RESULT 122
US-09-877-095-2
; Sequence 2, Application US/09877095
; Patent No. US20020123051A1
; GENERAL INFORMATION:
; APPLICANT: Danenberg, K. et al.
; TITLE OF INVENTION: METHOD OF DETERMINING A CHEMOTHERAPEUTIC
; TITLE OF INVENTION: REGIMEN BASED ON ERCC1 EXPRESSION
; FILE REFERENCE: 11220/127
; CURRENT APPLICATION NUMBER: US/09/877,095
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-09-877-095-2

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      410 GCGAGGCGAGGAGAGAG 427
Db      1 GCGAGGCGTGTAGGAAACAG 18

RESULT 123
US-09-969-373-2006
; Sequence 2006, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2006
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2006

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2057 CCCAAGCTTCCTCCATC 2074
Db      1 CCCAATCTACCTCCATC 18

RESULT 124
US-10-235-463-37/c
; Sequence 37, Application US/10235463
; Publication No. US20040043448A1
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/10/235,463
; CURRENT FILING DATE: 2003-01-10
```

```
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-235-463-37

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2304 CACAGTGGATGAAACCG 2321
Db      18 CACATGGAGGAACCG 1

RESULT 125
US-10-235-463-40/c
; Sequence 40, Application US/10235463
; Publication No. US20040043448A1
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/10/235,463
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-235-463-40

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2304 CACAGTGGATGAAACCG 2321
Db      18 CACATGGAGGAACCG 1

RESULT 126
US-10-235-463-66/c
; Sequence 66, Application US/10235463
; Publication No. US20040043448A1
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/10/235,463
```

```
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-235-463-66
```

```
Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2304 CACAGTGGATGGAACCG 2321
DB 18 CACATTGGGAGGAAACCG 1
```

```
RESULT 127
US-10-235-463-68/c
; Sequence 68; Application US/10235463
; Publication No. US20040043448A1
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/10/235,463
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-235-463-68
```

```
Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2304 CACAGTGGATGGAACCG 2321
DB 18 CACATTGGGAGGAAACCG 1
```

```
RESULT 128
US-10-108-260A-5373/c
; Sequence 5373; Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
```

```
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5373
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized r
US-10-108-260A-5373
```

```
Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 621 GGGCAGTATGATGACCA 638
DB 18 GGGCAGTATGATGACCA 1
```

```
RESULT 129
US-10-349-143-6054
; Sequence 6054; Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/062,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6054
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8638 for SEQ 2120,
US-10-349-143-6054
```

```
Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1987 GAGAAGAGAGAGGAG 2004
DB 1 GAGAAGAGAGAGGAG 18
```

```
RESULT 130
US-10-349-143-8778/c
; Sequence 8778; Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
```

```

; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8778
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-18198 for SEQ 913, in compleme
US-10-349-143-8778

Query Match
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 687 GCGATCAGATTCAGG 704
DB 18 CAAGTCACAGATCAGG 1

RESULT 131
US-10-349-143-11519/c
; Sequence 11519, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11519
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-899 for SEQ 3654, in compleme
US-10-349-143-11519

Query Match
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1930 GAGGACTTTAAAGAGC 1947
DB 18 GAGGCTTTTAAAGAGC 1

RESULT 132
US-10-453-784-2
; Sequence 2, Application US/10453784
; Publication No. US20040005621A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Danenberg, Kathleen
; TITLE OF INVENTION: METHOD OF DETERMINING A CHEMOTHERAPEUTIC
; TITLE OF INVENTION: REGIMEN BASED ON ESCC1 EXPRESSION
; FILE REFERENCE: 11220/145
; CURRENT APPLICATION NUMBER: US/10/453,784
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: US/09/988,784
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/877,095
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/796,491
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-453-784-2

Query Match
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 410 GCGAGGCGAGAGAG 427
DB 1 GCGAGGCGTGAAGAGAG 18

RESULT 133
US-10-444-795B-470
; Sequence 470, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - cdc25B.2
US-10-444-795B-470

Query Match
Best Local Similarity 72.2%; Pred. No. 74;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 1658 GCGGATTCAGAGCTTC 1875
DB 2 GCGGCTUACAGAGAGUUC 19

RESULT 134
US-10-444-795B-471/c
; Sequence 471, Application US/10444795B
; Publication No. US2004007574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
```

```

; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 471
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - cdc25B.2
US-10-444-795B-471

```

```

Query Match          0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.8%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1858 GGGGATACAGAGATTTC 1875

DB 18 GGGGGCTACAGAGATTTC 1

```

RESULT 135
US-09-927-046-879/c
; Sequence 879, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 879
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-879

```

```

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1175 TCTGACAGCTCTCT 1190

DB 16 TTTGACAGCTCTCT 1

```

RESULT 136
US-09-927-046-1525/c
; Sequence 1525, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 1525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1525

```

```

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1177 TGGACAGCTCTCTCG 1192

DB 16 TGGACAGCTCTCTCG 1

```

RESULT 137
US-09-927-046-1638
; Sequence 1638, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1638
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1638

```

```

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 85;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1997 AGAGGAGATGTACAG 2012

DB 1 ACAGGAGAGUACAG 16

```

RESULT 138
US-09-927-046-1907
; Sequence 1907, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 3450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1907
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1907

```

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 85;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1997 AGAGGAGATGTACAG 2012  
 DB 2 ACAGGAGAGUUGUACG 17

RESULT 139  
 US-09-927-046-2042/c  
 ; Sequence 2042, Application US/09927046  
 ; Publication No. US20030064946A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc  
 ; APPLICANT: McSwigen, Jim  
 ; APPLICANT: Thompson, Jim  
 ; APPLICANT: McKenzie, Jim  
 ; APPLICANT: Ayers, Dave  
 ; APPLICANT: Grupe, Andrew  
 ; APPLICANT: Szymkowski, Edmund  
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori  
 ; FILE REFERENCE: 249/021  
 ; CURRENT APPLICATION NUMBER: US/09/927,046  
 ; CURRENT FILING DATE: 2001-08-09  
 ; NUMBER OF SEQ ID NOS: 5450  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2042  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-927-046-2042

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 85;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1178 GGACAGCTCCTCCGT 1193  
 DB 17 GGACAGCTCCTCTAGT 2

RESULT 140  
 US-10-060-756A-137  
 ; Sequence 137, Application US/10060756A  
 ; Publication No. US20030046717A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Jian  
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
 ; FILE REFERENCE: PB0177  
 ; CURRENT APPLICATION NUMBER: US/10/060,756A  
 ; CURRENT FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/327,898  
 ; PRIOR FILING DATE: 2001-10-09  
 ; NUMBER OF SEQ ID NOS: 4804  
 ; SOFTWARE: Aecmca Sequence Listing Engine  
 ; SEQ ID NO 137

LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-060-756A-137  
 Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 85;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2049 AGCAGAGCCCAAGCT 2064  
 DB 2 AGCAGAGCCCAAGCT 17

RESULT 141  
 US-10-060-756A-138  
 ; Sequence 138, Application US/10060756A  
 ; Publication No. US20030046717A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Jian  
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
 ; FILE REFERENCE: PB0177  
 ; CURRENT APPLICATION NUMBER: US/10/060,756A  
 ; CURRENT FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 09/864,761  
 ; PRIOR FILING DATE: 2001-10-09  
 ; NUMBER OF SEQ ID NOS: 4804  
 ; SOFTWARE: Aecmca Sequence Listing Engine  
 ; SEQ ID NO 138  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-060-756A-138

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 85;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2049 AGCAGAGCCCAAGCT 2064  
 DB 1 AGCAGAGCCCAAGCT 16

RESULT 142  
 US-10-230-006-32/c  
 ; Sequence 32, Application US/10230006  
 ; Publication No. US20030191077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Fosnaugh, Kathy  
 ; APPLICANT: McSwigen, Jim  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
 ; FILE REFERENCE: 400/056 (METH01-1110)  
 ; CURRENT APPLICATION NUMBER: US/10/230,006  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: US 60/315,315  
 ; PRIOR FILING DATE: 2001-08-26  
 ; NUMBER OF SEQ ID NOS: 2678  
 ; SOFTWARE: PatentIn version 3.0

SEQ ID NO 32  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-230-006-32

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 85;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2023 AACCTCGAGGCGGC 2038  
DB 16 AACCTCGAGGCGGC 1

RESULT 143  
US-10-230-006-512/c  
Sequence 512, Application US/10230006  
Publication No. US20030191077A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Fosnagat, Kathy  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
FILE REFERENCE: 400/056 (MEHB01-1110)  
CURRENT APPLICATION NUMBER: US/10/230,006  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US 60/315,315  
PRIOR FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 2678  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 512  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-230-006-512

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 85;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2023 AACCTCGAGGCGGC 2038  
DB 17 AACCTCGAGGCGGC 2

RESULT 144  
US-10-138-674-2030/c  
Sequence 2030, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MEHB00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2030  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-138-674-2030

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 85;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 TCTTCATCATCTTTA 1404  
DB 17 TCTTCATCATCTTTA 2

RESULT 145  
US-10-138-674-5403/c  
Sequence 5403, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R  
FILE REFERENCE: MEHB00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5403  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-138-674-5403

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 85;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 163 CTTTGTTGGATTTA 178  
DB 17 CTTTGTTGGATTTA 2

RESULT 146  
US-10-138-674-8374/c  
Sequence 8374, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MEHB00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8374  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-138-674-8374

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 85;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 409 GGCGAGCGCAGAGAA 424  
DB 17 GGCGAGCGCAGAGAA 2

RESULT 147  
US-10-287-949A-2030/c  
Sequence 2030, Application US/10287949A  
Publication No. US20040102389A1

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Scinichcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2030
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-2030

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1389 TCTTCATCAGCTCTTA 1404
DB      17  TCTTCATCATCTTTA 2

RESULT 148
US-10-287-949A-5403/C
; Sequence 5403, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Scinichcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5403
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5403

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      163 CGTTGTTTGATTTA 178
DB      17  CTTTGTGTTGATTTA 2

RESULT 149
US-10-287-949A-8374/C
; Sequence 8374, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Scinichcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8374
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8374

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      409 GCGCGAGCGCAGAGAA 424
DB      17  GCGCGAGCGCAGAGAA 2

RESULT 150
US-10-418-819-52
; Sequence 52, Application US/10418819
; Publication No. US20030224493A1
; GENERAL INFORMATION:
; APPLICANT: Eirich, L. Dudley
; APPLICANT: Craft, David L.
; TITLE OF INVENTION: PATTY ALCOHOL OXIDASE GENES AND PROTEINS FROM Candida tropicalis
; FILE REFERENCE: U0154 (1010-92)
; CURRENT APPLICATION NUMBER: US/10/418,819
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/374,021
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-10-418-819-52

Query Match      0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      237 GCACCGGCGCTGTGG 252
DB      4  GCACCGATGCTGTGG 19

RESULT 151
US-10-151-542A-15
; Sequence 15, Application US/10151542A
; Publication No. US20030096348A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Fang
; APPLICANT: Chen, Fang
; TITLE OF INVENTION: DNA MOLECULES ENCODING MAMMALIAN NUCLEAR
; FILE REFERENCE: 20083PIA
; CURRENT APPLICATION NUMBER: US/10/151,542A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/326,755
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 09/581,033
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/26422
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/069,379
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 19
```

```
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8374
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8374

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      409 GCGCGAGCGCAGAGAA 424
DB      17  GCGCGAGCGCAGAGAA 2

RESULT 150
US-10-418-819-52
; Sequence 52, Application US/10418819
; Publication No. US20030224493A1
; GENERAL INFORMATION:
; APPLICANT: Eirich, L. Dudley
; APPLICANT: Craft, David L.
; TITLE OF INVENTION: PATTY ALCOHOL OXIDASE GENES AND PROTEINS FROM Candida tropicalis
; FILE REFERENCE: U0154 (1010-92)
; CURRENT APPLICATION NUMBER: US/10/418,819
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/374,021
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-10-418-819-52

Query Match      0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      237 GCACCGGCGCTGTGG 252
DB      4  GCACCGATGCTGTGG 19

RESULT 151
US-10-151-542A-15
; Sequence 15, Application US/10151542A
; Publication No. US20030096348A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Fang
; APPLICANT: Chen, Fang
; TITLE OF INVENTION: DNA MOLECULES ENCODING MAMMALIAN NUCLEAR
; FILE REFERENCE: 20083PIA
; CURRENT APPLICATION NUMBER: US/10/151,542A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/326,755
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 09/581,033
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/26422
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/069,379
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 19
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TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-10-151-542A-15

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 84;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1968 GAGCGGAGCCTGGGCA 1983  
DB 4 GAGCGGAGCCTGGGCA 19

RESULT 152  
US-10-665-951-1515/c  
Sequence 1515, Application US/10665951  
Publication No. US20040138163A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/131 (MEH02-742-F)  
CURRENT FILING DATE: US/10/665,951  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 10/664,668  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: PCT/US 03/05022  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 10/287,949  
PRIOR FILING DATE: 2002-11-04  
PRIOR APPLICATION NUMBER: US 10/306,747  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: PCT/US 02/17674  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2455  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1515  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1  
US-10-665-951-1515

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 84;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 253 CTGCTGGCTGGGCGCT 268  
DB 17 CCGGUGGCTGGGCGCT 2

RESULT 153  
US-10-665-951-1762  
Sequence 1762, Application US/10665951

Publication No. US20040138163A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/131 (MEH02-742-F)  
CURRENT FILING DATE: US/10/665,951  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 10/664,668  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: PCT/US 03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 10/287,949  
PRIOR FILING DATE: 2002-11-04  
PRIOR APPLICATION NUMBER: US 10/306,747  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: PCT/US 02/17674  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2455  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1762  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-665-951-1762

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 75.0%; Pred. No. 84;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 253 CTGCTGGCTGGGCGCT 268  
DB 3 CCGGUGGCTGGGCGCT 18

RESULT 154  
US-10-236-392-441/c  
Sequence 441, Application US/10236392  
Publication No. US20040067490A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Burgess, Catherine, E  
APPLICANT: Casman, Stacie J  
APPLICANT: Catterton, Elina  
APPLICANT: Chapoyal, Andrei  
APPLICANT: Crabtree, Julie  
APPLICANT: Edinger, Shlomit, R  
APPLICANT: Eilerman, Karen  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Grose, William M  
APPLICANT: Gusev, Vladimir  
APPLICANT: Kexuda, Ramesh  
APPLICANT: Larochele, William J  
APPLICANT: Li, Li

```

/ APPLICANT: MacDougall, John R
/ APPLICANT: Malpankar, Uriel M
/ APPLICANT: Miller, Charles E
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Patuajan, Meera
/ APPLICANT: Pena, Carol A
/ APPLICANT: Peyman, John A
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Reiger, Daniel K
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Shinkets, Richard A
/ APPLICANT: Smithson, Glenda
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-442A
/ CURRENT APPLICATION NUMBER: US/10/236,392
/ PRIOR FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US09/540,763
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US60/390,155
/ PRIOR FILING DATE: 2002-06-19
/ PRIOR APPLICATION NUMBER: US09/635,949
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: US60/318,765
/ PRIOR FILING DATE: 2001-09-12
/ PRIOR APPLICATION NUMBER: US60/357,303
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: US60/367,753
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: US60/369,479
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: US09/659,634
/ PRIOR FILING DATE: 2000-09-12
/ PRIOR APPLICATION NUMBER: US60/318,120
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US60/318,130
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 794
/ SOFTWARE: Custom
/ SEQ ID NO 441
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-441

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTGGGGCC 1347
DB      14 GCATGCTGGGGCC 1

RESULT 155
US-10-236-392-498/c
/ Sequence 498, Application US/10236392
/ Publication No. US20040067490A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, David W
/ APPLICANT: Boldog, Ferenc L
/ APPLICANT: Burgess, Catherine, E
/ APPLICANT: Casman, Stacie J
/ APPLICANT: Catterton, Elina
/ APPLICANT: Chapoval, Andrei
/ APPLICANT: Crabtree, Julie
/ APPLICANT: Edinger, Shlomil, R
/ APPLICANT: Ellemann, Karen
/ APPLICANT: Gerlach, Valerie

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/ APPLICANT: Gorman, Linda
/ APPLICANT: Grose, William M
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Larocheille, William J
/ APPLICANT: Li, Li
/ APPLICANT: MacDougall, John R
/ APPLICANT: Malpankar, Uriel M
/ APPLICANT: Miller, Charles E
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Patuajan, Meera
/ APPLICANT: Pena, Carol A
/ APPLICANT: Peyman, John A
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Reiger, Daniel K
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Shinkets, Richard A
/ APPLICANT: Smithson, Glenda
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-442A
/ CURRENT APPLICATION NUMBER: US/10/236,392
/ PRIOR FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US09/540,763
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US60/390,155
/ PRIOR FILING DATE: 2002-06-19
/ PRIOR APPLICATION NUMBER: US09/635,949
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: US60/318,765
/ PRIOR FILING DATE: 2001-09-12
/ PRIOR APPLICATION NUMBER: US60/357,303
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: US60/367,753
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: US60/369,479
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: US09/659,634
/ PRIOR FILING DATE: 2000-09-12
/ PRIOR APPLICATION NUMBER: US60/318,120
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US60/318,130
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 794
/ SOFTWARE: Custom
/ SEQ ID NO 498
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-498

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTGGGGCC 1347
DB      14 GCATGCTGGGGCC 1

RESULT 156
US-10-236-392-567/c
/ Sequence 567, Application US/10236392
/ Publication No. US20040067490A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, David W
/ APPLICANT: Boldog, Ferenc L
/ APPLICANT: Burgess, Catherine, E
/ APPLICANT: Casman, Stacie J

```

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APPLICANT: Caterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Grosse, William M
APPLICANT: Gusev, Vladimir
APPLICANT: Kekuda, Ramesh
APPLICANT: Larocheille, William J
APPLICANT: Li, Li
APPLICANT: MacDougall, John R
APPLICANT: Malvankar, Uriel M
APPLICANT: Miller, Charles E
APPLICANT: Milet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol A
APPLICANT: Peyman, John A
APPLICANT: Rastelli, Luca
APPLICANT: Reiger, Daniel K
APPLICANT: Rotenberg, Mark E
APPLICANT: Shenoy, Suresh
APPLICANT: Shinkets, Richard A
APPLICANT: Smithson, Glenda
APPLICANT: TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US60/390,155
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US09/635,949
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US60/318,765
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/357,303
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US60/367,753
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US60/369,479
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US09/659,634
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR FILING DATE: 2001-09-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NO 567
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-567

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTGGGGCC 1347
         |||||
Db       14 GCATGCTGGGGCC 1

```

```

Publication No. US20040067490A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Caterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Grosse, William M
APPLICANT: Gusev, Vladimir
APPLICANT: Kekuda, Ramesh
APPLICANT: Larocheille, William J
APPLICANT: Li, Li
APPLICANT: MacDougall, John R
APPLICANT: Malvankar, Uriel M
APPLICANT: Miller, Charles E
APPLICANT: Milet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol A
APPLICANT: Peyman, John A
APPLICANT: Rastelli, Luca
APPLICANT: Reiger, Daniel K
APPLICANT: Rotenberg, Mark E
APPLICANT: Shenoy, Suresh
APPLICANT: Shinkets, Richard A
APPLICANT: Smithson, Glenda
APPLICANT: TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US60/390,155
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US09/635,949
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US60/318,765
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/357,303
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US60/367,753
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US60/369,479
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US09/659,634
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR FILING DATE: 2001-09-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NO 597
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-597

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTGGGGCC 1347
         |||||

```

RESULT 157  
US-10-236-392-597/c  
Sequence 597, Application US/10236392

Db 14 GCATGCTGGGGCC 1

RESULT 158

```

US-10-236-392-630/c
; Sequence 630, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elna
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grose, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Laroche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 630
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-630

```

Query Match 0.6%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1334 GCATGCTGGGGCC 1347  
 Db 14 GCATGCTGGGGCC 1

RESULT 159

```

US-10-236-392-660/c
; Sequence 660, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elna
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grose, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Laroche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 660
; LENGTH: 15

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-660

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTCTGGGGCC 1347
Db      14 GCATGCTCTGGGGCC 1

RESULT 160
US-10-236-392-735/c
; Sequence 735, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larocheille, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Weera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
```

```

; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 735
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-735

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTCTGGGGCC 1347
Db      14 GCATGCTCTGGGGCC 1

RESULT 161
US-10-236-392-765/c
; Sequence 765, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larocheille, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Weera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
```

```

; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 765
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-765

Query Match          0.6%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1334 GCATGCTGGGGCC 1347
DB      14 GCATGCTGGGGCC 1

RESULT 162
US-09-927-046-1376
; Sequence 1376, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Avers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Symkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1376
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1376

Query Match          0.6%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 97;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1999 AGGAGATGTACAG 2012
DB      1 AGGAGAGUGUACAG 14

RESULT 163
US-10-238-700-3565/c
; Sequence 3565, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3565
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3565

Query Match          0.6%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2189 TGGAGCCCGAGGCA 2202
DB      14 TGGAGCCCGAGGCA 1

RESULT 164
US-10-138-674-1037/c
; Sequence 1037, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1037
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1037

Query Match          0.6%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      165 TTGCTTGATTTA 178
DB      17 TTGCTTGATTTA 4

RESULT 165
US-10-138-674-5402/c
; Sequence 5402, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5402
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5402
```

US-10-138-674-5402

Query Match 0.6%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
 |||||  
 DB 16 TTGTGTTGATTTA 3

RESULT 166  
 US-10-287-949A-1037/c  
 ; Sequence 1037, Application US/10287949A  
 ; Publication No. US20040102389A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Payco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; FILE REFERENCE: MEB00-876-N (400/049)  
 ; CURRENT APPLICATION NUMBER: US/10/287,949A  
 ; CURRENT FILING DATE: 2003-04-11  
 ; NUMBER OF SEQ ID NOS: 20822  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1037  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-287-949A-1037

Query Match 0.6%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
 |||||  
 DB 17 TTGTGTTGATTTA 4

RESULT 167  
 US-10-287-949A-5402/c  
 ; Sequence 5402, Application US/10287949A  
 ; Publication No. US20040102389A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Payco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; FILE REFERENCE: MEB00-876-N (400/049)  
 ; CURRENT APPLICATION NUMBER: US/10/287,949A  
 ; CURRENT FILING DATE: 2003-04-11  
 ; NUMBER OF SEQ ID NOS: 20822  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5402  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-287-949A-5402

Query Match 0.6%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
 |||||  
 DB 16 TTGTGTTGATTTA 3

RESULT 168  
 US-09-878-582-14/c  
 ; Sequence 14, Application US/09878582  
 ; Patent No. US20020058639A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Lex M. Cowseert  
 ; APPLICANT: Robert McKay  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION  
 ; FILE REFERENCE: ISPH-0463  
 ; CURRENT APPLICATION NUMBER: US/09/878,582  
 ; CURRENT FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: 09/577,902  
 ; PRIOR FILING DATE: 2000-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/358,381  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: PCT/US99/29594,  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 51  
 ; SEQ ID NO 14  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-878-582-14

Query Match 0.6%; Score 14; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 GTGGCTGTACCA 586  
 |||||  
 DB 15 GTGGCTGTACCA 2

RESULT 169  
 US-10-336-213B-14/c  
 ; Sequence 14, Application US/10336213B  
 ; Publication No. US20040002153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Lex M. Cowseert  
 ; APPLICANT: Robert McKay  
 ; APPLICANT: Tim Vickers  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION  
 ; FILE REFERENCE: ISIS0004-100  
 ; CURRENT APPLICATION NUMBER: US/10/336,213B  
 ; CURRENT FILING DATE: 2003-01-03  
 ; PRIOR APPLICATION NUMBER: US 60/411,780  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: US 09/878,582  
 ; PRIOR FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: US 09/577,902  
 ; PRIOR FILING DATE: 2000-05-24  
 ; PRIOR APPLICATION NUMBER: PCT/US99/29594  
 ; PRIOR FILING DATE: 1999-12-14  
 ; PRIOR APPLICATION NUMBER: US 09/358,381  
 ; PRIOR FILING DATE: 1999-07-21  
 ; NUMBER OF SEQ ID NOS: 88  
 ; SEQ ID NO 14  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide  
 US-10-336-213B-14

Query Match 0.6%; Score 14; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 573 GTGCGCTGTACCA 586  
Db 15 GTGCGCTGTACCA 2

Search completed: September 20, 2004, 10:10:40  
Job time : 6 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 10:11:26 / Search time 1 Seconds  
(without alignments)  
0.097 Million cell updates/sec

Title: US-08-864-955-1

Sequence: 2415  
1 CGAAGCGCCGCGCTTGCTG.....GCTGCCCAATAGCAAGAG 2419

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 1 segs, 20 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 10

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database: rst1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.2	0.6	20	1 AZ792281	ACCESSION:AZ792281

#### ALIGNMENTS

RESULT 1  
AZ792281/c 20 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0043F09R Mouse 10kb plasmid UUGCJM library Mus musculus genomic  
DEFINITION clone UUGC2M0043F09 R, genomic survey sequence.  
ACCESSION AZ792281  
VERSION AZ792281.1 GI:12936051  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
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Class: plasmid ends  
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/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	Best Local Similarity	Score	DB 1	Length	20
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	85.0%;	Pred. No. 0;			
	Mismatches 3;	Indels 0;	Gaps 0;		
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DB 20 CCACCTGCACGTATGTC 1					

Search completed: September 20, 2004, 10:11:27  
Job time : 1 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 10:04:58 ; Search time 5 Seconds

(without alignments)  
3,547 Million cell updates/sec

Title: US-08-864-955-1

Perfect score: 2419

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 190 seqs, 3666 residues

Total number of hits satisfying chosen parameters: 380

Minimum DB seq length: 10

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 194 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	24	1.0	24	1	AR197877
6	24	1.0	24	1	AR260030
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VERSION  
AX164904.1 GI:14545733

KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1  
AUTHORS  
Shinketsu, R.A. and leach, W.  
TITLE  
Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL  
Patent: WO 0138586-A 99 31-MAY-2001;  
Curagen Corporation (US)

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ACCESSION  
AR090841.1 GI:10017596  
VERSION  
AR090841.1  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.

ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
Chenichik, A., Jochhadze, G. and Bibilashvili, R.  
TITLE  
Methods of assaying differential expression  
JOURNAL  
Patent: US 5994076-A 961 30-NOV-1999;  
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DEFINITION Sequence 962 from patent US 5994076.
ACCESSION  AR090842
VERSION     AR090842.1 GI:10017597
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 5994076-A 962 30-NOV-1999;
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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6352829-A 961 05-MAR-2002;
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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6352829-A 962 05-MAR-2002;
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ACCESSION  AR260030
VERSION     AR260030.1 GI:27310541
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6489455-A 961 03-DEC-2002;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1632 GGGAGGCCACATCAAGGTCGAGT 1655
      |||
      1 GGGAGGCCACATCAAGGTCGAGT 24
      |||

RESULT 7
LOCUS      AR260031      24 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 962 from patent US 6489455.
ACCESSION  AR260031
VERSION     AR260031.1 GI:27310542
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Chenchik,A., Johhadze,G. and Bibilashvili,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6489455-A 962 03-DEC-2002;
FEATURES
            Location/Qualifiers
            source
              1..24
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No.3.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1954 AAGTCCGACCAAGCGGACC 1977

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DB 24 AAGTCCGACCAAGAGCCGAC 1

RESULT 8  
LOCUS AX096478 21 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 1656 from Patent WO0118250.  
ACCESSION AX096478  
VERSION AX096478.1 GI:13512732  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Lander, E.S., Garfili, M., Ireland, J.S., Bol, S., Daley, G.O. and  
McCarthy, J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: WO 0118250-A 1656 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium  
Pharmaceuticals, Inc. (US)

FEATURES  
source location/Qualifiers  
1..21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 9.6;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1339 TCTGGGGCCGACCCCAAGAG 1359

DB 1 TCTGGGGCCGACCCCAAGAG 21

RESULT 9  
LOCUS AX468631 20 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 26 from Patent WO0240710.  
ACCESSION AX468631  
VERSION AX468631.1 GI:21901429  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.  
TITLE Method for detecting methylation states for a toxicological  
JOURNAL diagnostic  
Patent: WO 0240710-A 26 23-MAY-2002;  
EpiGenomics AG (DE)

FEATURES  
source location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="chemically treated genomic DNA (Homo sapiens)"

Query Match 0.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 164 GTTGTGGATTATCTT 163

DB 20 GTTGTGGATTATCTT 1

RESULT 10  
LOCUS AX599169 20 bp DNA linear PAT 14-FEB-2003  
DEFINITION Sequence 509 from Patent WO02077272.

ACCESSION AX599169  
VERSION AX599169.1 GI:26399311  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Berlin, K., Braun, A., Dietler, J., Guetig, D., Howe, A., Mueller, J.,  
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Liu, E.,  
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,  
Pellet, C. and Ziebarth, H.  
TITLE Methods and nucleic acids for the analysis of hematopoietic cell  
JOURNAL proliferative disorders  
Patent: WO 02077272-A 509 03-OCT-2002;  
EpiGenomics AG (DE)

FEATURES  
source location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection primer for CDC25A"

Query Match 0.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 164 GTTGTGGATTATCTT 163

DB 20 GTTGTGGATTATCTT 1

RESULT 11  
LOCUS A51842 23 bp DNA linear PAT 10-MAR-1997  
DEFINITION Sequence 6 from Patent WO9620011.  
ACCESSION A51842  
VERSION A51842.1 GI:4530005  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE  
AUTHORS Blakey, D.C., Davies, D.H., Dowell, R.I., Hennam, J.F., Marsham, P.R.,  
Slater, Anthony, M. and Hennequin, L.F.  
TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS  
JOURNAL Patent: WO 9620011-A 6 04-JUL-1996;  
ZENEGA LTD (GB)  
COMMENT On Mar 27, 1999 this sequence version replaced gi:2304590.  
Other publication AU 4269796 960719.

FEATURES  
source location/Qualifiers  
1..23  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 28;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACCACTGCGAGGCTG 621

DB 23 CTATGACCACTGCGAGGCTG 1

RESULT 12  
LOCUS A51879 23 bp DNA linear PAT 10-MAR-1997  
DEFINITION Sequence 43 from Patent WO9620011.  
ACCESSION A51879  
VERSION A51879.1 GI:2304627  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

```

REFERENCE
  AUTHORS
    1 (bases 1 to 23)
    Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R.,
    Slater,Anthony,M. and Hennequin,L.F.
  TITLE
    CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
  JOURNAL
    ZENECA LTD (GB)
  COMMENT
    Other publication AU 4269796 960719.
  FEATURES
    source
      1..23
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db
  599 CTATGACCACTGCTGACAGTCTG 621
  23 CTGTGACCTGCTGACAGTCTG 1

RESULT 13
  A51891/c
  LOCUS
    A51891 Sequence 55 from Patent WO9620011.
  DEFINITION
    A51891
  ACCESSION
    A51891.1 GI:2304639
  VERSION
    A51891.1 GI:2304639
  KEYWORDS
    unidentified
  SOURCE
    unidentified
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 23)
    Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R.,
    Slater,Anthony,M. and Hennequin,L.F.
  TITLE
    CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS
  JOURNAL
    ZENECA LTD (GB)
  COMMENT
    Other publication AU 4269796 960719.
  FEATURES
    source
      1..23
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db
  599 CTATGACCACTGCTGACAGTCTG 621
  23 CTGTGACCTGCTGACAGTCTG 1

RESULT 14
  A87525/c
  LOCUS
    A87525 Sequence 6 from Patent WO9835988.
  DEFINITION
    A87525
  ACCESSION
    A87525.1 GI:6736174
  VERSION
    A87525.1 GI:6736174
  KEYWORDS
    unidentified
  SOURCE
    unidentified
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 23)
    Edge,M.D.
  TITLE
    PROTEINS
  JOURNAL
    ZENECA LTD (GB); EDGE MICHAEL DEREK (GB)
  COMMENT
    Patent: WO 9835988-A 6 20-AUG-1998;
    Location/Qualifiers
      1..23
      /organism="unidentified"

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db
  599 CTATGACCACTGCTGACAGTCTG 621
  23 CTGTGACCTGCTGACAGTCTG 1

RESULT 15
  A87543/c
  LOCUS
    A87543 Sequence 24 from Patent WO9835988.
  DEFINITION
    A87543
  ACCESSION
    A87543.1 GI:6736191
  VERSION
    A87543.1 GI:6736191
  KEYWORDS
    unidentified
  SOURCE
    unidentified
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 23)
    Edge,M.D.
  TITLE
    PROTEINS
  JOURNAL
    ZENECA LTD (GB); EDGE MICHAEL DEREK (GB)
  COMMENT
    Patent: WO 9835988-A 24 20-AUG-1998;
    Location/Qualifiers
      1..23
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db
  599 CTATGACCACTGCTGACAGTCTG 621
  23 CTGTGACCTGCTGACAGTCTG 1

RESULT 16
  A8085844/c
  LOCUS
    A8085844 Sequence 39 from patent US 5985281.
  DEFINITION
    A8085844
  ACCESSION
    A8085844
  VERSION
    A8085844.1 GI:10012610
  KEYWORDS
    Unknown.
  SOURCE
    Unknown.
  ORGANISM
    Unknown.
    unclassified.
  REFERENCE
    1 (bases 1 to 23)
    Taylorson,C.John., Eggelte,H.Johannes., Tarragona-Fiol,A.,
    Rabin,B.Robert., Boyle,F.Thomas., Hennam,J.Frederick.,
    Blakey,D.Charles., Marsham,P.Robert., Heaton,D.William.,
    Davies,D.Huw., Slater,A.Michael. and Hennequin,L.Francois.Andre.
  TITLE
    Chemical compounds
  JOURNAL
    Patent: US 5985281-A 39 16-NOV-1999;
    Location/Qualifiers
      1..23
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db
  599 CTATGACCACTGCTGACAGTCTG 621
  23 CTGTGACCTGCTGACAGTCTG 1

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RESULT 17  
AR085856/c 23 bp DNA linear PAT 07-SEP-2000  
LOCUS AR085856  
DEFINITION Sequence 51 from patent US 5985281.  
ACCESSION AR085856  
VERSION AR085856.1 GI:10012622  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Taylorson,C.John., Eggelte,H.Johannes., Tarragona-Fiol,A.,  
Rabin,B.Robert., Boyle,F.Thomas., Henman,J.Friderick.,  
Blakey,D.Charles., Marsham,P.Robert., Heaton,D.William.,  
Davies,D.Huw., Slater,A.Michael. and Hennequin,L.Francois.Andre.  
Chemical compounds  
Patent: US 5985281-A 51 16-NOV-1999;  
LOCATION/Qualifiers  
1. 23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 28;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACCACTGCAGGCTCTG 621  
DB 23 CTGTGACCTGCTGCAGACTCTG 1

RESULT 18  
BOVINE04/c 21 bp DNA linear MAM 06-FEB-1999  
LOCUS BOVINE04  
DEFINITION Bovine DNA for microsatellite marker, 3' terminus.  
ACCESSION D83284  
VERSION D83284.1 GI:1199701  
KEYWORDS PCR primer.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
REFERENCE 1 (sites)  
AUTHORS Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,  
Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.  
Characterization of 42 highly polymorphic bovine microsatellite  
markers  
JOURNAL Anim. Genet. 27 (5), 365-368 (1996)  
MEDLINE 97083737  
PUBMED 8930081  
REFERENCE 2 (bases 1 to 21)  
AUTHORS Hirano,T., Nakane,S., Mizoshita,K., Inoue-Murayama,M., Watanabe,T.,  
Barendse,W. and Sugimoto,Y.  
Characterization of 42 bovine microsatellite markers  
Unpublished  
3 (bases 1 to 21)  
TITLE Direct Submission  
AUTHORS Sugimoto,Y.  
JOURNAL Submitted (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock  
Technology Association, Shikawa Institute of Animal Genetics;  
Nishigo Odakura, Nishishikawa, Fukushima 961, Japan  
(E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,  
Fax:0248-25-5725)  
LOCATION/Qualifiers  
1. 21  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
1. 21  
/note="microsatellite DIK062 PCR antisense primer"

Query Match 0.7%; Score 18; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 GTATGTGAGAGAGAGA 1802  
DB 21 GTATGTGAGAGAGAGA 4

RESULT 19  
ARI45501 21 bp DNA linear PAT 08-AUG-2001  
LOCUS ARI45501  
DEFINITION Sequence 6 from patent US 6211440.  
ACCESSION ARI45501  
VERSION ARI45501.1 GI:15107368  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Briggs,S.P., Johal,G. and Multani,D.Singh.  
TITLE Hm2 cDNA from maize encoding disease resistance polypeptide  
JOURNAL Patent: US 6211440-A 6 03-APR-2001;  
LOCATION/Qualifiers  
1. 21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1980 GCGAGGGGAGAGAGAGAG 2000  
DB 1 GGAAGGGGAGAGAGAGAG 21

RESULT 20  
AR257361 21 bp DNA linear PAT 20-DEC-2002  
LOCUS AR257361  
DEFINITION Sequence 6 from patent US 6486302.  
ACCESSION AR257361  
VERSION AR257361.1 GI:27307314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Briggs,S.P., Johal,G. and Multani,D.S.  
TITLE Hm2 cDNA and related polypeptide  
JOURNAL Patent: US 6486302-A 6 26-NOV-2002;  
LOCATION/Qualifiers  
1. 21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1980 GCGAGGGGAGAGAGAGAG 2000  
DB 1 GGAAGGGGAGAGAGAGAG 21

RESULT 21  
AR311198 20 bp DNA linear PAT 12-JUN-2003  
LOCUS AR311198  
DEFINITION Sequence 1735 from patent US 6559294.  
ACCESSION AR311198  
VERSION AR311198.1 GI:31704624  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

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REFERENCE      Unclassified.
AUTHORS        1 (bases 1 to 20)
               Griffiths,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
               Sankaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 1735 06-MAY-2003;
FEATURES       Location/Qualifiers
SOURCE         1..20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match    0.7%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            1386 GACTCTTCATCAGTCTT 1402
              |||||
              1 GACTCTTCATCAGTCTT 17

Db
RESULT 22
LOCUS       AR370191          20 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION  Sequence 12 from patent US 6300132.
ACCESSION   AR370191
VERSION     AR370191.1  GI:34606697
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Monia,B.P. and Cowser,L.M.
TITLE        Antisense inhibition of telomeric repeat binding factor 2
             expression
JOURNAL      Patent: US 6300132-A 12 09-OCT-2001;
FEATURES     Location/Qualifiers
SOURCE       1..20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match    0.7%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY            283 CCCGCCGCCGCCGCCGCTT 302
              |||||
              1 CCCGCCGCCGCCGCCGCTT 20

Db
RESULT 23
LOCUS       AR298434          21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION  Sequence 10169 from patent US 6537751.
ACCESSION   AR298434
VERSION     AR298434.1  GI:31685718
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE        Biallelic markers for use in constructing a high density
             disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 10169 25-MAR-2003;
FEATURES     Location/Qualifiers
SOURCE       1..21
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match    0.7%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY            1037 CAGGAAATTCATCCTCTT 1056
              |||||
              1 CAGGAAATTCATCCTCTT 20

Db
RESULT 24
LOCUS       AR230362          22 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION  Sequence 95 from patent US 6451578.
ACCESSION   AR230362
VERSION     AR230362.1  GI:27270501
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,
               Desai,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buik,S.L. and
               Mushawar,I.K.
TITLE        Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods
             for their use
JOURNAL      Patent: US 6451578-A 95 17-SEP-2002;
FEATURES     Location/Qualifiers
SOURCE       1..22
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match    0.7%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY            834 TCTTGACCATGACATCTTTC 853
              |||||
              3 TCTTGACCATGACATCTTTC 22

Db
RESULT 25
LOCUS       AR310057          22 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION  Sequence 95 from patent US 6558898.
ACCESSION   AR310057
VERSION     AR310057.1  GI:31702335
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,
               Desai,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buik,S.L. and
               Mushawar,I.K.
TITLE        Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods
             for their use
JOURNAL      Patent: US 6558898-A 95 06-MAY-2003;
FEATURES     Location/Qualifiers
SOURCE       1..22
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match    0.7%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY            834 TCTTGACCATGACATCTTTC 853
              |||||
              3 TCTTGACCATGACATCTTTC 22

Db
RESULT 26
LOCUS       AR350469          22 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION  Sequence 95 from patent US 6586568.
ACCESSION   AR350469
VERSION     AR350469.1  GI:33751612

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KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 22)  
Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,  
Desai,S.M., Leary,T.P., Muerhoff,A.S., Ecker,U.C., Buljck,S.U. and  
Mushahwar,I.K.  
Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods  
for their use  
Patent: US 6586568-A 95 01-JUL-2003;  
Location/Qualifiers  
1..22  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 16.4; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTTGACATGACATCTTTC 853  
DB 3 TCTTGACATGACACTTTC 22

RESULT 27  
AX599245 18 bp DNA linear PAT 14-FEB-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX599245  
Sequence 585 from Patent WO02077272.  
AX599245  
AX599245.1 GI:28399387  
synthetic construct  
synthetic construct  
artificial sequences.  
1  
Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,  
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,  
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,  
Pelei,C. and Ziebarth,H.  
Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
Patent: WO 02077272-A 95 03-OCT-2002;  
Epigenomics AG (DE)  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 GTGTAGGTCGGCTTGTT 56  
DB 1 GTGTAGGTCGGTTGTT 18

RESULT 28  
AX599819 18 bp DNA linear PAT 14-FEB-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX599819  
Sequence 1159 from Patent WO02077272.  
AX599819  
AX599819.1 GI:28399967  
synthetic construct  
synthetic construct  
artificial sequences.  
1  
Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,  
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 22)  
Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,  
Desai,S.M., Leary,T.P., Muerhoff,A.S., Ecker,U.C., Buljck,S.U. and  
Mushahwar,I.K.  
Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods  
for their use  
Patent: US 6586568-A 95 01-JUL-2003;  
Location/Qualifiers  
1..22  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 GTGTAGGTCGGCTTGTT 56  
DB 1 GTGTAGGTCGGTTGTT 18

RESULT 29  
AX599821/c 18 bp DNA linear PAT 14-FEB-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX599821  
Sequence 1161 from Patent WO02077272.  
AX599821  
AX599821.1 GI:28399969  
synthetic construct  
synthetic construct  
artificial sequences.  
1  
Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,  
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,  
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,  
Pelei,C. and Ziebarth,H.  
Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
Patent: WO 02077272-A 95 03-OCT-2002;  
Epigenomics AG (DE)  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 GTGTAGGTCGGCTTGTT 56  
DB 18 GTGTAGGTCGGTTGTT 1

RESULT 30  
AX767689 18 bp DNA linear PAT 02-JUL-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX767689  
Sequence 337 from Patent WO03044226.  
AX767689  
AX767689.1 GI:32436294  
synthetic construct  
synthetic construct  
artificial sequences.  
1  
Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and  
Nimmrich,I.  
Method and nucleic acids for the analysis of a lymphoid cell  
proliferative disorder  
Patent: WO 03044226-A 337 30-MAY-2003;

FEATURES  
source  
Epigenomics AG (BE)  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 GTGTAGTGTGGCTTGCTT 56  
|||||  
1 GTGTAGTGTGGCTTGCTT 18

RESULT 31  
BD233265/c 19 bp DNA linear PAT 17-JUL-2003  
LOCUS BD233265  
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.  
ACCESSION BD233265.1 GI:33043035  
VERSION JP 2002518065-A/361.  
KEYWORDS JP 2002518065-A/361.  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
Viruses; Retrovirdae.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Stuyver, L.  
TITLE Method of detecting mutation selected by drug in HIV protease gene  
JOURNAL Patent: JP 2002518065-A 361 25-JUN-2002;  
COMMENT INNOGENETICS NV  
OS Aids-associated retrovirus  
PN JP 2002518065-A/361  
PD 25-JUN-2002  
PF 22-JUN-1999 JP 2000556068  
PR 24-JUN-1998 EP 98870143.9  
PI LIEVEN STUYVER  
PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00  
CC Method of detecting mutation selected by drug in HIV protease  
CC gene  
FH Key Location/Qualifiers  
FT source 1..19 /organism="Aids-associated retrovirus".  
FT Location/Qualifiers  
1..18  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
|||||  
19 CCTCGAGTCAACAGATT 2

RESULT 32  
AX007819/c 19 bp DNA linear PAT 06-SEP-2000  
LOCUS AX007819  
DEFINITION Sequence 361 from Patent WO9967428.  
ACCESSION AX007819  
VERSION AX007819.1 GI:9995516  
KEYWORDS Aids-associated retrovirus  
SOURCE Aids-associated retrovirus  
ORGANISM Viruses; Retrovirdae.  
REFERENCE 1  
AUTHORS Stuyver, L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene

JOURNAL Patent: WO 9967428-A 361 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
Location/Qualifiers  
1..19  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
|||||  
19 CCTCGAGTCAACAGATT 2

RESULT 33  
BD233264/c 20 bp DNA linear PAT 17-JUL-2003  
LOCUS BD233264  
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.  
ACCESSION BD233264.1 GI:33043034  
VERSION JP 2002518065-A/360.  
KEYWORDS JP 2002518065-A/360.  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
Viruses; Retrovirdae.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Stuyver, L.  
TITLE Method of detecting mutation selected by drug in HIV protease gene  
JOURNAL Patent: JP 2002518065-A 360 25-JUN-2002;  
COMMENT INNOGENETICS NV  
OS Aids-associated retrovirus  
PN JP 2002518065-A/360  
PD 25-JUN-2002  
PF 22-JUN-1999 JP 2000556068  
PR 24-JUN-1998 EP 98870143.9  
PI LIEVEN STUYVER  
PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00  
CC Method of detecting mutation selected by drug in HIV protease  
CC gene  
FH Key Location/Qualifiers  
FT source 1..20 /organism="Aids-associated retrovirus".  
FT Location/Qualifiers  
1..20  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
|||||  
20 CCTCGAGTCAACAGATT 3

RESULT 34  
AX007818/c 20 bp DNA linear PAT 06-SEP-2000  
LOCUS AX007818  
DEFINITION Sequence 360 from Patent WO9967428.  
ACCESSION AX007818  
VERSION AX007818.1 GI:9995515  
KEYWORDS Aids-associated retrovirus  
SOURCE Aids-associated retrovirus  
ORGANISM Viruses; Retrovirdae.  
REFERENCE 1  
AUTHORS Stuyver, L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene

JOURNAL Patent: WO 9967428-A 360 29-DEC-1999;  
 INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
 FEATURES Location/Qualifiers  
 source 1..20  
 /organism="Aids-associated retrovirus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 45;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
 DB 20 CCTCGAGTCAACAGATT 3

RESULT 35  
 BD233266/c  
 LOCUS BD233266 21 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Method of detecting mutation selected by drug in HIV protease gene.  
 ACCESSION BD233266  
 VERSION BD233266.1 GI:33043036  
 KEYWORDS JP 2002518065-A/362.  
 SOURCE Aids-associated retrovirus  
 ORGANISM Aids-associated retrovirus  
 Viruses; Retrovird viruses; Retroviridae.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Stuyver, L.  
 TITLE Method of detecting mutation selected by drug in HIV protease gene  
 JOURNAL Patent: JP 2002518065-A 362 25-JUN-2002;  
 INNOGENETICS NV

COMMENT OS Aids-associated retrovirus  
 PN JP 2002518065-A/362  
 PD 25-JUN-2002 JP 2000556068  
 PE 22-JUN-1999 JP 98870143.9  
 FR 24-JUN-1998 EP 98870143.9  
 PI LIEVEN STUYVER  
 PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00  
 CC Method of detecting mutation selected by drug in HIV protease  
 gene

FEATURES  
 source Location/Qualifiers  
 1..21  
 /organism="Aids-associated retrovirus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 21;  
 Best Local Similarity 94.4%; Pred. No. 48;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
 DB 21 CCTCGAGTCAACAGATT 4

RESULT 36  
 AX007820/c  
 LOCUS AX007820 21 bp DNA linear PAT 06-SEP-2000  
 DEFINITION Sequence 362 from Patent WO9967428.  
 ACCESSION AX007820  
 VERSION AX007820.1 GI:9995517  
 KEYWORDS Aids-associated retrovirus  
 SOURCE Aids-associated retrovirus  
 ORGANISM Viruses; Retrovird viruses; Retroviridae.  
 REFERENCE 1  
 AUTHORS Stuyver, L.  
 TITLE Method for detection of drug-selected mutations in the hiv protease  
 gene

JOURNAL Patent: WO 9967428-A 362 29-DEC-1999;  
 INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="Aids-associated retrovirus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:11966"

Query Match 0.7%; Score 16.4; DB 1; Length 21;  
 Best Local Similarity 94.4%; Pred. No. 48;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 683 CCTCGAGTCAACAGATT 700  
 DB 21 CCTCGAGTCAACAGATT 4

RESULT 37  
 AR038804  
 LOCUS AR038804 21 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 110 from patent US 5807681.  
 ACCESSION AR038804  
 VERSION AR038804.1 GI:5958167  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Giordano, A. and Baldi, A.  
 TITLE Human retinoblastoma-related (pRb2/p130) genomic DNA and methods  
 for detecting mutations therein  
 JOURNAL Patent: US 5807681-A 110 15-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 51;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TTAAACCTACTGCCACCTC 2181  
 DB 1 TTAAACCTACTGCCACCTC 21

RESULT 38  
 AR059690  
 LOCUS AR059690 21 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 110 from patent US 5840506.  
 ACCESSION AR059690  
 VERSION AR059690.1 GI:5986140  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Giordano, A.  
 TITLE Methods for the diagnosis and prognosis of cancer  
 JOURNAL Patent: US 5840506-A 110 24-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 51;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TTAAACCTACTGCCACCTC 2181  
 DB 1 TTAAACCTACTGCCACCTC 21

RESULT 39  
ARI69510/c 20 bp DNA linear PAT 17-DEC-2001  
LOCUS Sequence 6 from patent US 6291173.  
ACCESSION ARI69510  
VERSION ARI69510.1 GI:17907377  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bartel,P.L. and Tavtigian,S.V.  
TITLE MMS22-an MMS1 interacting protein  
JOURNAL Patent: US 6291173-A 6 18-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1317 TACAAAGAGGAGGAG 1332  
DB 16 TACAAAGAGGAGGAG 1

RESULT 40  
AX154203 21 bp DNA linear PAT 22-JUN-2001  
LOCUS Sequence 301 from Patent WO0138576.  
ACCESSION AX154203  
VERSION AX154203.1 GI:14535817  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0138576-A 301 31-MAY-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES Location/Qualifiers  
source 1..21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.7%; Score 16; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 55;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1104 TGGCTTCGTGACCTTCT 1121  
DB 4 TGGCTTCGTGACCTTCT 21

RESULT 41  
A51892 19 bp DNA linear PAT 10-MAR-1997  
LOCUS Sequence 56 from Patent WO9620011.  
ACCESSION A51892  
VERSION A51892.1 GI:2304640  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Blakey,D.C., Davies,D.H., Dowell,R.I., Hennam,J.F., Marsham,P.R.,  
Slater, Anthony,M. and Hennequin,L.F.

TITLE CHEMICAL COMPOUNDS CHEMICAL COMPOUNDS.  
JOURNAL Patent: WO 9620011-A 56 04-JUL-1996;  
COMMENT ZENECA LTD (GB)  
FEATURES Other publication AU 4269796 960719.  
source 1..19  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACCTGCTGAGGCTG 621  
DB 1 GGACCTGCTGAGGCTG 19

RESULT 42  
A67354 19 bp DNA linear PAT 05-MAY-1999  
LOCUS Sequence 110 from Patent WO9742329.  
ACCESSION A67354  
VERSION A67354.1 GI:4756298  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Copley,C.G., Edge,M.D. and Emery,S.C.  
TITLE MONOCLONAL ANTIBODY TO CEA, CONJUGATES COMPRISING SAID ANTIBODY,  
AND THEIR THERAPEUTIC USE IN AN ADEPT SYSTEM  
JOURNAL Patent: WO 9742329-A 110 13-NOV-1997;  
ZENECA LTD (GB)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACCTGCTGAGGCTG 621  
DB 1 GGACCTGCTGAGGCTG 19

RESULT 43  
A87526 19 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 7 from Patent WO9835988.  
ACCESSION A87526  
VERSION A87526.1 GI:6736175  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Edge,M.D.  
TITLE PROTEINS  
JOURNAL Patent: WO 9835988-A 7 20-AUG-1998;  
ZENECA LTD (GB); EDGE MICHAEL DEREK (GB)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACCACTGCGAGGCTGTG 621  
1 GGACCTGCTGCAGAGTCTG 19

RESULT 44  
LOCUS AR085857 19 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 52 from patent US 5985281.  
ACCESSION AR085857  
VERSION AR085857.1 GI:10012623  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Taylorson,C.John., Eggelte,H.Johannes., Tarragona-Piol,A.,  
Rabin,B.Robert., Boyle,F.Thomas., Hennam,J.Frederick.,  
Blakey,D.Charles., Harsham,P.Robert., Heaton,D.William.,  
Davies,D.Huw., Slater,A.Michael. and Hennequin,L.Francois.Andre.  
Chemical compounds  
Patent: US 5985281-A 52 16-NOV-1999;

TITLE Location/Qualifiers  
JOURNAL 1..19  
FEATURES /mol\_type="unknown"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACCACTGCGAGGCTGTG 621  
1 GGACCTGCTGCAGAGTCTG 19

RESULT 45  
LOCUS AR101705 19 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 5 from patent US 6083699.  
ACCESSION AR101705  
VERSION AR101705.1 GI:12812503  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Leusner,J., Hul,M., Dunn,J.M., Larson,M.T., Lacroix,J.-M. and  
Shipman,R.  
Method for bi-directional sequencing of nucleic acid polymers

JOURNAL Patent: US 6083699-A 5 04-JUL-2000;  
FEATURES Location/Qualifiers  
1..19  
source /organism="unknown"

/mol\_type="unassigned DNA"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CCGGAGCCCGGACCGGCC 489  
19 CCGGAGCCCGGACCGGCC 1

RESULT 46  
LOCUS AR101709 19 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6083699.  
ACCESSION AR101709  
VERSION AR101709.1 GI:12812507

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Leusner,J., Hul,M., Dunn,J.M., Larson,M.T., Lacroix,J.-M. and  
Shipman,R.  
Method for bi-directional sequencing of nucleic acid polymers

JOURNAL Patent: US 6083699-A 9 04-JUL-2000;  
FEATURES Location/Qualifiers  
1..19  
source /organism="unknown"

/mol\_type="unassigned DNA"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CCGGAGCCCGGACCGGCC 489  
19 CCGGAGCCCGGACCGGCC 1

RESULT 47  
LOCUS E29777 19 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for discriminating and detecting human coagulation factor V  
gene polymorphism.  
ACCESSION E29777  
VERSION E29777.1 GI:13016873  
KEYWORDS JP 1999313676-A/24.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 19)  
AUTHORS Takashi,F., Shigetoshi,K., Makoto,H. and Keizo,S.  
TITLES Method for discriminating and detecting human coagulation factor V  
gene polymorphism  
Patent: JP 1999313676-A 24 16-NOV-1999;

JOURNAL OTSUKA PHARMACEUT CO LTD

COMMENT OS Unidentified  
PN JP 1999313676-A/24  
PD 16-NOV-1999  
PF 30-APR-1998 JP 1998120217  
PR

PI TAKASHI FUKUI, SHIGETOSHI KINOSHITA, MAKOTO HASHIZUME, PI  
KEIZO SUGIMACHI

PC C12N15/09,C12Q1/68,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;

FM Key Location/Qualifiers  
FT source 1..19  
1..19 /organism="Unidentified".

FEATURES Location/Qualifiers  
1..19  
source /organism="unidentified"

/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 961 AAGATCTCTTCACACAGA 979  
1 AAGATCTCTTCACACAGA 19

RESULT 48  
LOCUS AR294930 19 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 6665 from patent US 6537751.  
ACCESSION AR294930

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VERSION      AR294930.1  GI:31682214
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 19)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
JOURNAL     Patent: US 6537751-A 6665 25-MAR-2003;
FEATURES
SOURCE       Location/Qualifiers
              1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.7%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2095 CAGAGAACTTAAGCAAG 2113
Db      19 CAGGAACTTAACAGAG 1

RESULT 49
LOCUS      AR139318      20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 26 from patent US 6207372.
ACCESSION  AR139318
VERSION    AR139318.1  GI:14481814
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Shuber,A.P.
TITLE     Universal primer sequence for multiplex DNA amplification
JOURNAL   Patent: US 6207372-A 26 27-MAR-2001;
FEATURES
SOURCE     Location/Qualifiers
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.7%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      205 CCCGCCGCTGGCCTGCG 223
Db      19 CTCGGCCGCTGGCCTGCG 1

RESULT 50
LOCUS      AR139319/c    20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 27 from patent US 6207372.
ACCESSION  AR139319
VERSION    AR139319.1  GI:14481815
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Shuber,A.P.
TITLE     Universal primer sequence for multiplex DNA amplification
JOURNAL   Patent: US 6207372-A 27 27-MAR-2001;
FEATURES
SOURCE     Location/Qualifiers
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.7%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2341 CAGCATCTCATGAGGAGG 2359
Db      19 CAGCATTTCTGAGGAGG 1

RESULT 53
LOCUS      AR315798      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 6335 from patent US 6559294.
ACCESSION  AR315798
VERSION    AR315798.1  GI:31709224
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      205 CCCGCCGCTGGCCTGCG 223
Db      19 CTCGACCGCTGGCCTGCG 1

RESULT 51
LOCUS      AR139320/c    20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 28 from patent US 6207372.
ACCESSION  AR139320
VERSION    AR139320.1  GI:14481816
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Shuber,A.P.
TITLE     Universal primer sequence for multiplex DNA amplification
JOURNAL   Patent: US 6207372-A 28 27-MAR-2001;
FEATURES
SOURCE     Location/Qualifiers
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.7%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      205 CCCGCCGCTGGCCTGCG 223
Db      19 CTCGACCGCTGGCCTGCG 1

RESULT 52
LOCUS      I83478        20 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION Sequence 14 from patent US 5714329.
ACCESSION  I83478
VERSION    I83478.1  GI:3407008
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dracopoli,N., Tucker,M. and Goldstein,A.
TITLE     Methods for the diagnosis of a genetic predisposition to cancer
JOURNAL   associated with variant CDK4 allele
JOURNAL   Patent: US 5714329-A 14 03-FEB-1998;
FEATURES
SOURCE     Location/Qualifiers
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.7%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2341 CAGCATCTCATGAGGAGG 2359
Db      19 CAGCATTTCTGAGGAGG 1

RESULT 53
LOCUS      AR315798      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 6335 from patent US 6559294.
ACCESSION  AR315798
VERSION    AR315798.1  GI:31709224
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,I.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6335 06-MAY-2003;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 20;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2297 TCTGACCCACAGTGGATG 2315
Db 2 TCTGACCCACAGTGGAGG 20

RESULT 54
LOCUS AX718888 20 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 10 from Patent WO02101048.
ACCESSION AX718888
VERSION AX718888.1 GI:23891454
KEYWORDS
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
REFERENCE
    Escary,J.L.
    New polynucleotides and polypeptides of the ifn_g(a)-7 gene
    JOURNAL Patent: WO 02101048-A 10 19-DEC-2002;
    Genodyssee (FR)
FEATURES
    Location/Qualifiers
        1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 20;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1497 TCATCAGTCTGCTGGAAA 1515
Db 2 TCATCAGTCTGCTGTAAA 20

RESULT 55
LOCUS AR001304 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 17 from patent US 5739026.
ACCESSION AR001304
VERSION AR001304.1 GI:3963371
KEYWORDS
SOURCE
    Unknown.
ORGANISM
    Unknown.
REFERENCE
    Unclassified.
    1 (bases 1 to 21)
AUTHORS Garoff,H. and Liljestrom,P.
TITLE DNA expression systems based on alphavirus
JOURNAL Patent: US 5739026-A 17 14-APR-1998;
FEATURES
    Location/Qualifiers
        1..21
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 356 CGGCGCCCGGTGGCGCGC 374
Db 21 CGGCGCCCGGTGGCGCGC 3

RESULT 56
LOCUS AR130402 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6190666.
ACCESSION AR130402
VERSION AR130402.1 GI:14118727
KEYWORDS
SOURCE
    Unknown.
ORGANISM
    Unknown.
REFERENCE
    Unclassified.
    1 (bases 1 to 21)
AUTHORS Garoff,H. and Liljestrom,P.
TITLE DNA expression systems based on alphavirus
JOURNAL Patent: US 6190666-A 17 20-FEB-2001;
FEATURES
    Location/Qualifiers
        1..21
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 356 CGGCGCCCGGTGGCGCGC 374
Db 21 CGGCGCCCGGTGGCGCGC 3

RESULT 57
LOCUS AR278808 21 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 14 from patent US 6512095.
ACCESSION AR278808
VERSION AR278808.1 GI:29713191
KEYWORDS
SOURCE
    Unknown.
ORGANISM
    Unknown.
REFERENCE
    Unclassified.
    1 (bases 1 to 21)
AUTHORS Baum,P.R.
TITLE Molecules designated B7L-1
JOURNAL Patent: US 6512095-A 14 28-JAN-2003;
FEATURES
    Location/Qualifiers
        1..21
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 492 CCTGCTCTTGGCCTGCAGC 510
Db 1 CCTGCTCTTGGCCTGCTGC 19

RESULT 58
LOCUS AX164904 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 99 from Patent WO0138586.
ACCESSION AX164904
VERSION AX164904.1 GI:14545733
KEYWORDS
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
REFERENCE
    Unclassified.
    1 (bases 1 to 51)
AUTHORS Garoff,H. and Liljestrom,P.
TITLE DNA expression systems based on alphavirus
JOURNAL Patent: US 6190666-A 17 20-FEB-2001;
FEATURES
    Location/Qualifiers
        1..51
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 15.8; DB 1; Length 21;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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REFERENCE 1
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
PATENT: WO 0138586-A 99 31-MAY-2001;
JOURNAL Curagen Corporation (US)
FEATURES
SOURCE Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism
Accession number CG43088901"
variation

Query Match 0.7%; Score 15.8; DB 1; Length 51;
Best Local Similarity 65.7%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2264 CACATGCAGTCTGAGCACCCTGTCAAGCTGCTC 2238
DB 35 CCCACTGTGACTGAGAGCAGCTTGACACCGCTGCTC 1

RESULT 59
AR116129 18 bp DNA linear PAT 16-MAY-2001
LOCUS AR116129
DEFINITION Sequence 17 from patent US 6133007.
ACCESSION AR116129
VERSION AR116129.1 GI:14096451
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Loughney, K.
TITLE Phosphodiesterase 8A
JOURNAL Patent: US 6133007-A 17 17-OCT-2000;
FEATURES
SOURCE Location/Qualifiers
1..18
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAATAGCAA 17

RESULT 60
AR254388 18 bp DNA linear PAT 20-DEC-2002
LOCUS AR254388
DEFINITION Sequence 31 from patent US 6480791.
ACCESSION AR254388
VERSION AR254388.1 GI:27303185
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Strathmann, M.P.
TITLE Parallel methods for genomic analysis
JOURNAL Patent: US 6480791-A 31 12-NOV-2002;
FEATURES
SOURCE Location/Qualifiers
1..18
/organism="unassigned DNA"
/mol_type="genomic DNA"

Query Match 0.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAATAGCAA 17

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1112 TGAACCTTCTGATGGA 1128
DB 18 TGAACCTTCTGATGGA 2

RESULT 61
AR322346 18 bp DNA linear PAT 17-AUG-2003
LOCUS AR322346
DEFINITION Sequence 17 from patent US 6566087.
ACCESSION AR322346
VERSION AR322346.1 GI:33707978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Loughney, K.
TITLE Phosphodiesterase 8A
JOURNAL Patent: US 6566087-A 17 20-MAY-2003;
FEATURES
SOURCE Location/Qualifiers
1..18
/organism="unassigned DNA"
/mol_type="genomic DNA"

Query Match 0.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAATAGCAA 17

RESULT 62
BD062484 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD062484
DEFINITION Phosphodiesterase 8A.
ACCESSION BD062484
VERSION BD062484.1 GI:22608087
KEYWORDS JP 2001512327-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Loughney, K.
TITLE Phosphodiesterase 8A
JOURNAL Patent: JP 2001512327-A 13 21-AUG-2001;
COMMENT ICOS CORP
OS Artificial Sequence
PN JP 2001512327-A/13
PD 21-AUG-2001
PF 16-OCT-1998 JP 1999522750
PR 16-OCT-1997 US 08/951648
PI KATE LOUGHNEY
PC C12N15/55, C12N9/16, C12N15/11, C07K16/40, C07K16/42, G01N33/68, PC
C12Q1/68
CC Description of Artificial Sequence: primer
FH Key
FEATURES
SOURCE Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAATAGCAA 17

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RESULT 63
AX348014/c      19 bp      DNA      linear      PAT 06-FEB-2002
LOCUS           AX348014
DEFINITION      Sequence 47 from Patent EP172444.
ACCESSION       AX348014
VERSION         AX348014.1 GI:18614124
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE
  1             Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE        Diagnostic use of polymorphisms in the gene coding for the tnfr
  JOURNAL      receptor II and method for detecting non-responders to anti-tnf
  PATENT       therapy
  PATENT       Patent: EP 1172444-A 47 16-JAN-2002;
  SOURCE       Conaris Research Institute GmbH (DE)
FEATURES
  source
    1..19
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Forward Primer"

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 493 CTGCTCTGCGCTGCAG 509
Db 17 CTGCTCTTGGCTGCAG 1

RESULT 64
A97000/c      20 bp      DNA      linear      PAT 07-SEP-2000
LOCUS           A97000
DEFINITION      Sequence 5 from Patent WO921992.
ACCESSION       A97000
VERSION         A97000.1 GI:6780441
KEYWORDS
SOURCE          unidentified
ORGANISM        unidentified
                unclassified.
REFERENCE
  1             Laxhuber,L. and Metzger,R.
  AUTHORS       Nucleic acid molecules encoding a glutamate receptor
  TITLE        Patent: WO 921992-A 5 06-MAY-1992;
  JOURNAL      LAXHUBER LUDWIG (DE); METZGER RAINER (DE); GANIMED PHARMACEUTICALS
  PATENT       GMBH (DE)
FEATURES
  source
    1..20
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

modified_base 6 /mod_base=i
modified_base 11 /mod_base=i
modified_base 12 /mod_base=i
modified_base 15 /mod_base=i

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2069 TCCATCCCTTACC 2085
Db 20 TCCATCCCTTCCC 4

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RESULT 65
AR074809/c      20 bp      DNA      linear      PAT 28-AUG-2000
LOCUS           AR074809
DEFINITION      Sequence 17 from patent US 5955277.
ACCESSION       AR074809
VERSION         AR074809.1 GI:10001562
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
                unclassified.
REFERENCE
  1             Hansen,T., Andersen,C.Bo. and Pedersen,O.Bobye.
  AUTHORS       Mutant cDNA encoding the p85.alpha. subunit of phosphatidylinositol
  TITLE        3-kinase
  JOURNAL      Patent: US 5955277-A 17 21-SEP-1999;
  PATENT       location/Qualifiers
  SOURCE       1..20
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1940 AAGAGACTTGAGAG 1956
Db 18 AAGAGACTTGAGAG 2

RESULT 66
AR170368/c      20 bp      DNA      linear      PAT 17-DEC-2001
LOCUS           AR170368
DEFINITION      Sequence 19 from patent US 6291430.
ACCESSION       AR170368
VERSION         AR170368.1 GI:17908327
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
                unclassified.
REFERENCE
  1             Chauv,P., Strobant,V., Boon-Falleur,T., van der Bruggen,F.,
  AUTHORS       Thielemans,K. and Kurthals,J.
  TITLE        Mage-3 peptides presented by HLA class II molecules
  JOURNAL      Patent: US 6291430-A 19 18-SEP-2001;
  PATENT       location/Qualifiers
  SOURCE       1..20
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGCGCGCCATG 463
Db 20 GCCGGGCGCGCCATG 4

RESULT 67
BD233818/c      20 bp      DNA      linear      PAT 17-JUL-2003
LOCUS           BD233818
DEFINITION      Transcriptional activation factor of fungi useful in the production
ACCESSION       BD233818
VERSION         BD233818.1 GI:33043588
KEYWORDS       process of polypeptide.
SOURCE         JP 2002526112-A/8.
ORGANISM       Homo sapiens (human)
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1             Hoyer,C., J.C.A.M.J., Puntel,P.J. and Schuren,F.H.
  PATENT       (bases 1 to 20)

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TITLE Transcriptional activation factor of fungi useful in the production  
JOURNAL Process of polypeptide  
Patent: JP 2002526112-A 8 20-AUG-2002;  
COMMENT NOVOZYMES AS  
OS Homo sapiens (human)  
PN JP 2002526112-A/8  
PD 20-AUG-2002  
PR 05-OCT-1999 JP 2000574691  
PR 05-OCT-1998 DK PA 199801258  
PI CARSTEN HOORT,CEBS A M J J VAN DEN HONDEL,PETER J PUNT,FRANK H  
PI SCHUREN  
PC C12N15/09,C07K14/37,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/  
PC 62,  
C12P21/02//C12N1/15,C12R1:685),(C12N9/62,C12R1:685),(C12N9/62,PC  
C12R1:69),  
PC (C12P21/02,C12R1:685),C12N15/00,C12N5/00  
CC Transcriptional activation factor of fungi useful in the CC  
production  
CC process of polypeptide  
FT Key Location/Qualifiers  
FT source 1..20  
FT Location/Qualifiers  
/organism="Homo sapiens (human)".  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match  
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGCGCGCCATGG 463  
DB 20 GCCGGGCGCGCCATGG 4

RESULT 68  
BD237168/c  
LOCUS BD237168 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION MAGE-A3 peptide presented by HLA class II molecule.  
ACCESSION BD237168  
VERSION BD237168.1 GI:33046938  
KEYWORDS JP 2002526110-A/8;  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 20)  
Chaux,P., Stroobant,V., Falleur,T.B., Burggen,P.V.D., Schultz,E.S.,  
Snick,J.V., Lethe,B., Thielemans,K., Cortals,J. and Heitman,C.  
MAGE-A3 peptide presented by HLA class II molecule  
Patent: JP 2002526110-A 8 20-AUG-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH,VRIJE UNIVERSITEIT BRUSSELS  
OS Homo sapiens (human)  
PN JP 2002526110-A/8  
PD 20-AUG-2002  
PR 15-SEP-1999 JP 2000574676  
PR 05-OCT-1998 US 09/166448  
PI PASCAL CHAUX,VINCENT STROOBANT,THIERRY BOON FALLEUR PI  
PI PIERRE VAN DER BRUGEN,  
PI ERWIN S SCHULTZ,JACQUES VAN SNICK,BERNARD LETHE,KRIS PI  
THIELEMANS,  
PI JURGEN CORTALS,CARLO HEITMAN  
PC C12N15/09,A61K35/14,A61K38/00,A61K45/00,A61P35/00,A61P37/04,  
PC C07K7/06  
PC C07K7/08,C07K14/82,C07K16/32,C12N5/06,C12O1/02,G01N33/53// PC  
PC C12P21/08,  
PC (C12N5/06,C12R1:91),C12N15/00,C12N5/00,A61K37/02,(C12N5/00,PC  
C12R1:91)  
CC MAGE-A3 peptide presented by HLA class II molecule FH Key

TITLE Location/Qualifiers  
JOURNAL FT source 1..20  
Patent: US 5523391-A 5 04-JUN-1996;  
COMMENT Location/Qualifiers  
/organism="Homo sapiens (human)".  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match  
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGCGCGCCATGG 463  
DB 20 GCCGGGCGCGCCATGG 4

RESULT 69  
121716/c  
LOCUS 121716 20 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 5 from patent US 5523391.  
ACCESSION 121716  
VERSION 121716.1 GI:1602070  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Komurasaki,T., Toyoda,H., Yoshimoto,M. and Hanada,K.  
TITLE DNA fragment encoding tumor cell growth inhibitors  
JOURNAL Patent: US 5523391-A 5 04-JUN-1996;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2243 CCGTCATATCAGACT 2259  
DB 18 CCGTCATATCAGACT 2

RESULT 70  
121719  
LOCUS 121719 20 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 8 from patent US 5523391.  
ACCESSION 121719  
VERSION 121719.1 GI:1602073  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Komurasaki,T., Toyoda,H., Yoshimoto,M. and Hanada,K.  
TITLE DNA fragment encoding tumor cell growth inhibitors  
JOURNAL Patent: US 5523391-A 8 04-JUN-1996;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2243 CCGTCATATCAGACT 2259  
DB 3 CCGTCATATCAGACT 19

RESULT 71  
 AR194294/c 20 bp DNA linear PAT 20-APR-2002  
 LOCUS AR194294  
 DEFINITION Sequence 11 from patent US 6348450.  
 ACCESSION AR194294  
 VERSION AR194294.1 GI:20240886  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 20)  
 Tang, D.-C.C., Marks, D.H., Curjel, D.T., Shi, Z. and van Kampen, K.R. 1999.  
 Noninvasive genetic immunization, expression products therefrom and uses thereof  
 TITLE Patent: US 6348450-A 11-19-FEB-2002;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source 1..20  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGCTAATGAATACCCCA 1825  
 DB 18 GGCTGATGAATACCCCA 2

RESULT 72  
 AR221344/c 20 bp DNA linear PAT 26-SEP-2002  
 LOCUS AR221344  
 DEFINITION Sequence 19 from patent US 6426217.  
 ACCESSION AR221344  
 VERSION AR221344.1 GI:23328323  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 20)  
 Chauv, P., Stroobant, V., Boon-Falleur, T., van der Bruggen, P., Thielemans, K. and Kurthals, J.  
 MAGE-3 peptides presented by HLA class II molecules  
 TITLE Patent: US 6426217-A 19-30-JUL-2002;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source 1..20  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGCGCGCCCATG3 463  
 DB 20 GCCGGCGCGCCCATG3 4

RESULT 73  
 AX117251 20 bp DNA linear PAT 11-MAY-2001  
 LOCUS AX117251  
 DEFINITION Sequence 2374 from Patent WO0129262.  
 ACCESSION AX117251  
 VERSION AX117251.1 GI:14034202  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE  
 1 Picoult-Newburg, L. and Pohl, M.  
 AUTHORS Genotyping reagents, kits and methods of use thereof  
 TITLE

JOURNAL Patent: WO 0129262-A 2374 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
 FEATURES  
 source 1..20  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2266 CAATGCAATCTGAGCA 2282  
 DB 4 CAATGCAATCTGAGCA 20

RESULT 74  
 AX721032/c 20 bp DNA linear PAT 07-MAY-2003  
 LOCUS AX721032  
 DEFINITION Sequence 4 from Patent EP1298141.  
 ACCESSION AX721032  
 VERSION AX721032.1 GI:30421868  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE  
 1 Interleukin-4 (il-4) promoter sequences specifically interacting with ilrf-1 and ilrf-2  
 TITLE Patent: EP 1298141-A 4 02-APR-2003;  
 JOURNAL Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DB)  
 FEATURES  
 source 1..20  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide"

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 878 AGGAAATGAAGCTTT 894  
 DB 17 AGGAAATGAAGCTTT 1

RESULT 75  
 BD075110 20 bp DNA linear PAT 27-AUG-2002  
 LOCUS BD075110/c  
 DEFINITION MAGE-3 peptide presented by HLA class II molecule.  
 ACCESSION BD075110  
 VERSION BD075110.1 GI:22620713  
 KEYWORDS  
 SOURCE JP 2001516579-A/8.  
 ORGANISM Homo sapiens (human)  
 REFERENCE  
 1 (bases 1 to 20)  
 Thieremance, C., Hiernan, C., Colatus, C., Shaw, P., Stroobant, V., Falleur, T.B., Bruggen, P.V.D. and Rutten, R.  
 MAGE-3 peptide presented by HLA class II molecule  
 TITLE Patent: JP 2001516579-A 8 02-OCT-2001;  
 JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH, Vrije Universiteit BRUSSELS  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001516579-A/8  
 PD 02-OCT-2001  
 PF 04-SEP-1998 JP 2000511865  
 PR 12-SEP-1997 US 08/928615

PI CHRIS THIERNANCE, CARLO HIERMAN, JURGEN COLTANUS, PASCAL SHAM,  
 PI VINCENT SHTROBANT, THIERRY BOON FALLEUR, PIERRE VAN DER BRUGEN,  
 PI ROZARIE RHITTEN  
 PC C12N15/09, A61K35/26, A61K38/00, A61P35/00, C07K14/705, C07K16/30,  
 PC C07K19/00,  
 PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12N15/00, A61K37/ PC  
 02, C12N5/00  
 CC MAGE-3 peptide presented by HLA class II molecule FH Key  
 Location/Qualifiers  
 FT source 1..20  
 /organism='Homo sapiens (human)'.  
 Location/Qualifiers  
 1..20  
 /organism='Homo sapiens'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGCGCGCCGATCG 463  
 DB 20 GCCGGGCGCGCCGATCG 4

RESULT 76  
 LOCUS BD089209/c 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION A method of arraying genome clone.  
 ACCESSION BD089209  
 VERSION BD089209.1 GI:22634819  
 KEYWORDS JP 2001321190-A/1453.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Soeda, E.  
 TITLE A method of arraying genome clone  
 JOURNAL Patent: JP 2001321190-A 1453 20-NOV-2001;  
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA  
 GENOTECNS  
 COMMENT OS Artificial Sequence  
 PN JP 2001321190-A/1453  
 PD 20-NOV-2001  
 PF 12-MAR-2001 JP 2001068285  
 PI EIICHI SOEDA  
 PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC  
 C12N15/00,  
 PC C12N15/00  
 CC Description of Artificial Sequence: Synthetic DNA FH Key  
 Location/Qualifiers  
 FT source 1..20  
 /organism='Artificial Sequence'.  
 Location/Qualifiers  
 1..20  
 /organism='synthetic construct'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32630'

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1955 AGTTCGCGACCAAGAGC 1971  
 DB 18 AGTTCGCGACCAAGAGC 2

RESULT 77  
 LOCUS AB068420/c 20 bp DNA linear SYN 21-MAY-2003

DEFINITION Synthetic construct DNA, forward primer for human STS sts-R79G21F  
 at 1p36.  
 ACCESSION AB068420  
 VERSION AB068420.1 GI:15129224  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Chen, Y.-Z., Hayashi, Y., Wu, J.-G., Takaoka, E., Maekawa, K.,  
 Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,  
 Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.  
 and Soeda, E.  
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human  
 JOURNAL chromosome 1p35-p36  
 MEDLINE Genomics 74 (1), 55-70 (2001)  
 PUBMED 21269192  
 PUBMED 11374902  
 REFERENCE 2 (bases 1 to 20)  
 AUTHORS Horii, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
 Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
 Tel: 81-22-717-8042, Fax: 81-22-717-8047)

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 64;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1955 AGTTCGCGACCAAGAGC 1971  
 DB 18 AGTTCGCGACCAAGAGC 2

RESULT 78  
 LOCUS AR036620/c 20 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 20 from patent US 5872242.  
 ACCESSION AR036620  
 VERSION AR036620.1 GI:5953288  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Monia, B.P., Cowser, L.M. and Manoharan, M.  
 TITLE Antisense oligonucleotide inhibition of ras  
 JOURNAL Patent: US 5872242-A 20 16-FEB-1999;  
 Location/Qualifiers  
 FT source 1..20  
 /organism='unknown'  
 /mol\_type='unassigned DNA'

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 69;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTGGCGGCGAGCGAG 419  
 DB 20 GCGCGGCGCGGCGAGCGAG 1

RESULT 79

AR042895  
LOCUS AR042895 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5811636.  
ACCESSION AR042895  
VERSION AR042895.1 GI:5963391  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Hanna, W.W., Ozias-Akins, P. and Dujardin, M.  
TITLE Apomixis for producing true-breeding plant progenies  
JOURNAL Patent: US 5811636-A 2 22-SEP-1998;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CTGCAGAGATGGCTCTC 686  
Db 1 CTGCAGATATGGCTCTC 20

RESULT 80  
AR079640/c  
LOCUS AR079640 20 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 20 from patent US 5965722.  
ACCESSION AR079640  
VERSION AR079640.1 GI:10006381  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ecker, D.J., Cook, P.Dan., Monia, B.P., Freier, S.M. and Sanghvi, Y.S.  
TITLE Antisense inhibition of ras gene with chimeric and alternating oligonucleotides  
JOURNAL Patent: US 5965722-A 20 12-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTCGCGCGGAGGCGAG 419  
Db 20 GCGCGCGCGCGCGGAGGCGAG 1

RESULT 81  
AR093056/c  
LOCUS AR093056 20 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 151 from patent US 5998383.  
ACCESSION AR093056  
VERSION AR093056.1 GI:10019808  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Wright, J.A. and Young, A.H.  
TITLE Antitumor antisense sequences directed against ribonucleotide reductase  
JOURNAL Patent: US 5998383-A 151 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..20

/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAAGAAGAGTTGAAGACT 1687  
Db 20 GGAAGCAGGTTGAAGACT 1

RESULT 82  
AR102403/c  
LOCUS AR102403 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 28 from patent US 6083923.  
ACCESSION AR102403  
VERSION AR102403.1 GI:12813201  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Hardee, G.E., Geary, R.S., Levin, A., Templin, M.V., Howard, R. and Mehta, R.C.  
TITLE Liposomal oligonucleotide compositions for modulating RAS gene expression  
JOURNAL Patent: US 6083923-A 28 04-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTCGCGCGGAGGCGAG 419  
Db 20 GCGCGCGCGCGCGGAGGCGAG 1

RESULT 83  
AR107593/c  
LOCUS AR107593 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 33 from patent US 6110664.  
ACCESSION AR107593  
VERSION AR107593.1 GI:12823080  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cowser, L.M.  
TITLE Antisense inhibition of G-alpha-S1 expression  
JOURNAL Patent: US 6110664-A 33 29-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 CCATGACATCTTCACTCA 859  
Db 20 CCATGACATCTTCACTCA 1

RESULT 84  
AR150345  
LOCUS AR150345 20 bp DNA linear PAT 08-AUG-2001

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DEFINITION Sequence 421 from patent US 6228642.
ACCESSION AR150345
VERSION AR150345.1 GI:15114936
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Baker,B.F., Bennett,C.Frank., Butler,M.M. and Sharanan,W.R. Jr.
TITLE Antisense oligonucleotide modulation of tumor necrosis
factor-(alpha.) (TNF-alpha.) expression
JOURNAL Patent: US 6228642-A 421 08-MAY-2001;
FEATURES
  Location/Qualifiers
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        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1783 CGGTATGTGAGAGAGAGA 1802
Db 1 CAGTATGTGAGAGAGAGA 20

RESULT 85
LOCUS AR158609 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 231 from patent US 6251588.
ACCESSION AR158609
VERSION AR158609.1 GI:16220701
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 231 26-JUN-2001;
FEATURES
  Location/Qualifiers
    source
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 775 TCCCTACCTCAAAAGCTGTT 794
Db 1 TCCCCACCTCAACAGATGTT 20

RESULT 86
LOCUS AR158610 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 232 from patent US 6251588.
ACCESSION AR158610
VERSION AR158610.1 GI:16220703
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 232 26-JUN-2001;
FEATURES
  Location/Qualifiers
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      1..20
        /organism="unknown"

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      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 776 CCTTACTCAAAAGCTGTTG 795
Db 1 CCCCACCTCAACAGATGTTG 20

RESULT 87
LOCUS BD228218 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide regulation of expression of tumor
necrosis factor-alpha (TNF-alpha).
ACCESSION BD228218
VERSION BD228218.1 GI:33037988
KEYWORDS JP 2002526125-A/421.
SOURCE Synthetic construct
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.U.S.
TITLE Antisense oligonucleotide regulation of expression of tumor
necrosis factor-alpha (TNF-alpha)
JOURNAL Patent: JP 2002526125-A 421 20-AUG-2002;

COMMENT
  ISIS PHARMACEUTICALS INC
  OS Artificial Sequence
  PN JP 2002526125-A/421
  PD 20-AUG-2002
  PF 05-OCT-1999 JP 2000574737
  PR 05-OCT-1998 US 09/166186,18-MAY-1999 US 09/313932 PT
  BRENDIA F BAKER, FRANK C BENNETT, WADELINE M BUTLER, WILLIAM U PI
  SHANAHAN JR
  PC C12N15/09,A61K31/7115,A61K31/712,A61K48/00,A61P1/
  PC 00,A61P1/16,
  PC A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
  C07H21/02,
  CC C07H21/04,C12N15/00
  CC Synthetic
  FH Key
  FT source
    1..20
      Location/Qualifiers
        /organism="Artificial Sequence".
        /mol_type="synthetic construct"
        /db_xref="taxon:32630"

FEATURES
  source
    1..20
      Location/Qualifiers
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1783 CGGTATGTGAGAGAGAGA 1802
Db 1 CAGTATGTGAGAGAGAGA 20

RESULT 88
LOCUS AR201438 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6359124.
ACCESSION AR201438
VERSION AR201438.1 GI:20252326
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Becker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
TITLE Antisense inhibition of ras gene with chimeric and alternating
oligonucleotides

```

JOURNAL Patent: US 6359124-A 20 19-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/mol\_type="unknown"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GGGCGTCGCGCGAGGAGCAG 419  
DB 20 GGCGCGCGCGCGAGGAGCAG 1

RESULT 89  
AR230778/c 20 bp DNA linear PAT 20-DEC-2002  
LOCUS AR230778 Sequence 38 from patent US 6451602.  
DEFINITION AR230778  
ACCESSION AR230778  
VERSION AR230778.1 GI:27271565  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Popoff, I. and Cowser, L. M.  
TITLE Antisense modulation of PARP expression  
JOURNAL Patent: US 6451602-A 38 17-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/mol\_type="unknown"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2297 TCTGAGCCACAGTGGATGA 2316  
DB 20 TCTGAGCTTCGGTGGATGA 1

RESULT 90  
AR243571 20 bp DNA linear PAT 20-DEC-2002  
LOCUS AR243571 Sequence 21 from patent US 6475797.  
DEFINITION AR243571  
ACCESSION AR243571  
VERSION AR243571.1 GI:27290936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Wyatt, J.  
TITLE Antisense modulation of SR-CYP expression  
JOURNAL Patent: US 6475797-A 21 05-NOV-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/mol\_type="unknown"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1730 TCATGTGTGTTCACTGC 1749  
DB 1 TCATTGTGTGTTTACAGC 20

RESULT 91  
AR295125

LOCUS AR295125 20 bp DNA linear PAT 12-JUN-2003  
DEFINITION AR295125 Sequence 6860 from patent US 6537751.  
ACCESSION AR295125  
VERSION AR295125.1 GI:31682409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Balleic markers for use in constructing a high density disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 6860 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/mol\_type="unknown"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2385 TTACACGAAATGCTGCTG 2404  
DB 1 TGAACAGAAATGAGACTGG 20

RESULT 92  
AR359558/c 20 bp DNA linear PAT 17-AUG-2003  
LOCUS AR359558 Sequence 151 from patent US 6593305.  
DEFINITION AR359558  
ACCESSION AR359558  
VERSION AR359558.1 GI:33766281  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Wright, J. A.  
TITLE Antitumor antisense sequences directed against R1 and R2 components of ribonucleotide reductase  
JOURNAL Patent: US 6593305-A 151 15-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/mol\_type="unknown"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAAGAGAGGTTGAAGACT 1687  
DB 20 GGAAGCAGGTTGAAGACT 1

RESULT 93  
AR370194 20 bp DNA linear PAT 12-SEP-2003  
LOCUS AR370194 Sequence 15 from patent US 6300132.  
DEFINITION AR370194  
ACCESSION AR370194  
VERSION AR370194.1 GI:34606700  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Montia, B. P. and Cowser, L. M.  
TITLE Antisense inhibition of telomeric repeat binding factor 2 expression  
JOURNAL Patent: US 6300132-A 15 09-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..20

/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 199 CGCCCGCCCGCCGCTGACC 218  
DB 1 CGCCCGCCCTGCAGCTGCC 20

RESULT 94  
LOCUS AX613566 20 bp DNA linear PAT 17-FEB-2003  
DEFINITION Sequence 4591 from Patent WO02072882.  
ACCESSION AX613566  
VERSION AX613566.1 GI:28408995  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Cullen,P. and Seedorf,U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 4591 19-SEP-2002;  
OGHAM GmbH (DE)

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1557 TGTTCGATGCGAGTTTG 1576  
DB 1 TGTTCGATGCGTAAAGTG 20

RESULT 95  
LOCUS AX699210 20 bp DNA linear PAT 29-MAY-2003  
DEFINITION Sequence 151 from Patent WO03000727.  
ACCESSION AX699210  
VERSION AX699210.1 GI:29499860  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Zhang,Y., Moffatt,M., Cookson,W. and Tinsley,J.O.  
TITLE Atopy  
JOURNAL Patent: WO 03000727-A 151 03-JAN-2003;  
ISIS INNOVATION LIMITED (GB)

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2375 GTAGAGAGTTTACACAGAA 2394  
DB 20 GTAGAGATGTTTACACAGAA 1

RESULT 96  
LOCUS AX785708 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Sequence 217 from Patent WO03050299.  
ACCESSION AX785708  
VERSION AX785708.1 GI:32953328  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Cullen,P. and Seedorf,U.  
TITLE Method for analysing hereditary masculine infertility  
JOURNAL Patent: WO 03050299-A 217 19-JUN-2003;  
OGHAM GmbH (DE)

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 AATTCATTCCTCTTTTAC 1061  
DB 1 AATTCATTCATCTTGTTAC 20

RESULT 97  
LOCUS AX920995 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1 from Patent WO03080865.  
ACCESSION AX920995  
VERSION AX920995.1 GI:40214723  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Badmapriya,B.P., Ramesh,A.C., Chandrasekar,A. and Varadaraj,M.C.  
TITLE Primers for detecting food poisoning bacteria and a use thereof  
JOURNAL Patent: WO 03080865-A 1 02-OCT-2003;  
Council of Scientific and Industrial Research (IN)

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="A forward primer for detecting enterotoxin A target  
gene in Staph ylococcus aureus."

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 83 GGTGGGAGAACGCGAGA 102  
DB 1 GTAGCGAGAAAAGCGAGA 20

RESULT 98  
LOCUS BD006253 20 bp DNA linear PAT 31-JAN-2002  
DEFINITION Antisense inhibition of ras gene with chimeric and alternating  
oligonucleotides.  
ACCESSION BD006253  
VERSION BD006253.1 GI:18634624  
KEYWORDS JP 2001500530-A/20.  
SOURCE synthetic construct

QY 2001500530-A/20.  
SOURCE synthetic construct

ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 20)  
REFERENCE Ecker,D.J., Cook,P.D., Monia,B.P., Freier,S.M. and Sang,Y.S.  
AUTHORS Antisense inhibition of ras gene with chimeric and alternating  
TITLE oligonucleotides  
JOURNAL Patent: JP 2001500530-A 20 16-JAN-2001;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2001500530-A/20  
PD 16-JAN-2001  
PR 30-APR-1998 JP 1998547418  
PI 30-APR-1997 US 08/848840  
PI DAVID J ECKER, PHILIP DAN COOK, BRETT P MONIA, SUSAN M FREIER, PI  
YOGESH S SANGHVI  
PC C12Q1/68,C12P19/34,C07H19/16,C07H19/167,C07H19/173,C07H19/067,  
PC C07H19/06,  
PC C07H19/09,C07H21/04,A61K48/00  
CC  
FH Key Location/Qualifiers  
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source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 400 GGCGTCGGCGCGGAGCGCAG 419  
Db 20 GGCGCGCGCGCGGAGCGCAG 1  
RESULT 99  
BD073147 20 bp DNA linear PAT 27-AUG-2002  
LOCUS Antisense oligonucleotide inhibition of RAS.  
DEFINITION BD073147  
ACCESSION BD073147 GI:22618750  
VERSION JP 2001509394-A/20.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P., Cowcert,L.M. and Manoharan,M.  
TITLE Antisense oligonucleotide inhibition of RAS  
JOURNAL Patent: JP 2001509394-A 20 24-JUL-2001;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Unidentified  
PN JP 2001509394-A/20  
PD 24-JUL-2001  
PR 06-JUL-1998 JP 2000502223  
PI 08-JUL-1997 US 08/889286  
PI BRETT P MONIA, LEX M COWCERT, MUSIA MANOHARAN  
PC C12N15/09,A61K31/7083,A61K48/00,A61P35/00,C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
CC Antisense oligonucleotide inhibition of RAS  
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Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 400 GGCGTCGGCGCGGAGCGCAG 419  
Db 20 GGCGCGCGCGCGGAGCGCAG 1  
RESULT 100  
BD138197 20 bp DNA linear PAT 16-SEP-2002  
LOCUS Antisense modulation of human MDM2 expression.  
DEFINITION BD138197  
ACCESSION BD138197 GI:23233142  
VERSION JP 2002508944-A/123.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowcert,L.M.  
TITLE Antisense modulation of human MDM2 expression  
JOURNAL Patent: JP 2002508944-A 123 26-MAR-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Unidentified  
PN JP 2002508944-A/123  
PD 26-MAR-2002 JP 2000538025  
PR 26-MAR-1999 US 09/048810  
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M  
PI CONCERT  
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
PC C12Q1/68,  
PC C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Antisense modulation of human MDM2 expression FH Key  
CC Location/Qualifiers  
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/db\_xref="taxon:32644"  
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Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1005 GCTTTCCTCAATGAAGAG 1024  
Db 1 GCTTTCATCAAGGAAGG 20  
RESULT 101  
A87890 18 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 38 from Patent WO9833904.  
DEFINITION A87890  
ACCESSION A87890 GI:6736460  
VERSION  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Brysch,W. and Schlengensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 38 06-AUG-1998;  
BIOGONOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
PC Location/Qualifiers  
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/organism="unclassified"  
/mol\_type="unassigned DNA"

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 400 GGCGTCGGCGCGGAGCGCAG 419  
Db 20 GGCGCGCGCGCGGAGCGCAG 1  
RESULT 100  
BD138197 20 bp DNA linear PAT 16-SEP-2002  
LOCUS Antisense modulation of human MDM2 expression.  
DEFINITION BD138197  
ACCESSION BD138197 GI:23233142  
VERSION JP 2002508944-A/123.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowcert,L.M.  
TITLE Antisense modulation of human MDM2 expression  
JOURNAL Patent: JP 2002508944-A 123 26-MAR-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Unidentified  
PN JP 2002508944-A/123  
PD 26-MAR-2002 JP 2000538025  
PR 26-MAR-1999 US 09/048810  
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M  
PI CONCERT  
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
PC C12Q1/68,  
PC C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Antisense modulation of human MDM2 expression FH Key  
CC Location/Qualifiers  
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Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1005 GCTTTCCTCAATGAAGAG 1024  
Db 1 GCTTTCATCAAGGAAGG 20  
RESULT 101  
A87890 18 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 38 from Patent WO9833904.  
DEFINITION A87890  
ACCESSION A87890 GI:6736460  
VERSION  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Brysch,W. and Schlengensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 38 06-AUG-1998;  
BIOGONOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
PC Location/Qualifiers  
FT source 1..18  
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/mol\_type="unassigned DNA"

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/db_xref="taxon:32644"
Query Match      0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 GGGGGGGGGGGGGGGG 404
      |||
Db      2 GGGGGGGGGGGGGGGG 16

RESULT 102
A89857
LOCUS      A89857      18 bp      DNA      linear      PAT 22-JUN-2000
DEFINITION Sequence 38 from Patent EP0856579.
ACCESSION A89857
VERSION    A89857.1 GI:6738371
KEYWORDS
SOURCE     unidentified
           unidentified
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Brysch,W.D. and Schlingensiepen,K.D.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: EP 0856579-A 38 05-AUG-1998;
           BIOLOGISTIK GES. (DE)
FEATURES
  source    1. .18
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 GGGGGGGGGGGGGGGG 404
      |||
Db      2 GGGGGGGGGGGGGGGG 16

RESULT 103
A8296787
LOCUS      A8296787      18 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 8522 from patent US 6537751.
ACCESSION A8296787
VERSION    A8296787.1 GI:31684071
KEYWORDS
SOURCE     Unknown.
           Unclassified.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
           disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 8522 25-MAR-2003;
           Location/Qualifiers
FEATURES
  source    1. .18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      864 CCCAGATGAGAACAA 878
      |||
Db      3 CCCAGATGAGAACAA 17

RESULT 104
BD065403
LOCUS      BD065403      18 bp      DNA      linear      PAT 27-AUG-2002

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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065403
VERSION    BD065403.1 GI:22611006
KEYWORDS
SOURCE     unidentified
           unidentified
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 200151000-A 38 07-AUG-2001;
           BIOLOGISTIK GESELLSCHAFT FUR BIOLOGIEKULARE DIAGNOSTIK MBH
COMMENT
  OS Unknown
  PN JP 200151000-A/38
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 97101531.8
  PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
  PC C12N15/11,C07H21/04,A61K31/70
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FEATURES
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Query Match      0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 GGGGGGGGGGGGGGGG 404
      |||
Db      2 GGGGGGGGGGGGGGGG 16

RESULT 105
A8154594
LOCUS      A8154594/c      20 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238921.
ACCESSION A8154594
VERSION    A8154594.1 GI:15122647
KEYWORDS
SOURCE     Unknown.
           Unclassified.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J. and Montia,B.P.
TITLE      Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL    Patent: US 6238921-A 11 28-MAY-2001;
           Location/Qualifiers
FEATURES
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            /organism="unknown"
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Query Match      0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1707 TGTACTACTGATGG 1721
      |||
Db      19 TGTACTACTGATGG 5

RESULT 106
E29883
LOCUS      E29883      20 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION HIV cofactor inhibitor.
ACCESSION E29883
VERSION    E29883.1 GI:13021278
KEYWORDS   JP 1999297795-A/37.

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SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 20)  
AUTHORS Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.  
TITLE HIV cofactor inhibitor  
JOURNAL Patent: JP 1999292795-A 37 26-OCT-1999;  
YAMANOUCHI PHARMACEUT CO LTD

COMMENT OS Unidentified  
FN JP 1999292795-A/37  
PD 26-OCT-1999  
PR 02-APR-1998 JP 1998125452

PI HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI  
AKIRA WADA  
PC A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC  
FH Key Location/Qualifiers  
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FEATURES  
source 1..20

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 GCGGCGAGACCGCC 2048  
DB 5 GCGGCGAGACCGCC 19

RESULT 107  
AR333603/c 20 bp DNA linear PAT 20-DEC-2002  
LOCUS AR333603  
DEFINITION Sequence 6 from patent US 6458534.  
ACCESSION AR333603  
VERSION AR333603.1 GI:27276205  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Concanon,P.J., Vissinga,C.S., Cerosaletti,K.M., Varon-Mateeva,R., Sperling,K. and Reis,A.W.S.  
TITLE Gene associated with Nijmegen breakage syndrome, it's gene product and methods for their use  
JOURNAL Patent: US 6458534-A 6 01-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/organism='unknown'  
/mol\_type='genomic DNA'

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 GTATGTGAGAGAG 1799  
DB 15 GTATGTGAGAGAG 1

RESULT 108  
AR268875/c 20 bp DNA linear PAT 10-APR-2003  
LOCUS AR268875  
DEFINITION Sequence 45 from patent US 6500637.  
ACCESSION AR268875  
VERSION AR268875.1 GI:29699571  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.  
TITLE Neurogenesis inducing genes  
JOURNAL Patent: US 6500637-A 45 31-DEC-2002;  
FEATURES Location/Qualifiers  
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/mol\_type='genomic DNA'

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1106 GCTTCGTGACCTTC 1120  
DB 17 GCTTCGTGACCTTC 3

RESULT 109  
AR373452 20 bp DNA linear PAT 18-DEC-2003  
LOCUS AR373452  
DEFINITION Sequence 22 from patent US 6602713.  
ACCESSION AR373452  
VERSION AR373452.1 GI:40075581  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Wylie,J.  
TITLE Antisense modulation of protein phosphatase 2 catalytic subunit beta expression  
JOURNAL Patent: US 6602713-A 22 05-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/organism='unknown'  
/mol\_type='genomic DNA'

Query Match 0.6%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 CCGGCCCGCCGCCG 297  
DB 2 CCGGCCCGCCGCCG 16

RESULT 110  
BD138085/c 20 bp DNA linear PAT 18-SEP-2002  
LOCUS BD138085  
DEFINITION Antisense modulation of human MDM2 expression.  
ACCESSION BD138085  
VERSION BD138085.1 GI:23233030  
KEYWORDS JP 2002508944-A/11.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 20)  
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowse, L.M.  
TITLE Antisense modulation of human MDM2 expression  
JOURNAL Patent: JP 2002508944-A 11 26-MAR-2002;  
ISIS PHARMACEUTICALS INC

COMMENT OS Unidentified  
FN JP 2002508944-A/11  
PD 26-MAR-2002  
PR 26-MAR-1999 JP 2000538025  
PR 26-MAR-1998 US 09/048810  
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSE  
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//  
PC C12O1/68,

PC C12N15/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 CC Antisense modulation of human MDM2 expression FH  
 Location/Qualifiers  
 FT source 1..20  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1707 TGTACCTACTGATGG 1721  
 Db 19 TGTACTACTGATGG 5

RESULT 111  
 A89509 18 bp DNA linear PAT 22-JAN-2000  
 LOCUS Sequence 1657 from Patent WO9833904.  
 DEFINITION A89509  
 ACCESSION A89509.1 GI:6738079  
 VERSION  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Brysch, W. and Schlingensiepen, K.  
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
 JOURNAL Patent: WO 9833904-A 1657 06-AUG-1998;  
 BIOCHEMIST GEB (DE); BRYSCH WOLFGANG (DE)  
 FEATURES  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 70;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 878 AGGAAATGAGCCCTTG 895  
 Db 1 AAGAGATGAGCCCTTG 18

RESULT 112  
 AR074781 18 bp DNA linear PAT 28-AUG-2000  
 LOCUS Sequence 78 from patent US 5955276.  
 DEFINITION AR074781  
 ACCESSION AR074781  
 VERSION AR074781.1 GI:10001534  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Morgante, M. and Vogel, J. Marie.  
 TITLE Compound microsatellite primers for the detection of genetic polymorphisms  
 JOURNAL Patent: US 5955276-A 78 21-SEP-1999;  
 FEATURES  
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 /mol\_type="unassigned DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 70;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1785 GTATGTGAGAGAGAGA 1802  
 Db 1 GTGTGTGAGAGAGAGA 18

RESULT 113  
 AR106764 18 bp DNA linear PAT 14-FEB-2001  
 LOCUS Sequence 12 from patent US 6107091.  
 DEFINITION AR106764  
 ACCESSION AR106764  
 VERSION AR106764.1 GI:12821294  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Cowsett, L. M.  
 TITLE Antisense inhibition of G-alpha-16 expression  
 JOURNAL Patent: US 6107091-A 12 22-AUG-2000;  
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Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 70;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2149 GACTTCATGCGCTTAAC 2166  
 Db 1 GACTTCCTGCTGCAAC 18

RESULT 114  
 AR236591 18 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 37 from patent US 6465213.  
 DEFINITION AR236591  
 ACCESSION AR236591  
 VERSION AR236591.1 GI:27280660  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Ekstrand, J.  
 TITLE Nucleotide sequences  
 JOURNAL Patent: US 6465213-A 37 15-OCT-2002;  
 FEATURES  
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 /mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 70;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2304 CACAGTGAGTAACCG 2321  
 Db 18 CACATTGGAGAACG 1

RESULT 115  
 AR236594/c 18 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 40 from patent US 6465213.  
 DEFINITION AR236594  
 ACCESSION AR236594  
 VERSION AR236594.1 GI:27280663  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS  
TITLE Nucleotide sequences  
JOURNAL Patent: US 6465213-A 40 15-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGAGTGAACAG 2321  
18 CACATTGGAGGAGACAG 1

RESULT 116  
AR236612/C 18 bp DNA linear PAT 20-DEC-2002  
LOCUS AR236612 Sequence 66 from patent US 6465213.  
DEFINITION AR236612  
ACCESSION AR236612  
VERSION AR236612.1 GI:27280681  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Ekstrand,J.  
TITLE Nucleotide sequences  
JOURNAL Patent: US 6465213-A 66 15-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGAGTGAACAG 2321  
18 CACATTGGAGGAGACAG 1

RESULT 117  
AR236614/C 18 bp DNA linear PAT 20-DEC-2002  
LOCUS AR236614 Sequence 68 from patent US 6465213.  
DEFINITION AR236614  
ACCESSION AR236614  
VERSION AR236614.1 GI:27280683  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Ekstrand,J.  
TITLE Nucleotide sequences  
JOURNAL Patent: US 6465213-A 68 15-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGAGTGAACAG 2321  
18 CACATTGGAGGAGACAG 1

RESULT 118  
AR281556 18 bp DNA linear PAT 10-APR-2003  
LOCUS AR281556 Sequence 2 from patent US 6518416.  
DEFINITION AR281556  
ACCESSION AR281556  
VERSION AR281556.1 GI:29717311  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Danenberg,K.D.  
TITLE Method of determining a chemotherapeutic regimen based on ERCC1  
expression  
JOURNAL Patent: US 6518416-A 2 11-FEB-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 GCGGAGCGAGAGAGAG 427  
1 GCGGAGGCTGAGGACAG 18

RESULT 119  
AR294319 18 bp DNA linear PAT 12-JUN-2003  
LOCUS AR294319 Sequence 6054 from patent US 6537751.  
DEFINITION AR294319  
ACCESSION AR294319  
VERSION AR294319.1 GI:31681603  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Ballelic markers for use in constructing a high density  
JOURNAL Patent: US 6537751-A 6054 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1987 GAGAGAGGAGAGGAG 2004  
1 GAGAGAGGAGAGGAG 18

RESULT 120  
AR297043/C 18 bp DNA linear PAT 12-JUN-2003  
LOCUS AR297043 Sequence 8778 from patent US 6537751.  
DEFINITION AR297043  
ACCESSION AR297043  
VERSION AR297043.1 GI:31684327  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Ballelic markers for use in constructing a high density

JOURNAL disequilibrium map of the human genome  
Patent: US 6537751-A 8778 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 687 CGAGTCAACGATTCAGG 704  
DB 18 CAAGTCAACGATTCAGG 1

RESULT 121  
AR299784/c 18 bp DNA linear PAT 12-JUN-2003  
LOCUS AR299784  
DEFINITION Sequence 11519 from patent US 6537751.  
ACCESSION AR299784  
VERSION AR299784.1 GI:31687068  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 11519 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1930 GAGACTTTAAGAGAC 1947  
DB 18 GAGGCTTTAAGAGAC 1

RESULT 122  
AR340545 18 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340545  
DEFINITION Sequence 2 from patent US 6573052.  
ACCESSION AR340545  
VERSION AR340545.1 GI:33732191  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 18)  
AUTHORS Danenberg,K.D.  
TITLE Method of determining a chemotherapeutic regimen based on ERCC1  
JOURNAL Patent: US 6573052-A 2 03-JUN-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 GCGGAGCGAGGAGAG 427  
DB 1 GCGGAGCGTGAAGAACAG 18

RESULT 123  
AR373063 18 bp DNA linear PAT 18-DEC-2003  
LOCUS AR373063  
DEFINITION Sequence 2 from patent US 6602670.  
ACCESSION AR373063  
VERSION AR373063.1 GI:40074994  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 18)  
AUTHORS Danenberg,K.D.  
TITLE Method of determining a chemotherapeutic regimen based on ERCC1  
JOURNAL Patent: US 6602670-A 2 05-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 GCGGAGCGAGGAGAG 427  
DB 1 GCGGAGCGTGAAGAACAG 18

RESULT 124  
AX574419 18 bp DNA linear PAT 07-JAN-2003  
LOCUS AX574419  
DEFINITION Sequence 2 from Patent WO02061128.  
ACCESSION AX574419  
VERSION AX574419.1 GI:27551745  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE Unclassified.  
1  
AUTHORS Danenberg,K.D.  
TITLE Method of determining a chemotherapeutic regimen based on ercc1  
JOURNAL Patent: WO 02061128-A 2 08-AUG-2002;  
FEATURES Response Genetics, Inc. (US)  
source Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide Primer"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 GCGGAGCGAGGAGAG 427  
DB 1 GCGGAGCGTGAAGAACAG 18

RESULT 125  
AX599246 18 bp DNA linear PAT 14-FEB-2003  
LOCUS AX599246  
DEFINITION Sequence 586 from Patent WO02077272.  
ACCESSION AX599246  
VERSION AX599246.1 GI:28399368  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE artificial sequences.  
1

AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pellet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

JOURNAL Patent: WO 02077272-A 586 03-OCT-2002;

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 39 GTGTAGTGGCTTGGTT 56  
Db 1 GTGTAGTGGCTTGGTT 18

RESULT 126  
AX599249 18 bp DNA linear PAT 14-FEB-2003  
LOCUS Sequence 589 from Patent WO02077272.  
DEFINITION AX599249  
ACCESSION AX599249.1 GI:28399391  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pellet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

JOURNAL Patent: WO 02077272-A 589 03-OCT-2002;

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 88 GGAGAGACGGAAGACAG 105  
Db 1 GGAGATACGGAAGATAG 18

RESULT 127  
AX599820 18 bp DNA linear PAT 14-FEB-2003  
LOCUS Sequence 1160 from Patent WO02077272.  
DEFINITION AX599820  
ACCESSION AX599820.1 GI:28399968  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pellet, C. and Ziebarth, H.

Pellet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

JOURNAL Patent: WO 02077272-A 1160 03-OCT-2002;

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 39 GTGTAGTGGCTTGGTT 56  
Db 1 GTGTAGTGGCTTGGTT 18

RESULT 125  
AX599822/c 18 bp DNA linear PAT 14-FEB-2003  
LOCUS Sequence 1162 from Patent WO02077272.  
DEFINITION AX599822  
ACCESSION AX599822.1 GI:28399970  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pellet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

JOURNAL Patent: WO 02077272-A 1162 03-OCT-2002;

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 39 GTGTAGTGGCTTGGTT 56  
Db 1 GTGTAGTGGCTTGGTT 1

RESULT 129  
AX599831 18 bp DNA linear PAT 14-FEB-2003  
LOCUS Sequence 1171 from Patent WO02077272.  
DEFINITION AX599831  
ACCESSION AX599831.1 GI:28399979  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pellet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

JOURNAL Patent: WO 02077272-A 1171 03-OCT-2002;  
EpiGenomics AG (DE)  
FEATURES  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 GAGAACAGCGAAGACAGC 106  
|||||  
1 GAGAAATAGCGAAGATAGC 18

RESULT 130  
AX599833/C  
LOCUS Sequence 1173 from Patent WO02077272.  
DEFINITION AX599833  
ACCESSION AX599833  
VERSION AX599833.1 GI:28399981  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1  
AUTHORS Berlin, K., Braun, A., Distler, U., Guefig, D., Howe, A., Mueller, J.,  
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Lau, E.,  
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,  
Pelest, C., and Ziebarth, H.  
TITLE Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
JOURNAL Patent: WO 02077272-A 1173 03-OCT-2002;  
EpiGenomics AG (DE)  
FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 GAGAACAGCGAAGACAGC 106  
|||||  
18 GAGAAATAGCGAAGATAGC 1

RESULT 131  
AX767690  
LOCUS Sequence 338 from Patent WO03044226.  
DEFINITION AX767690  
ACCESSION AX767690  
VERSION AX767690.1 GI:32436295  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1  
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and  
Nimmich, I.  
TITLE Method and nucleic acids for the analysis of a lymphoid cell  
proliferative disorder  
JOURNAL Patent: WO 03044226-A 338 30-MAY-2003;  
EpiGenomics AG (DE)  
FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 39 GTGTAGGTCGCGCTTGCTT 56  
|||||  
1 GTGTAGGTCGCTTGCTT 18

RESULT 132  
AX767693  
LOCUS Sequence 341 from Patent WO03044226.  
DEFINITION AX767693  
ACCESSION AX767693  
VERSION AX767693.1 GI:32436298  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
1  
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and  
Nimmich, I.  
TITLE Method and nucleic acids for the analysis of a lymphoid cell  
proliferative disorder  
JOURNAL Patent: WO 03044226-A 341 30-MAY-2003;  
EpiGenomics AG (DE)  
FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for CDC25A"

Query Match  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 88 GGAGAACAGCGAAGACAGC 105  
|||||  
1 GGAGAAATAGCGAAGATAGC 18

RESULT 133  
AX838249/C  
LOCUS Sequence 5373 from Patent EP1347046.  
DEFINITION AX838249  
ACCESSION AX838249  
VERSION AX838249.1 GI:39921941  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1  
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,  
Yamamoto, U. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,  
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and  
Masuno, Y.  
TITLE Full-length cDNA sequences  
JOURNAL Patent: EP 1347046-A 5373 24-SEP-2003;  
Research Association for Biotechnology (JP)  
FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of Artificial Sequence: an artificially  
synthesized primer se q"

Query Match  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 88 GGAGAACAGCGAAGACAGC 105  
|||||  
1 GGAGAAATAGCGAAGATAGC 18

RESULT 133  
AX838249/C  
LOCUS Sequence 5373 from Patent EP1347046.  
DEFINITION AX838249  
ACCESSION AX838249  
VERSION AX838249.1 GI:39921941  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1  
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,  
Yamamoto, U. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,  
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and  
Masuno, Y.  
TITLE Full-length cDNA sequences  
JOURNAL Patent: EP 1347046-A 5373 24-SEP-2003;  
Research Association for Biotechnology (JP)  
FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of Artificial Sequence: an artificially  
synthesized primer se q"

Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 621 GGCGAGTGTATGAGCA 638  
18 GGCGAGTGTATGAGCA 1

## RESULT 134

BD067022 18 bp DNA linear PAT 27-AUG-2002  
LOCUS An antisense oligonucleotide preparation method.  
DEFINITION BD067022  
ACCESSION BD067022 GI:22612625  
VERSION JP 2001511000-A/1657.  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Schlingsensiepen, K.H. and Brysch, W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1657 07-AUG-2001;  
BIOLOGISTIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/1657  
PD 07-AUG-2001  
PR 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGSSENSIEPEN, WOLFGANG BRYSCH  
PC C12N15/11, C07H21/04, A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
LOCATION/Qualifiers  
FT source 1.18  
/organism='Unknown'.  
location/Qualifiers  
source 1.18  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 AGGAAATGAGCCTTTG 895  
1 AAGAGATGAGCCTTTG 18

RESULT 135  
BD261781 19 bp DNA linear PAT 17-JUL-2003  
LOCUS Controlled release formulation comprising GNRH-II.  
DEFINITION BD261781  
ACCESSION BD261781 GI:33071549  
VERSION JP 2002531411-A/2.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Qi, S., Akinsanya, K. and Hayward, A.  
TITLE Controlled release formulation comprising GNRH-II  
JOURNAL Patent: JP 2002531411-A 2 24-SEP-2002;  
FERRING BV

COMMENT OS Artificial Sequence  
PN JP 2002531411-A/2  
PD 24-SEP-2002  
PR 02-DEC-1999 JP 2000584909  
PR 03-DEC-1998 GB 9826652.0  
PI STEVE QI, KAREN AKINSANYA, AMANDA HAYWARD  
PC A61K38/00, A61K9/50, A61K47/34, A61P3/10, A61P13/08, A61P19/00, PC  
A61P19/10//  
PC C07K14/59, A61K37/02.

CC Description of Artificial Sequence: Synthetic PCR primer FH  
Key Location/Qualifiers  
FT source 1.19  
/organism="Artificial Sequence".  
location/Qualifiers  
source 1.19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 GGCGGGCGGGGCTCG 407  
2 GGCGGGCGGGGCTCG 19

RESULT 136  
AX025392 19 bp DNA linear PAT 16-SEP-2000  
LOCUS Sequence 2 from Patent GB2344287.  
DEFINITION AX025392  
ACCESSION AX025392 GI:10187076  
VERSION AX025392.1  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Akinsanya, K., Hayward, A. and Qi, S.  
TITLE Controlled release pharmaceutical formulation  
JOURNAL Patent: GB 2344287-A 2 07-JUN-2000;  
FERRING BV (NL)  
location/Qualifiers  
source 1.19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic PCR primer"

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 GGCGGGCGGGGCTCG 407  
2 GGCGGGCGGGGCTCG 19

RESULT 137  
AX128870 19 bp DNA linear PAT 15-MAY-2001  
LOCUS AX128870/c  
DEFINITION AX128870  
ACCESSION AX128870  
VERSION AX128870.1 GI:14135175  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
JOURNAL Robbins, J.M. and Tritz, R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye  
diseases  
Patent: WO 0130362-A 88 03-MAY-2001;  
IMMUSOL, INC. (US)  
location/Qualifiers  
source 1.19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cdk1 ribozyme binding site"

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 75;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1988 AGAAGAGCAAGAGGAGA 2005  
 |||||  
 DB 18 AGCAGAGCAAGAGGAGA 1

RESULT 138  
 AX132503 19 bp DNA PAT 15-MAY-2001  
 LOCUS Sequence 3721 from Patent WO0130362.  
 DEFINITION AX132503  
 ACCESSION AX132503  
 VERSION AX132503.1 GI:14138808  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Robbins, J.M. and Trletz, R.  
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
 JOURNAL Patent: WO 0130362-A 3721 03-MAY-2001;  
 IMMUSOL, INC. (US)  
 FEATURES  
 source  
 1.19  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="cdcc25 hs ribozyme binding site"

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 75;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 ACTCTTATTGAAGAGC 1702  
 |||||  
 DB 2 ACTCTTCTGAAGAGC 19

RESULT 139  
 AX822079 19 bp DNA PAT 10-DEC-2003  
 LOCUS Sequence 2 from Patent EP1340768.  
 DEFINITION AX822079  
 ACCESSION AX822079  
 VERSION AX822079.1 GI:39725261  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE 1  
 AUTHORS Akinsanya, K., Hayward, A. and Qi, S.  
 TITLE LHRH analogues for the treatment of osteoporosis  
 JOURNAL Patent: EP 1340768-A 2 03-SEP-2003;  
 (NL)  
 FEATURES  
 source  
 1.19  
 Location/Qualifiers  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32844"

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 75;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 GGGGGGGGGGGGGGGGTCG 407  
 |||||  
 DB 2 GGGGGGGGGGGGGGGGCTCTCG 19

RESULT 140  
 AR010014 16 bp DNA PAT 04-DEC-1998  
 LOCUS Sequence 26 from patent US 5756684.  
 DEFINITION AR010014  
 ACCESSION AR010014  
 VERSION AR010014.1 GI:3966819  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Johnson, E.M. and Bergemann, A.D.  
 TITLE Cloning and expression of PUR protein  
 JOURNAL Patent: US 5756684-A 26 26-MAY-1998;  
 FEATURES  
 source  
 1.16  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 70;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GGCAGAGGAGAGGGA 430  
 |||||  
 DB 1 GGCAGAGGAGAGGGA 16

RESULT 141  
 AR034749 16 bp DNA PAT 29-SEP-1999  
 LOCUS Sequence 26 from patent US 5869622.  
 DEFINITION AR034749  
 ACCESSION AR034749  
 VERSION AR034749.1 GI:5950354  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Johnson, E.M. and Bergemann, A.D.  
 TITLE Monoclonal antibodies to the pur protein  
 JOURNAL Patent: US 5869622-A 26 09-SEP-1999;  
 FEATURES  
 source  
 1.16  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 70;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GGCAGAGGAGAGGGA 430  
 |||||  
 DB 1 GGCAGAGGAGAGGGA 16

RESULT 142  
 BD233305 16 bp DNA PAT 17-JUN-2003  
 LOCUS Method of detecting mutation selected by drug in HIV protease gene.  
 DEFINITION BD233305  
 ACCESSION BD233305  
 VERSION BD233305.1 GI:33043075  
 KEYWORDS  
 SOURCE Aids-associated retrovirus  
 ORGANISM Aids-associated retrovirus  
 Viruses; Retroid viruses; Retroviridae.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Stuyver, L.  
 TITLE Method of detecting mutation selected by drug in HIV protease gene  
 JOURNAL Patent: JP 2002518065-A 401 25-JUN-2002;  
 INNOGENETICS NV  
 OS Aids-associated retrovirus  
 PN JP 2002518065-A/401

PD 25-JUN-2002  
PF 22-JUN-1999 JP 2000556068  
PR 24-JUN-1998 EP 98870143.9  
PI LIEVEN STUYVER  
PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00  
CC Method of detecting mutation selected by drug in HIV protease  
C1  
Key gene  
FH source  
FT Location/Qualifiers  
1.16  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

Query Match  
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 16;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 684 CTCGAGTCACAGAT 699  
16 CTCGAGTCACAGAT 1

RESULT 143  
LOCUS AX007859/c 16 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 401 from Patent WO967428.  
ACCESSION AX007859  
VERSION AX007859.1 GI:9995556  
KEYWORDS  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
REFERENCE 1  
AUTHORS Stuyver,L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene  
JOURNAL Patent: WO 967428-A 401 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
LOCATION/Qualifiers  
1.16  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

FEATURES  
source

Query Match  
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 16;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 684 CTCGAGTCACAGAT 699  
16 CTCGAGTCACAGAT 1

RESULT 144  
LOCUS 126797 17 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 20 from patent US 5561041.  
ACCESSION 126797  
VERSION 126797.1 GI:1606667  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sidransky,D.  
TITLE Nucleic acid mutation detection by analysis of sputum  
JOURNAL Patent: US 5561041-A 20 01-OCT-1996;  
LOCATION/Qualifiers  
1.17  
/organism="unknown"

/mol\_type="unassigned DNA"  
0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 275 TCCGACACCCGCCG 290  
2 TCCGACACCCGCCG 17

RESULT 145  
LOCUS 191538 17 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 20 from patent US 5726019.  
ACCESSION 191538  
VERSION 191538.1 GI:3936008  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sidransky,D.  
TITLE Analysis of sputum by amplification and detection of mutant nucleic acid sequences  
JOURNAL Patent: US 5726019-A 20 10-MAR-1998;  
LOCATION/Qualifiers  
1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 275 TCCGACACCCGCCG 290  
2 TCCGACACCCGCCG 17

RESULT 146  
LOCUS AR188775/c 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4263 from patent US 6346398.  
ACCESSION AR188775  
VERSION AR188775.1 GI:20234740  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Becobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 4263 12-FEB-2002;  
LOCATION/Qualifiers  
1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

FEATURES  
source

Query Match  
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 TCTTCATCAGTCTTA 1404  
17 TCTTCATCAGTCTTA 2

RESULT 147  
LOCUS AR324628/c 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 2030 from patent US 6566127.

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ACCESSION   AR324628
VERSION     AR324628.1  GI:33710436
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2010 20-MAY-2003;
FEATURES
source      1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1389 TCTTCATCAGCTCTTA 1404
DB      17 TCTTCATCAGCTCTTA 2

RESULT 148
LOCUS     AR328001 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5403 from patent US 6566127.
ACCESSION AR328001
VERSION   AR328001.1 GI:33713809
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 5403 20-MAY-2003;
FEATURES
source    1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      163 CGTTTGTGGATTTA 178
DB      17 CTTTGTGGATTTA 2

RESULT 149
LOCUS     AX423695 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2031 from Patent WO0188124.
ACCESSION AX423695
VERSION   AX423695.1 GI:21527077
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., McLaughlin,F.G. and
            Randi,A.M.
TITLE     Method and reagent for the inhibition of erg
JOURNAL   Patent: WO 0188124-A 2031 22-NOV-2001;
FEATURES  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
source    1..17

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            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1136 TGAAGATGAGGAGA 1151
DB      2 TGAAGAGAGGAGAGA 17

RESULT 150
LOCUS     AX423696 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2032 from Patent WO0188124.
ACCESSION AX423696
VERSION   AX423696.1 GI:21527078
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Jarvis,T., von Carlwiltz,I., Mcswigen,J.A., McLaughlin,F.G. and
            Randi,A.M.
TITLE     Method and reagent for the inhibition of erg
JOURNAL   Patent: WO 0188124-A 2032 22-NOV-2001;
FEATURES  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
source    1..17
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            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1136 TGAAGATGAGGAGA 1151
DB      1 TGAAGAGAGGAGAGA 16

RESULT 151
LOCUS     AX475726 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 947 from Patent WO0224750.
ACCESSION AX475726
VERSION   AX475726.1 GI:22215011
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Zhang,J.
TITLE     Human kidney tumor overexpressed membrane protein 1
JOURNAL   Patent: WO 0224750-A 947 28-MAR-2002;
FEATURES  Aeomica, Inc. (US)
source    1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      247 CTGTGGCTGGTGGCTG 262

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Db 2 CTGTGGCTGCTGGCTG 17

RESULT 152

AX475727 17 bp DNA linear PAT 12-AUG-2002

LOCUS Sequence 948 from Patent WO0224750.

DEFINITION AX475727

ACCESSION AX475727

VERSION AX475727.1 GI:22215012

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Zhang J.

AUTHORS Human kidney tumor overexpressed membrane protein 1

JOURNAL Patent: WO 0224750-A 948 28-MAR-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 75;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 247 CTGTGGCTGCTGGCTG 262

Db 1 CTGTGGCTGCTGGCTG 16

RESULT 153

AX498830 17 bp DNA linear PAT 27-SEP-2002

LOCUS Sequence 137 from Patent EP1229046.

DEFINITION AX498830

ACCESSION AX498830

VERSION AX498830.1 GI:23381112

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Zhan, J.

AUTHORS Human testis expressed patched like protein

JOURNAL Patent: EP 1229046-A 137 07-AUG-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 75;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2049 AGCAGAGCCCAAGCT 2064

Db 2 AGCAGAGCCCAAGCT 17

RESULT 154

AX498831 17 bp DNA linear PAT 27-SEP-2002

LOCUS Sequence 138 from Patent EP1229046.

DEFINITION AX498831

ACCESSION AX498831

VERSION AX498831.1 GI:23381113

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Zhan, J.

AUTHORS Human testis expressed patched like protein

JOURNAL Patent: EP 1229046-A 138 07-AUG-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 75;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2049 AGCAGAGCCCAAGCT 2064

Db 1 AGCAGAGCCCAAGCT 16

RESULT 155

AX579041/c 17 bp RNA linear PAT 10-JAN-2003

LOCUS Sequence 879 from Patent WO0211674.

DEFINITION AX579041

ACCESSION AX579041.1 GI:27648243

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Thompson, J., Moswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D. E.

AUTHORS and Grube, A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)

JOURNAL Patent: WO 0211674-A 879 14-FEB-2002;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol\_type="unassigned RNA"

/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 75;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1175 TCTGACAGCTCTCT 1190

Db 16 TTGGACAGCTCTCT 1

RESULT 156

AX579687/c 17 bp RNA linear PAT 10-JAN-2003

LOCUS Sequence 1525 from Patent WO0211674.

DEFINITION AX579687

ACCESSION AX579687

VERSION AX579687.1 GI:27648889

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Thompson, J., Moswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D. E.

AUTHORS and Grube, A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)

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JOURNAL Patent: WO 0211674-A 1525 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 TGACAGCTCTCTCTCG 1192
Db 16 TGGACAGCTCTCTCTAG 1

RESULT 157
LOCUS AX579800 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1638 from Patent WO0211674.
ACCESSION AX579800
VERSION AX579800.1 GI:27649002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
Patent: WO 0211674-A 1638 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1997 AGAGGAGATGTACAG 2012
Db 1 ACAGGAGATGTACAG 16

RESULT 158
LOCUS AX580069 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1907 from Patent WO0211674.
ACCESSION AX580069
VERSION AX580069.1 GI:27649271
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
Patent: WO 0211674-A 1907 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
1. .17

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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1997 AGAGGAGATGTACAG 2012
Db 2 ACAGGAGATGTACAG 17

RESULT 159
LOCUS AX580204/c 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2042 from Patent WO0211674.
ACCESSION AX580204
VERSION AX580204.1 GI:27649406
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
Patent: WO 0211674-A 2042 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1178 GGACAGCTCTCTCTGT 1193
Db 17 GGACAGCTCTCTCTAGT 2

RESULT 160
LOCUS AX726898 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4585 from Patent WO03025176.
ACCESSION AX726898
VERSION AX726898.1 GI:30506241
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Teلمان,A., Amson,R. and Tuljinder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 4585 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 75;

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2249 ATATCAGACTGTGCC 2264  
|||  
2 ATCTCAGACTGTGCC 17

Db

RESULT 161  
AX760113 17 bp DNA linear PAT 25-JUN-2003  
LOCUS Sequence 3434 from Patent WO03040369.  
DEFINITION AX760113  
ACCESSION AX760113.1 GI:32254729  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 3434 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2249 ATATCAGACTGTGCC 2264  
|||  
2 ATCTCAGACTGTGCC 17

Db

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2072 ATCCCTTTACCCCTC 2087  
|||  
2 ATCTCTTTACCCCTC 17

Db

RESULT 162  
AX761912 17 bp DNA linear PAT 25-JUN-2003  
LOCUS Sequence 5233 from Patent WO03040369.  
DEFINITION AX761912  
ACCESSION AX761912.1 GI:32256528  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 5233 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2249 ATATCAGACTGTGCC 2264  
|||  
2 ATCTCAGACTGTGCC 17

Db

RESULT 163  
AX762380 17 bp DNA linear PAT 25-JUN-2003  
LOCUS Sequence 5701 from Patent WO03040369.  
DEFINITION AX762380  
ACCESSION AX762380.1 GI:32256996  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 5701 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1789 GTGAGAGAGAGATC 1804  
|||  
16 GAGAGAGAGAGATC 1

Db

RESULT 164  
A57394 18 bp DNA linear PAT 03-MAR-1998  
LOCUS Sequence 2 from Patent EP0729388.  
DEFINITION A57394  
ACCESSION A57394.1 GI:37132270  
VERSION  
KEYWORDS  
SOURCE Legionella sp.  
ORGANISM Legionella sp.  
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
Legionellaceae; Legionella.

REFERENCE  
1  
AUTHORS Heidrich, B., Robinson, P.D., Tiecke, F. and Rolfs, A.D.  
TITLE Method for genus and species specific identification of Legionella  
JOURNAL Patent: EP 0739988-A 2 30-OCT-1996;  
BOEHRINGER MANNHEIM GMBH (DE)  
COMMENT Other publication DE 19515891 961031.  
FEATURES Location/Qualifiers  
source 1..18  
/organism="Legionella sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:459"

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 CTGATTCCTTGACCA 842  
|||  
3 CTGATTCCTTGACCA 18

Db

RESULT 165  
A67603 18 bp DNA linear PAT 05-MAY-1999  
LOCUS Sequence 23 from Patent WO9744485.  
DEFINITION A67603  
ACCESSION A67603.1 GI:4756466  
VERSION  
KEYWORDS  
SOURCE unidentified

## ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)

AUTHORS Goodfellow,P.N.

TITLE METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST

JOURNAL Patent: WO 9744485-A 23 27-NOV-1997;

FEATURES HEXAGEN TECHNOLOGY LIMITED (GB)

SOURCE location/Qualifiers

1.18

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 GATTCTCTGGGCGCAT 730

Db 17 GGTTCCTCTGGGCGCAT 2

RESULT 166

AR089741/C

LOCUS AR089741

DEFINITION Sequence 23 from patent US 5994075.

ACCESSION AR089741

VERSION AR089741.1 GI:10016496

KEYWORDS

SOURCE Unknown.

ORGANISM Unassigned.

REFERENCE 1 (bases 1 to 18)

AUTHORS Goodfellow,P.N.

TITLE Methods for identifying a mutation in a gene of interest without a

JOURNAL Patent: US 5994075-A 23 30-NOV-1999;

FEATURES Location/Qualifiers

1.18

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 GATTCTCTGGGCGCAT 730

Db 17 GGTTCCTCTGGGCGCAT 2

RESULT 167

AR131439

LOCUS AR131439

DEFINITION Sequence 2 from patent US 6194145.

ACCESSION AR131439

VERSION AR131439.1 GI:14120342

KEYWORDS

SOURCE Unknown.

ORGANISM Unassigned.

REFERENCE 1 (bases 1 to 18)

AUTHORS Heidrich,B., Robinson,P.-N., Tjেকে,F. and Rolfe,A.

TITLE Genus and species-specific identification of Legionella

JOURNAL Patent: US 6194145-A 2 27-FEB-2001;

FEATURES Location/Qualifiers

1.18

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 827 CTGATTCCTTGACCA 842

Db 3 CTGATTCCTTGACCA 18

RESULT 168

AR242052

LOCUS AR242052

DEFINITION Sequence 340 from patent US 6472154.

ACCESSION AR242052

VERSION AR242052.1 GI:27287864

KEYWORDS

SOURCE Unknown.

ORGANISM Unassigned.

REFERENCE 1 (bases 1 to 18)

AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fordon,J.W. III.

TITLE Polymorphic repeats in human genes

JOURNAL Patent: US 6472154-A 340 29-OCT-2002;

FEATURES Location/Qualifiers

1.18

/organism="unassigned DNA"

/mol\_type="genomic DNA"

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2048 CAGCAGCAGCCCGCAGC 2063

Db 2 CAGCAGCAGCCCGCAGC 17

RESULT 169

AR382600

LOCUS AR382600

DEFINITION Sequence 22 from patent US 6610515.

ACCESSION AR382600

VERSION AR382600.1 GI:40091336

KEYWORDS

SOURCE Unknown.

ORGANISM Unassigned.

REFERENCE 1 (bases 1 to 18)

AUTHORS Yamamoto,A., Tuchiya,K., Iwata,A. and Ueda,S.

TITLE Feline granulocyte colony-stimulating factor

JOURNAL Patent: US 6610515-A 22 26-AUG-2003;

FEATURES Location/Qualifiers

1.18

/organism="unassigned DNA"

/mol\_type="genomic DNA"

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 607 CAGCTGCAGGCTCTGG 622

Db 1 CAGCTGCAGGCTCTGG 16

RESULT 170

AX796148

LOCUS AX796148

DEFINITION Sequence 491 from Patent WO03052135.

ACCESSION AX796148

VERSION AX796148.1 GI:37516814

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Burger, M., Field, J.K., Genc, B., Illoglou, T., Lipscher, E., Mater, S. and Nimrich, I.  
 TITLE Method and nucleic acids for the analysis of a lung cell  
 JOURNAL Proliferative disorder  
 Patent: WO 03052135-A 491 26-UTN-2003;  
 Epigenomics AG (DE)  
 FEATURES Location/Qualifiers  
 source 1..18  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Detection oligonucleotide for WT1"

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 81;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 165 TTTGTTTGATTTTAA 180  
 Db 3 TTTGTTTGATTTTAA 18

RESULT 171  
 HSPMLRARE HSPMLRARE 18 bp mRNA linear PRI 04-AUG-1992  
 LOCUS H.sapiens PML-RAR alpha-bcr2-13# gene.  
 DEFINITION X63641  
 ACCESSION X63641.1 GI:35545  
 VERSION PML-RAR alpha-bcr gene.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 18)  
 REFERENCE Pandolfi, P.P., Alcalay, M., Fagioli, M., Zangrilli, D., Mencarelli, A.,  
 AUTHORS Diverio, D., Bonaldi, A., Lo Coco, F., Rambaldi, A., Grignani, F.,  
 Rochette-Egly, C., Gaube, M.P., Chambon, P. and Pelicci, P.G.  
 TITLE Genomic variability and alternative splicing generate multiple  
 PML/RAR alpha transcripts that encode aberrant PML proteins and  
 PML/RAR alpha isoforms in acute promyelocytic leukaemia  
 JOURNAL EMBO J. 11 (4), 1397-1407 (1992)  
 MEDLINE 92224879  
 PUBMED 1314166  
 REFERENCE 2 (bases 1 to 18)  
 AUTHORS Fagioli, M., Alcalay, M., Pandolfi, P.P., Ventrutti, L., Mencarelli, A.,  
 TITLE Simone, A., Acampora, D., Grignani, F. and Pelicci, P.G.  
 JOURNAL Alternative splicing of PML transcripts predicts coexpression of  
 MEDLINE 92278759  
 PUBMED 1594241  
 REFERENCE 3 (bases 1 to 18)  
 AUTHORS Pandolfi, P.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JAN-1992) P.P. Pandolfi, Istituto di Clinica Medica  
 MEDLINE 1594241  
 PUBMED 1594241  
 REFERENCE 1, University of Perugia, Policlinico Monteluce, 06100 Perugia,  
 JOURNAL ITALY  
 FEATURES Location/Qualifiers  
 source 1..18  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /chromosome="15;17":15q(+) "  
 /cell\_line="patient #13 cells"  
 misc\_feature 1..18  
 /product="bcr2-jul3A"  
 gene 1..10  
 /gene="PML"  
 exon <1..10  
 /gene="PML"  
 /number=6  
 gene 11..18  
 /gene="RAR alpha"

exon 11..18  
 /gene="RAR alpha"  
 /number=3

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 81;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1422 CAAGGACACCATGAG 1437  
 Db 3 CATGAGACCATGAG 18

RESULT 172  
 AR230749/c AR230749 19 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 9 from patent US 6451602.  
 DEFINITION AR230749  
 ACCESSION AR230749.1 GI:27271536  
 VERSION AR230749.1  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Popoff, I. and Cowse, L.M.  
 TITLE Antisense modulation of PAB expression  
 JOURNAL Patent: US 6451602-A 9 17-SEP-2002;  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 86;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 244 TGCGTGTGCTGTG 259  
 Db 16 TGCGTGTGCTGTGAGG 1

RESULT 173  
 AX129983 AX129983 19 bp DNA linear PAT 15-MAY-2001  
 LOCUS Sequence 1201 from Patent WO0130362.  
 DEFINITION AX129983  
 ACCESSION AX129983.1 GI:14136288  
 VERSION AX129983.1  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 REFERENCE Robbins, J.M. and Tritz, R.  
 AUTHORS Robbins, J.M. and Tritz, R.  
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye  
 JOURNAL diseases  
 Patent: WO 0130362-A 1201 03-MAY-2001;  
 JOURNAL IMMUSOL, INC. (US)

FEATURES Location/Qualifiers  
 source 1..19  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="Cdk-we-hu ribozyme binding site"

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 86;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 622 GGCAGTGATTAGAGC 637  
 Db 1 GGCAGTGATTAGAGC 16

```

RESULT 174
LOCUS AX131110 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 2328 from Patent WO0130362.
ACCESSION AX131110
VERSION AX131110.1 GI:14137415
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Robbins,J.M. and Trletz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 2328 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin F ribozyme binding site"

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1137 GAAGATGAGAGAG 1152
DB 3 GAAGATGAGAGAG 18

RESULT 175
LOCUS BD087244 19 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA molecule encoding human nuclear receptor protein nmrs.
ACCESSION BD087244
VERSION BD087244.1 GI:22632854
KEYWORDS JP 2001525197-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Chen,F.
TITLE DNA molecule encoding human nuclear receptor protein nmrs
JOURNAL Patent: JP 2001525197-A 14 11-DEC-2001;
MERCK & CO INC
COMMENT
OS Artificial Sequence
PN JP 2001525197-A/14
PD 11-DEC-2001
PR 11-DEC-1998 JP 2000524316
PR 12-DEC-1997 US 60/0659379
PI FANG CHEN
PC C12N15/09,C07K14/47,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12N15/00,C12N5/00
CC Oligonucleotide
FH Key
FT source location/Qualifiers
1..19
/organism="Artificial Sequence"
Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1968 GAGCCGAGCTGGCA 1983

```

```

DB 4 GAGCCGAGCTGGCA 19

RESULT 176
LOCUS BD221612/c 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Upstream genome sequence of IFN-alpha2 gene code domain for producing and transporting protein.
ACCESSION BD221612
VERSION BD221612.1 GI:33031382
KEYWORDS JP 2002513580-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE Upstream genome sequence of IFN-alpha2 gene code domain for producing and transporting protein
JOURNAL Patent: JP 2002513580-A 314-MAY-2002;
TRANSFAROTIC THERAPIES INC
COMMENT
OS Homo sapiens (human)
PN JP 2002513580-A/3
PD 14-MAY-2002
PR 05-MAY-1999 JP 2000547246
PR 07-MAY-1998 US 60/084648,21-MAY-1998 US 60/086555 PI
DOUGLAS A TRECO, MICHAEL W HEARTLEIN, RICHARD F SELDEN PC
C12N15/09,A61K48/00,C07K14/56,C12N5/10,C12P21/02//C12N5/10, PC
C12R1:911,
PC (C12P21/02,C12R1:911),C12N15/00,C12N5/00,C12N5/00,C12R1:911) CC
Upstream genome sequence of IFN-alpha2 gene code domain for CC
producing and
transporting protein

CC Key location/Qualifiers
FH key source 1..19
FT source 1..19
/organism="Homo sapiens (human)"
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2287 GTCAGCTGCTCTGAG 2302
DB 19 GTCAGCTGCTCTGTG 4

RESULT 177
LOCUS BD234970 17 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234970
VERSION BD234970.1 GI:33044740
KEYWORDS JP 2002517434-A/74.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 74 18-JUN-2002;
BIOGENOSTIK GEBELSCHAF FUEER BIOWOLEKULARE DIAGNOSTIK MEH
OS Homo sapiens (human)
PN JP 2002517434-A/74
PD 18-JUN-2002
PR 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI

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KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI  
BRYSCH  
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/  
PC 00, A61P35/00  
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A  
method for stimulating the immune system  
FH Key Location/Qualifiers  
FT source 1.17  
/organism='Homo sapiens (human)'.  
Location/Qualifiers

# FEATURES

source 1.17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GCGGGGCGGGGCG 403  
Db 4 GCGGGGCGGGGCG 17

## RESULT 178

LOCUS 160477 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 10 from patent US 5656462.  
ACCESSION 160477  
VERSION 160477.1 GI:2478922  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Keller, C., Mitsunashi, M. and Akitaya, T.  
TITLE Method for synthesizing cDNA using a polynucleotide immobilized support  
JOURNAL Patent: US 5656462-A 10-12-AUG-1997;  
FEATURES Location/Qualifiers

source 1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 ATCTGCTGCTGCC 934  
Db 15 ATCTGCTGCTGCC 2

RESULT 179  
LOCUS AR187025/c 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2513 from patent US 6346398.  
ACCESSION AR187025  
VERSION AR187025.1 GI:20232990  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 2513 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
Db 17 TTGTGTTGATTTA 4

RESULT 180  
LOCUS AR323635/c 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1037 from patent US 6566127.  
ACCESSION AR323635  
VERSION AR323635.1 GI:33709443  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1037 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1.17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
Db 17 TTGTGTTGATTTA 4

RESULT 181  
LOCUS AR328000/c 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5402 from patent US 6566127.  
ACCESSION AR328000  
VERSION AR328000.1 GI:33713808  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5402 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1.17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTTA 178  
Db 16 TTGTGTTGATTTA 3

RESULT 182  
LOCUS AX009041 17 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 74 from Patent WO9963975.  
ACCESSION AX009041  
VERSION AX009041.1 GI:9996415

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1  
Brysch,W., Schlingensiepen,K.R. and Schlingensiepen,R.  
A method for stimulating the immune system  
Patent: WO 9963975-A 74 16-DEC-1999;  
BIOGENISTIK GBS (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL  
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred.No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GGCGGGGGGGCGGCG 403  
DB 4 GGCGGGGGGGGGCGGCG 17

RESULT 183  
AX579538 17 bp RNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 1376 from Patent WO0211674.  
ACCESSION AX579538  
VERSION AX579538.1 GI:27648740  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1  
Thompson,J., Mewissen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.  
and Grube,A.  
Method and reagent for the inhibition of calcium activated chloride  
channel-1 (Clca-1)  
Patent: WO 0211674-A 1376 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);  
Thompson, James (US)  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred.No. 87;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1999 AGGAGATGTACAG 2012  
DB 1 AGGAGATGTACAG 14

RESULT 184  
AX725743 17 bp DNA linear PAT 08-MAY-2003  
LOCUS  
DEFINITION Sequence 3430 from Patent WO03025176.  
ACCESSION AX725743  
VERSION AX725743.1 GI:30505086  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Mus musculus  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Telemann,A., Anson,R. and Tuijnder,M.

TITLE  
JOURNAL  
FEATURES  
source

Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
Patent: WO 03025176-A 3430 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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/organism="Mus musculus"  
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QY 1478 TCTCCAGGGTTAT 1491  
DB 3 TCTCCAGGGTTAT 16

RESULT 185  
AX750821 17 bp DNA linear PAT 20-JUN-2003  
LOCUS  
DEFINITION Sequence 37 from Patent WO03033703.  
ACCESSION AX750821  
VERSION AX750821.1 GI:32133149  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1  
Zhang,J.  
Human gtp-activator protein for rab-like gtpase  
Patent: WO 03033703-A 37 24-APR-2003;  
Amersham Biosciences (SV) Corp. (US)  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred.No. 87;  
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QY 209 CCGCTGGCCCTCGC 222  
DB 4 CCGCTGGCCCTCGC 17

RESULT 186  
AX750822 17 bp DNA linear PAT 20-JUN-2003  
LOCUS  
DEFINITION Sequence 38 from Patent WO03033703.  
ACCESSION AX750822  
VERSION AX750822.1 GI:32133150  
KEYWORDS  
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ORGANISM  
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AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1  
Zhang,J.  
Human gtp-activator protein for rab-like gtpase  
Patent: WO 03033703-A 38 24-APR-2003;  
Amersham Biosciences (SV) Corp. (US)  
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 Db 3 CCGGCTGGCCTGCGC 16

RESULT 187  
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 DEFINITION Sequence 39 from Patent WO03033703.  
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 VERSION AX750823.1 GI:32133151  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Zhang, J.  
 JOURNAL Human gtp-activator protein for rab-like gtpase  
 Patent: WO 03033703-A 39 24-APR-2003;  
 Amersham Biosciences (SV) Corp. (US)  
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 LOCUS AX750824 17 bp DNA linear PAT 20-JUN-2003  
 DEFINITION Sequence 40 from Patent WO03033703.  
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 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Zhang, J.  
 JOURNAL Human gtp-activator protein for rab-like gtpase  
 Patent: WO 03033703-A 40 24-APR-2003;  
 Amersham Biosciences (SV) Corp. (US)  
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RESULT 189  
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 DEFINITION Sequence 2349 from Patent WO03040369.  
 ACCESSION AX759028  
 VERSION AX759028.1 GI:32253644  
 KEYWORDS  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Teierman, A., Amson, R. and Tuijinder, M.  
 JOURNAL Sequences involved in tumoral suppression, tumoral reversion,  
 apoptosis and/or viral resistance phenomena and their use as  
 medicines  
 Patent: WO 03040369-A 2349 15-MAY-2003;  
 Molecular Engines Laboratories (FR)  
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RESULT 190  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Teierman, A., Amson, R. and Tuijinder, M.  
 JOURNAL Sequences involved in tumoral suppression, tumoral reversion,  
 apoptosis and/or viral resistance phenomena and their use as  
 medicines  
 Patent: WO 03040369-A 4511 15-MAY-2003;  
 Molecular Engines Laboratories (FR)  
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QY 247 CTGTGGCTGTGTGCTG 260  
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RESULT 191  
 LOCUS S71705 18 bp DNA linear PRI 07-MAY-1993  
 DEFINITION Lipoprotein lipase (exon 8) [human, Genomic Mutant, 18 nt].  
 ACCESSION S71705  
 VERSION S71705.1 GI:240932  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 18)  
 Gotooda,T., Yamada,N., Kawamura,M., Kozaki,K., Mori,N., Ishibashi,S., Shimano,H., Takaku,F., Yazaki,Y., Furuchi,Y. et.al.  
 Heterogeneous mutations in the human lipoprotein lipase gene in patients with familial lipoprotein lipase deficiency  
 JOURNAL U. Clin. Invest. 86 (6), 1856-1864 (1991)  
 MEDLINE 92091492  
 PUBMED  
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gisbseq 71705] from the original journal article.  
 This sequence comes from Fig.1.  
 nonsense mutation in exon 8 (TTP382 to Stop).  
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 QY 1011 CTCGAATGAAAGAG 1024  
 DB 4 CTCGAATGAAAGAG 17  
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 LOCUS A87890 18 bp DNA linear PAT 22-JAN-2000  
 DEFINITION Sequence 38 from Patent WO9833904.  
 ACCESSION A87890  
 VERSION A87890.1 GI:6736460  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Brysch,W. and Schlingensiepen,K.  
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
 JOURNAL Patent: WO 9833904-A 38 06-AUG-1998;  
 BIOLOGISTIK GES (DE); BRYSCH WOLFGANG (DE)  
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 DB 18 CCCCACCGCGCGCCG 2  
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 LOCUS A89857 18 bp DNA linear PAT 22-JAN-2000  
 DEFINITION Sequence 38 from Patent EP0856579.  
 ACCESSION A89857  
 VERSION A89857.1 GI:6738371  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: EP 0856579-A 38 05-AUG-1998;  
 BIOLOGISTIK GES (DE)  
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 DB 18 CCCCACCGCGCGCCG 2  
 RESULT 194  
 LOCUS BD065403/c 18 bp DNA linear PAT 27-AUG-2002  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD065403  
 VERSION BD065403.1 GI:22611006  
 KEYWORDS JP 2001511000-A/38.  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Schlingensiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 38 07-AUG-2001;  
 BIOLOGISTIK GESellschaft FUR BIOMOLEKULARE DIAGNOSTIK MBH  
 OS Unknown  
 PN JP 2001511000-A/38  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PR 31-JAN-1997 EP 97101531.8  
 PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH  
 CC C12N15/11.C07H21/04.A61K31/70  
 CC An antisense oligonucleotide preparation method FH Key  
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 Job time : 6 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 10:08:14; Search time 5 Seconds

(without alignments)  
3,411 Million cell updates/sec

Title: US-08-864-955-1

Perfect score: 2419

Sequence: 1 CCAAAAGCCGCGCTTGGCTG.....GCTGGCAATGCAAGAG 2419

Scoring table: IDENTITY NUC

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Searched: 191 seqs, 3525 residues

Total number of hits satisfying chosen parameters: 382

Minimum DB seq length: 10

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 191 summaries

Database: rml.seq\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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13	17	0.7	20	1	US-09-198-452A-1735
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26	15.8	0.7	19	1	US-09-422-978-6665
27	15.8	0.7	20	1	US-08-564-002-14
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C 100	14	0.6	17	1	US-08-584-040-2513	Sequence 1037, App1
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C 104	14	0.6	18	1	US-09-577-902-14	Sequence 527, App1
C 105	14	0.6	17	1	US-08-390-850-527	

C 180	1.3	0.5	17	1	US-08-292-620A-1760	Sequence 1760, Ap
C 181	13	0.5	17	1	US-09-071-845-1760	Sequence 1760, Ap
C 182	13	0.5	17	1	US-08-738-1688-10	Sequence 10, Appl
C 183	13	0.5	17	1	US-09-017-974-82	Sequence 82, Appl
C 184	13	0.5	17	1	US-08-682-255A-82	Sequence 82, Appl
C 185	13	0.5	17	1	US-08-584-040-205	Sequence 205, Ap
C 186	13	0.5	17	1	US-08-584-040-205	Sequence 205, Ap
C 187	13	0.5	17	1	US-09-429-130-82	Sequence 82, Appl
C 188	13	0.5	17	1	US-09-471-772B-600	Sequence 600, Appl
C 189	13	0.5	17	1	US-09-371-772B-601	Sequence 601, Appl
C 190	13	0.5	17	1	US-09-371-772B-490A	Sequence 490A, Ap
C 191	13	0.5	17	1	US-09-371-772B-5421	Sequence 5421, Ap

RESULT 1

Patent No. 5994076

APPLICANT: George Jakhadze,

TITLE OF INVENTION:	METHOD OF ASS
TITLE OF INTENTION:	EXPRESSION

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.  
 3300 Grand Hill Road, Suite 1000  
 Washington, D.C. 20007

STREET: 2200 SAIN  
CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READER  
MEDIUM TYPE:

COMPUTER: I

# OPERATING SY

```
; SOFTWARE: H
```

CURRENT APPLICATION

FILING DATE:

CLASSIFICATION

PRIOR APPLICATION

APPLCATION  
FILING DATE:

ATTORNEY/AGENT

NAME: Field

REGISTRATION  
;

REFERENCE/DOCUMENTATION

TELEPHONE:

TELEFAX: 41

; INFORMATION FOR

SEQUENCE CHARACTERISTICS: 24

TYPE: nucle

STRANDEDNESS

TOPOLOGY: 1

MOLECULE TYPE:

OTHER INFORMATION:

US-08-859-998-961

1

query match  
PostgreSQL simi

Best Local Limited  
Matches 24: CC

100

QY 1632 GGGAG

23

70 1000000

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RESULT 2
US-08-859-998-962/c
; Sequence 962, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 962:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-962

Query Match          1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
; US-09-225-928-961

Query Match          1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-225-928-962/c
; Sequence 962, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
```

ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 962:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-09-225-928-962  
Query Match 1.0%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1954 AAGTTCGACCAAGAGCCGAC 1977  
DB 24 AAGTTCGACCAAGAGCCGAC 1  
RESULT 5  
US-09-225-201B-961  
Sequence 961, Application US/09225201B  
Patent No. 6489455  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Jokhadze, George  
Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,201B  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 961:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-09-225-201B-962

OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 961:  
US-09-225-201B-961  
Query Match 1.0%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1632 GCGAGGCCACATCAAGGTCGACT 1655  
DB 1 GCGAGGCCACATCAAGGTCGACT 24  
RESULT 6  
US-09-225-201B-962/c  
Sequence 962, Application US/09225201B  
Patent No. 6489455  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Jokhadze, George  
Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,201B  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 962:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-09-225-201B-962  
Query Match 1.0%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1954 AAGTTCGACCAAGAGCCGAC 1977  
DB 24 AAGTTCGACCAAGAGCCGAC 1  
RESULT 7  
US-08-860-882A-39/c

Sequence 39, Application US/08860882A  
Patent No. 5985281  
GENERAL INFORMATION:  
APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGEITE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-FIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUM  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-39

Query Match 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACCACTGCTGAGGCTGTG 621  
DB 23 CTGTGACCTGCTGCTGAGAGTCTG 1

RESULT 8  
US-08-860-882A-51/c  
Sequence 51, Application US/08860882A  
Patent No. 5985281  
GENERAL INFORMATION:  
APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGEITE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-FIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUM  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-51

Query Match 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACCACTGCTGAGGCTGTG 621  
DB 23 CTGTGACCTGCTGCTGAGAGTCTG 1

RESULT 9  
US-08-011-769A-6/c  
Sequence 6, Application US/09011769A  
Patent No. 6436691  
GENERAL INFORMATION:  
APPLICANT: SLATER, Anthony M.  
APPLICANT: BLAKLEY, David C.  
APPLICANT: DAVIES, David H.  
APPLICANT: HENNAM, John F.  
APPLICANT: HENNEQUIN, Laurent F.A.  
APPLICANT: DOWELL, Robert I.  
APPLICANT: MARSHAM, Peter R.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975

FILED DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-011-769A-6

Query Match  
Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACGAGCTGCGAGGCTG 621  
DB 23 CTGTGACCTGCTGCGAGGCTG 1

RESULT 10  
US-09-011-769A-33/C  
Sequence 33, Application US/09011769A  
Patent No. 6436591  
GENERAL INFORMATION:  
APPLICANT: SLATER, Anthony M.  
BLAKLEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-011-769A-33

Query Match  
Best Local Similarity 0.8%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 CTATGACGAGCTGCGAGGCTG 621  
DB 23 CTGTGACCTGCTGCGAGGCTG 1

RESULT 11  
US-09-231-227-6  
Sequence 6, Application US/09231227  
Patent No. 6211440  
GENERAL INFORMATION:  
APPLICANT: Briggs, Steven P.  
APPLICANT: Mutani, Dilbag Singh  
TITLE OF INVENTION: Hm2 cDNA and Polypeptide  
FILE REFERENCE: 0846  
CURRENT APPLICATION NUMBER: US/09/231,227  
CURRENT FILING DATE: 1999-01-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-231-227-6

Query Match  
Best Local Similarity 0.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1980 GCGAGGCGAGAGAGCAAG 2000  
DB 1 GGAAGGCGAGAGAGCTAGAG 21

RESULT 12  
US-09-768-585-6  
Sequence 6, Application US/09768585  
Patent No. 6486302  
GENERAL INFORMATION:  
APPLICANT: Briggs, Steven P.  
APPLICANT: Jothal, Gurmukh  
APPLICANT: Mutani, Dilbag Singh  
TITLE OF INVENTION: Hm2 cDNA and Polypeptide  
FILE REFERENCE: 0846D  
CURRENT APPLICATION NUMBER: US/09/768,585  
CURRENT FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/071,684  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: US 09/231,227  
PRIOR FILING DATE: 1999-01-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-768-585-6

Query Match  
Best Local Similarity 0.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1980 GCGAGGCGAGAGAGCAAG 2000  
DB 1 GGAAGGCGAGAGAGCTAGAG 21

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RESULT 13
US-09-198-452A-1735
; Sequence 1735, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1735
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1735

Query Match          0.7%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1386 GACTCTTCATCAGTCTT 1402
DB      1 GACTCTTCATCAGTCTT 17

RESULT 14
US-09-467-642-12
; Sequence 12, Application US/09467642
; Patent No. 6300132
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowest
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRES
; FILE REFERENCE: RTS-0106
; CURRENT APPLICATION NUMBER: US/09/467,642
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-12

Query Match          0.7%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      283 CCGCGCCGCGCGCGCGCTT 302
DB      1 CCCTCCGCGCGCGCGCGCTT 20

RESULT 15
US-09-422-978-10169
; Sequence 10169, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
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; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10169
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-10267 for SEQ 2304, in complem
US-09-422-978-10169

Query Match          0.7%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1037 CAGGGAATTCATCCTCTT 1056
DB      1 CAGGGAATTCATCCTCTT 20

RESULT 16
US-08-469-260A-95
; Sequence 95, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIK
; APPLICANT: ISA K. MUSHAMWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/APed
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

US-08-469-260A-95

Query Match 0.7%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTTGACATGACATCTTC 853  
Db 3 TCTTGACATGACATCTTC 22

RESULT 17

US-08-488-446-95  
; Sequence 95, Application US/08488446  
; Patent No. 6558698  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-488-446-95

Query Match 0.7%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTTGACATGACATCTTC 853  
Db 3 TCTTGACATGACATCTTC 22

RESULT 18

US-08-467-344A-95  
; Sequence 95, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:  
US-08-467-344A-95

Query Match 0.7%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTTGACATGACATCTTC 853  
Db 3 TCTTGACATGACATCTTC 22

RESULT 19

US-08-832-883-110  
; Sequence 110, Application US/08832883  
; Patent No. 5807681  
; GENERAL INFORMATION:  
; APPLICANT: Giordano, Antonio  
; APPLICANT: Baldi, Alphonso  
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS  
; TITLE OF INVENTION: OF CANCER  
; NUMBER OF SEQUENCES: 115

Query Match 0.7%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 834 TCTTGACATGACATCTTC 853  
Db 3 TCTTGACATGACATCTTC 22

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.  
;; STREET: Suite 1800 Two Penn Center Plaza  
;; CITY: Philadelphia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19102  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/832,863  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Monaco, Daniel A  
;; REGISTRATION NUMBER: 30,480  
;; REFERENCE/DOCKET NUMBER: 8321-13 US1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-8383  
;; TELEFAX: (215) 568-5549  
;; INFORMATION FOR SEQ ID NO: 110:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; US-08-832-863-110  
;  
Query Match                    0.7%; Score 16.2; DB 1; Length 21;  
Best Local Similarity       85.7%; Pred. No. 41;  
Matches    18; Conservative    0; Mismatches    3; Indels    0; Gaps    0;  
;  
QY                    2161 TTAACCTACTCTCCACACTC 2181  
DB                    1 TTAACCTACTCTCCACACTC 21  
;  
RESULT 20  
US-08-832-877-110  
; Sequence 110, Application US/08832877  
; Patent No. 5840506  
; GENERAL INFORMATION:  
; APPLICANT: Giordano, Antonio  
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF  
; TITLE OF INVENTION: CANCER  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.  
; STREET: Suite 1800 Two Penn Center Plaza  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/832,877  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-13 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549

;; INFORMATION FOR SEQ ID NO: 110:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; US-08-832-877-110  
;  
Query Match                    0.7%; Score 16.2; DB 1; Length 21;  
Best Local Similarity       85.7%; Pred. No. 41;  
Matches    18; Conservative    0; Mismatches    3; Indels    0; Gaps    0;  
;  
QY                    2161 TTAACCTACTCTCCACACTC 2181  
DB                    1 TTAACCTACTCTCCACACTC 21  
;  
RESULT 21  
US-09-306-998-6/C  
; Sequence 6, Application US/09306998  
; Patent No. 6291173  
; GENERAL INFORMATION:  
; APPLICANT: Bartel, Paul L.  
; APPLICANT: Tavtigian, Sean V.  
; TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein  
; FILE REFERENCE: MMSC2  
; CURRENT APPLICATION NUMBER: US/09/306,998  
; CURRENT FILING DATE: 1999-05-07  
; EARLIER APPLICATION NUMBER: US 60/084,740  
; EARLIER FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-306-998-6  
;  
Query Match                    0.7%; Score 16; DB 1; Length 20;  
Best Local Similarity       100.0%; Pred. No. 40;  
Matches    16; Conservative    0; Mismatches    0; Indels    0; Gaps    0;  
;  
QY                    1317 TACAAGAGGAGGAG 1332  
DB                    16 TACAAGAGGAGGAG 1  
;  
RESULT 22  
US-08-860-882A-52  
; Sequence 52, Application US/0860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGELTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKEIV, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/23853  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-52

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 GGACGAGCTGACAGGCTGTG 621  
DB 1 GGACCTGCTGCAGAGCTGTG 19

RESULT 23  
US-09-009-483A-5/C  
Sequence 5, Application US/09009483A  
Patent No. 6083699  
GENERAL INFORMATION:  
APPLICANT: Leushner, James  
APPLICANT: Hui, May  
APPLICANT: Dunn, James M.  
APPLICANT: Larson, Marina T.  
APPLICANT: Lacroix, Jean-Michel  
APPLICANT: Shipman, Robert  
TITLE OF INVENTION: METHOD FOR BI-DIRECTIONAL SEQUENCING OF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Opdeadl & Larson  
STREET: 1992 Commerce Street Suite 309  
CITY: Yorktown  
STATE: NY  
COUNTRY: US  
ZIP: 10598  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,483A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330

TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: yes  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE:  
OTHER INFORMATION: primer for sequencing of exon 3 of HLA-A  
OTHER INFORMATION: gene  
US-09-009-483A-5

Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CCCGAGCCCCGACCCGCC 489  
DB 19 CCCGAGCCCCGCCCCGCC 1

RESULT 24  
US-09-009-483A-9/C  
Sequence 9, Application US/09009483A  
Patent No. 6083699  
GENERAL INFORMATION:  
APPLICANT: Leushner, James  
APPLICANT: Hui, May  
APPLICANT: Dunn, James M.  
APPLICANT: Larson, Marina T.  
APPLICANT: Lacroix, Jean-Michel  
APPLICANT: Shipman, Robert  
TITLE OF INVENTION: METHOD FOR BI-DIRECTIONAL SEQUENCING OF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Opdeadl & Larson  
STREET: 1992 Commerce Street Suite 309  
CITY: Yorktown  
STATE: NY  
COUNTRY: US  
ZIP: 10598  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,483A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: double

```

; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: primer for sequencing of exon 3 of HLA-B
; US-09-009-483A-9
;
Query Match      0.7%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY      471 CCCGAGCCCCGACGCGCC 489
Db      19 CCCGAGCCCCGCGCCGCC 1

RESULT 25
US-09-171-945-110
; Sequence 110, Application US/091712945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-110

Query Match      0.7%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY      603 GGACGAGCTGCAGGCTCG 621
Db      1 GGACCTGCTGCAGAGTCTG 19

RESULT 26
US-09-011-769A-34
; Sequence 34, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; APPLICANT: BLAKEY, David C.
; APPLICANT: DAVIES, David H.
; APPLICANT: HENNAM, John F.
; APPLICANT: HENBOUJIN, Laurent F.A.
; APPLICANT: MARSHAM, Peter R.
; APPLICANT: DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Suro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1995
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-011-769A-34
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```

Query Match      0.7%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

CY      603 GGACGAGCTGCAGGCTCG 621
Db      1 GGACCTGCTGCAGAGTCTG 19
```

```

RESULT 27
US-09-422-978-6665/c
; Sequence 6665, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020C21
; CURRENT APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6665
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-16401 for SEQ 2731.
; US-09-422-978-6665
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Query Match 0.7%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2095 CAGAGAACTTAACCAAG 2113

DB 19 CAGAGAACTTAACCAAG 1

RESULT 28  
US-08-564-002-14/c  
Sequence 14, Application US/08564002

Patent No. 5714329  
GENERAL INFORMATION:  
APPLICANT: Diacopoli, Niccolias  
APPLICANT: Tucker, Margaret  
APPLICANT: Goldstein, Ailsa  
TITLE OF INVENTION: Methods for the Diagnosis of a Genetic  
TITLE OF INVENTION: Predisposition to Cancer Associated with Variant CDK4  
TITLE OF INVENTION: Allele  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBERTSON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,002

FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J.

REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: A-62562

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989

TELEFAX: (415) 396-3249  
INFORMATION FOR SEQ. ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Primer"  
US-08-564-002-14

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2341 CAGCATCTCATGGGGAG 2359

DB 19 CAGCATCTCTGAGGGAG 1

RESULT 29

US-08-983-466-26/c

Sequence 26, Application US/08983466  
Patent No. 6207372

GENERAL INFORMATION:  
APPLICANT: SHUBER, ANTHONY P.

TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX  
TITLE OF INVENTION: DNA AMPLIFICATION  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 Sheridan Ave., Ste. 440  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,466

FILING DATE: 10-FEB-1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/474,450

FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/06/41012

FILING DATE: 06-JUNE-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara

REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: GECO.001.01US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477

INFORMATION FOR SEQ. ID NO: 26:  
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide primer"

US-08-983-466-26

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 205 CCGCGCCGCTGCGCTCGCG 223

DB 19 CTGGCGCGCTGCGCTCGCG 1

RESULT 30  
US-08-983-466-27/c  
Sequence 27, Application US/08983466  
Patent No. 6207372

GENERAL INFORMATION:  
APPLICANT: SHUBER, ANTHONY P.

TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX  
TITLE OF INVENTION: DNA AMPLIFICATION  
NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP

STREET: 260 Sheridan Ave., Ste. 440  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,466

FILING DATE: 10-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

US-08-983-466-26/c

Sequence 26, Application US/08983466  
Patent No. 6207372

GENERAL INFORMATION:  
APPLICANT: SHUBER, ANTHONY P.

TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX  
TITLE OF INVENTION: DNA AMPLIFICATION  
NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP

STREET: 260 Sheridan Ave., Ste. 440  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,466

APPLICATION NUMBER: 08/474,450  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA: WO96/41012  
APPLICATION NUMBER: WO96/41012  
FILING DATE: 06-JUNE-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: GEO.001.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide primer"  
US-08-983-466-27

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 205 CCGGCCGCTGGCGCTGCG 223  
DB 19 CTCGACCGCTGGCTGCG 1

RESULT 31  
US-08-983-466-28/c  
Sequence 28, Application US/08983466  
Patent No. 6207372  
GENERAL INFORMATION:  
APPLICANT: SHUBER, ANTHONY P.  
TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RAE-VENTER LAW GROUP  
STREET: 260 Sheridan Ave., Ste. 440  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,466  
FILING DATE: 10-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/474,450  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO96/41012  
FILING DATE: 06-JUNE-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: GEO.001.01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide primer"  
US-08-983-466-28

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 205 CCGGCCGCTGGCGCTGCG 223  
DB 19 CTCGACCGCTGGCTGCG 1

RESULT 32  
US-09-198-452A-6335  
Sequence 6335, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Griffiths, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev  
FILE REFERENCE: 9710-003-599  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO: 6335  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-6335

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2297 TCTGAGCCACAGTGGAGT 2315  
DB 2 TCTGAGCCACAGTGGAGT 20

RESULT 33  
US-07-920-281C-17/c  
Sequence 17, Application US/07920281C  
Patent No. 5739026  
GENERAL INFORMATION:  
APPLICANT: Garoff, Henrik  
TITLE OF INVENTION: DNA Expression Systems Based on  
TITLE OF INVENTION: Alphaviruses  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/920,281C  
FILING DATE: 13-AUG-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 828-103P

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..21  
OTHER INFORMATION: /label= primer  
OTHER INFORMATION: /note= "SP2 downstream sequencing primer"  
US-07-920-281C-17

Query Match 0.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 48;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 356 CGGCGCGCGGTGGCGCGC 374  
DB 21 CGGCGCGCGGTGGCGCGC 3

RESULT 34  
US-08-466-277-17/C  
Sequence 17, Application US/08466277  
Patent No. 6190666  
GENERAL INFORMATION:  
APPLICANT: Garoff, Henrik  
Liljestrom, Peter  
TITLE OF INVENTION: DNA Expression Systems Based on  
Alphaviruses  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,277  
FILING DATE: 06-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/920,281  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 828-103P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO  
ANTI-SENSE: YES  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..21  
OTHER INFORMATION: /label= primer  
OTHER INFORMATION: /note= "SP2 downstream sequencing primer"  
US-08-466-277-17

Query Match 0.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 48;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 356 CGGCGCGCGGTGGCGCGC 374  
DB 21 CGGCGCGCGGTGGCGCGC 3

RESULT 35  
US-09-778-510-14  
Sequence 14, Application US/09778510  
Patent No. 6512095  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
TITLE OF INVENTION: Molecules Designated B7L1  
FILE REFERENCE: 2844-US  
CURRENT APPLICATION NUMBER: US/09/778,510  
CURRENT FILING DATE: 2001-02-07  
PRIOR APPLICATION NUMBER: PCT/US99/17906  
PRIOR FILING DATE: 1999-08-05  
PRIOR APPLICATION NUMBER: 60/095,663  
PRIOR FILING DATE: 1998-08-07  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 14  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer from Homo sapien  
US-09-778-510-14

Query Match 0.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 48;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 492 CCGCTCTTGGCTCGAGC 510  
DB 1 CCGCTCTTGGCTCGCTGC 19

RESULT 36  
US-08-951-648-17  
Sequence 17, Application US/08951648  
Patent No. 5932465  
GENERAL INFORMATION:  
APPLICANT: Loughney, Kate  
TITLE OF INVENTION: Phosphodiesterase 8  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker, Sears Tower Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-951-648-17

Query Match
Best Local Similarity 0.6%; Score 15.4; DB 1; Length 18;
Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAAGTAGCAA 17

RESULT 37
US-09-174-437-17
; Sequence 17, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
; US-09-174-437-17

Query Match
Best Local Similarity 0.6%; Score 15.4; DB 1; Length 18;
Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAAGTAGCAA 17

RESULT 38
US-09-427-834A-31/C
; Sequence 31, Application US/09427834A
; Patent No. 6480791
; GENERAL INFORMATION:
; APPLICANT: Strathmann, Michael P.
; TITLE OF INVENTION: PARALLEL METHODS FOR GENOMIC ANALYSIS
; FILE REFERENCE: 20946-701
; CURRENT APPLICATION NUMBER: US/09/427,834A
; CURRENT FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: US 60/105,914
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 31
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-427-834A-31

Query Match
Best Local Similarity 0.6%; Score 15.4; DB 1; Length 18;
Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1112 TGACCTTCTCGATGGA 1128
DB 18 TGACCTTCTCGATGGA 2

RESULT 39
US-09-686-055A-17
; Sequence 17, Application US/09686055A
; Patent No. 656087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
; US-09-686-055A-17

Query Match
Best Local Similarity 0.6%; Score 15.4; DB 1; Length 18;
Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2399 TGCTGGCCCAATAGCAA 2415
DB 1 TGCTGGCCCAAGTAGCAA 17

RESULT 40
US-08-244-309-5/C
; Sequence 5, Application US/08244309
; Patent No. 5523391
; GENERAL INFORMATION:
; APPLICANT: KOMORASAKI, Toshi
; APPLICANT: TOYODA, Hitoshi
; APPLICANT: YOSHIMOTO, Makoto
; APPLICANT: HANADA, Kazunori
; TITLE OF INVENTION: DNA FRAGMENT ENCODING TUMOR CELL GROWTH
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LORUSSO & LOUD
; STREET: 745 South 23rd Street, Suite 301
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/244,309  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: ASA-B074  
TELEPHONE: (703)892-8882  
TELEFAX: (703)892-8884  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-244-309-5

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2243 CCGTCATATCAGAACT 2259  
DB 18 CCGTCATATCAGAACT 2

RESULT 41  
US-08-244-309-8  
Sequence 8, Application US/08244309  
Patent No. 5523391  
GENERAL INFORMATION:  
APPLICANT: KOMURASAKI, Toshii  
APPLICANT: TOYODA, Hitoshi  
APPLICANT: YOSHIWOTO, Nakoto  
APPLICANT: HANADA, Kazunori  
TITLE OF INVENTION: DNA FRAGMENT ENCODING TUMOR CELL GROWTH  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: IORUSSO & LOUD  
STREET: 745 South 23rd Street, Suite 301  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,309  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: ASA-B074  
TELEPHONE: (703)892-8882  
TELEFAX: (703)892-8884  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-244-309-8

Query Match 0.6%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2243 CCGTCATATCAGAACT 2259  
DB 3 CCGTCATATCAGAACT 19

RESULT 42  
US-08-850-993-17/c  
Sequence 17, Application US/08850993  
Patent No. 5952877  
GENERAL INFORMATION:  
APPLICANT: Hansen, Torben  
APPLICANT: Andersen, Carsten  
APPLICANT: Pedersen, Oluf B.  
TITLE OF INVENTION: Mutant cDNA Encoding The p53alpha  
TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase  
FILE REFERENCE: 4802.200-US  
CURRENT APPLICATION NUMBER: US/08/850,993  
CURRENT FILING DATE: 1997-05-05  
EARLIER APPLICATION NUMBER: 0539/96  
EARLIER FILING DATE: 1996-05-06  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 20  
TYPE: DNA  
ORGANISM: human  
US-08-850-993-17

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1940 AAGAAGACCTGAAGAAG 1956  
DB 18 AAGAAGACCTGAAGAAG 2

RESULT 43  
US-09-166-448-19/c  
Sequence 19, Application US/09166448  
Patent No. 6291830  
GENERAL INFORMATION:  
APPLICANT: Chau, Pascal  
APPLICANT: Vantomme, Valrie  
APPLICANT: Strobant, Vincent  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Thielemans, Kris  
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
FILE REFERENCE: 10461/7052  
CURRENT APPLICATION NUMBER: US/09/166,448  
CURRENT FILING DATE: 1998-10-05  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 19  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-166-448-19

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGCGCCGCAATGG 463  
DB 20 GCCGGGCGCCGCAATGG 4

RESULT 44

US-09-563-826-11/c  
Sequence 11, Application US/09563826  
Patent No. 6348450  
GENERAL INFORMATION:  
APPLICANT: Tang, et al.  
TITLE OF INVENTION: NONINVASIVE GENETIC IMMUNIZATION, EXPRESSION PRODUCTS THEREFROM, A  
FILE REFERENCE: 858610-2003.1  
CURRENT APPLICATION NUMBER: US/09/563,826  
CURRENT FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 09/533,149  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: 09/402,527  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/132,216  
PRIOR FILING DATE: 1999-05-03  
PRIOR APPLICATION NUMBER: PCT/US98/16739  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: 60/075,113  
PRIOR FILING DATE: 1998-02-11  
PRIOR APPLICATION NUMBER: 60/055,520  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: primer  
LOCATION: (1)..(20)  
OTHER INFORMATION: primer  
US-09-563-826-11

Query Match

Best Local Similarity 0.6%; Score 15.4; DB 1; Length 20;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1809 GGGTAAATGATACCCCA 1825

DB 18 GGGTAAATGATACCCCA 2

RESULT 45

US-09-697-884-19/c  
Sequence 19, Application US/09697884  
Patent No. 6426217  
GENERAL INFORMATION:  
APPLICANT: Chaux, Pascal  
APPLICANT: Vanomme, Val,rie  
APPLICANT: Stroobant, Vincent  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Thielemans, Kris  
APPLICANT: Cortals, Jurgen  
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
FILE REFERENCE: L0461/7052  
CURRENT APPLICATION NUMBER: US/09/697,884  
CURRENT FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: 09/166,448  
PRIOR FILING DATE: 1998-10-05  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 19  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-697-884-19

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

447 GCCGCGCGCCGCGCATGG 463

DB 20 GCCGCGCGCGCCGCGCATGG 4

RESULT 46

US-08-532-050-2  
Sequence 2, Application US/08532050  
Patent No. 581636  
GENERAL INFORMATION:  
APPLICANT: HANNA, WAYNE  
APPLICANT: Ozias-Akins, Peggy  
APPLICANT: Dujardin, Michel  
TITLE OF INVENTION: APOPIXIS FOR PRODUCING TRUE-BREEDING  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: USDA-ARS-OTT  
STREET: ROOM 409, BLDG. 005, BARC-W  
CITY: BELTSVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20705  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,050  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: POULOS, GAIL E.  
REGISTRATION NUMBER: 36,327  
REFERENCE/DOCKET NUMBER: 0173,93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-504-6558  
TELEFAX: 301-504-5060  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-532-050-2

Query Match

Best Local Similarity 0.6%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

667 CTCGAGAGATGGGCTCCTC 686

DB 1 CTCGAGAGATGGGCTCCTC 20

RESULT 47

US-08-889-296A-20/c  
Sequence 20, Application US/0889296A  
Patent No. 5872242  
GENERAL INFORMATION:  
APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.  
TITLE OF INVENTION: Antisense Oligonucleotide  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESS: Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill

STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/889,296A  
FILING DATE: herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/411,734  
FILING DATE: April 3, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09346  
FILING DATE: October 1, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 958,134  
FILING DATE: October 5, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/007,996  
FILING DATE: January 21, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0213  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-889-296A-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GGCGGTGCGCGCGAGGAGCAG 419  
Db 20 GGCGCGCGCGCGCGAGGAGCAG 1

RESULT 48  
US-08-848-840A-20/c  
Sequence 20, Application US/08848840A  
Patent No. 5965722  
GENERAL INFORMATION:  
APPLICANT: Morita, et al.  
TITLE OF INVENTION: ANTISENSE INHIBITION OF ras GENE WITH  
TITLE OF INVENTION: CHIMERIC AND ALTERNATING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5965722xis LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,840A  
FILING DATE: 30-APR-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/317,289  
FILING DATE: 03-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/794,493  
FILING DATE: 04-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/335,046  
FILING DATE: 07-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/468,256  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,666  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/468,037  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/411,734  
FILING DATE: 03-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,180  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Luccl  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-2458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-848-840A-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GGCGGTGCGCGCGAGGAGCAG 419  
Db 20 GGCGCGCGCGCGCGAGGAGCAG 1

RESULT 49  
US-08-904-901-151/c  
Sequence 151, Application US/08904901  
Patent No. 5998383  
GENERAL INFORMATION:  
APPLICANT: Wright, Jim A.  
TITLE OF INVENTION: ANTITUMOR ANTISENSE SEQUENCES DIRECTED  
TITLE OF INVENTION: AGAINST RIBONUCLEOTIDE REDUCTASE  
NUMBER OF SEQUENCES: 163  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KOHN & ASSOCIATES  
STREET: 30500 No. 5998383thwestern Hwy. Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/904,901

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 0227.00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 151:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
ANTI-SENSE: YES  
US-08-904-901-151

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAGAGAGGTTGAAGACT 1687  
DB 20 GGAGAGAGGTTGAAGACT 1

RESULT 50  
US-08-445-515-20

Sequence 20, Application US/08445515  
Patent No. 6043088  
GENERAL INFORMATION:  
APPLICANT: Bookstein, Robert  
TITLE OF INVENTION: A No. 6043088el Prostate/Colon Tumor Suppressor  
TITLE OF INVENTION: Gene Located on Human Chromosome 8  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,515  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-CU 1607  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-445-515-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 36;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1665 CATGAGAGAGGTTGAAG 1684  
DB 1 CACTGAGAGAGGTTGAAG 20

RESULT 51  
US-08-961-469A-28/C  
Sequence 28, Application US/08961469A  
Patent No. 6083923  
GENERAL INFORMATION:  
APPLICANT: Greg Hardee, Richard Geary, Arthur Levin,  
APPLICANT: Mike Templyn, Randy Howard, Rahul Mehra  
TITLE OF INVENTION: LIPOSOMAL OLIGONUCLEOTIDE COMPOSITIONS  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: PENTIUM  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,469A  
FILING DATE: October 31, 1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0219  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-779-2400  
TELEFAX: 609-810-1454  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-961-469A-28

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GGCGTGGCGCGGAGGAG 419  
DB 20 GGCGGCGCGCGGAGGAG 1

RESULT 52  
US-09-344-914-33/C  
Sequence 33, Application US/09344914  
Patent No. 6110664  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-S1 EXPRESSION  
FILE REFERENCE: RTS-0068  
CURRENT APPLICATION NUMBER: US/09/344,914  
CURRENT FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 33  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-344-914-33

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 CCATGACATCTTCAGCTCA 859  
DB 20 CCCTGACATCATTCAGCGCA 1

RESULT 53  
US-09-128-494-20/c  
Sequence 20, Application US/09128494  
Patent No. 6117848  
GENERAL INFORMATION:  
APPLICANT: Monia, B.P., Cowsett, L.M. and Manoharan, M.  
TITLE OF INVENTION: Antisense Oligonucleotide  
TITLE OF INVENTION: Inhibition of ras  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09128,494  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/889,296  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/411,734  
FILING DATE: April 3, 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09346  
FILING DATE: October 1, 1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 958,134  
FILING DATE: October 5, 1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/007,996  
FILING DATE: January 21, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0213  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-09-128-494-20

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTCGCGCGGAGCGAG 419  
DB 20 GCGCGCGCGCGCGGAGCGAG 1

RESULT 54  
US-09-249-730-151/c  
Sequence 151, Application US/09249730  
Patent No. 6121000  
GENERAL INFORMATION:  
APPLICANT: WRIGHT, Jim A.  
APPLICANT: YOUNG, Alping H.  
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and  
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase  
FILE REFERENCE: 032386-040  
CURRENT APPLICATION NUMBER: US/09/249,730  
CURRENT FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 220  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 151  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Human  
US-09-249-730-151

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAAGAAGAGGTTGAAGACT 1687  
DB 20 GGAAGAAGAGGTTGAAGACT 1

RESULT 55  
US-09-280-805-123  
Sequence 123, Application US/09280805  
Patent No. 6184212  
GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
TITLE OF INVENTION: Grahm, Brett P. Monia  
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2  
NUMBER OF SEQUENCES: 271  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PC  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,805  
FILING DATE: herewith  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/048,810  
FILING DATE: March 26, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane Massey  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0346  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-810-1515  
TELEFAX: 609-810-1454  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-09-280-805-123

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1005 GCTTTCCTCAATGAAGAG 1024  
DB 1 GCTTTCATCAAGAGAGG 20

RESULT 56  
US-09-313-932-421  
Sequence 421, Application US/09313932A  
Patent No. 6228642  
GENERAL INFORMATION:  
APPLICANT: Baker, Brenda  
APPLICANT: Bennett, C. Frank  
APPLICANT: Butler, Madeline M.  
APPLICANT: Shanahan, William R.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-  
FILE REFERENCE: ISPH-0356  
CURRENT APPLICATION NUMBER: US/09/313,932A  
NUMBER OF SEQ ID NOS: 501  
SEQ ID NO 421  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-313-932-421

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1783 CGGTATGTGAGAGAGAGA 1802  
DB 1 CAGTATGTGAGAGAGAGA 20

RESULT 57  
US-09-021-701-231

Sequence 231, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-231

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 775 TCCTTACTCTCAAGCTGTT 794  
DB 1 TCCCACCTCAACAGATGTT 20

RESULT 58  
US-09-021-701-232  
Sequence 232, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 232:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-232

Query Match  
Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 776 CCCCTACTCAAAAGCTGTTG 795  
DB 1 CCCCACTCAGACAGATGTTG 20

RESULT 59  
US-09-467-642-15  
Sequence 15, Application US/09467642  
Patent No. 6300132  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRES  
FILE REFERENCE: RTS-0106  
CURRENT APPLICATION NUMBER: US/09/467,642  
CURRENT FILING DATE: 1999-12-20  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 15  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-467-642-15

Query Match  
Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 199 CGCCCGCCCGCCCGCTGACC 218  
DB 1 CGCCCGCCCTGCAGCTGCCCC 20

RESULT 60  
US-09-248-386-20/c  
Sequence 20, Application US/09248386  
Patent No. 6359124  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P  
APPLICANT: Freier, Susan M  
APPLICANT: Sanghvi, Yogesh S  
APPLICANT: Cook, Phillip D  
APPLICANT: Ecker, David J  
TITLE OF INVENTION: Antisense Inhibition of RAS Gene with Chimeric and  
FILE REFERENCE: ISIS3350  
CURRENT APPLICATION NUMBER: US/09/248,386  
CURRENT FILING DATE: 1999-01-12  
EARLIER APPLICATION NUMBER: 08/848,840  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 07/411,734  
EARLIER FILING DATE: 1989-09-25  
EARLIER APPLICATION NUMBER: PCT/US93/09346  
EARLIER FILING DATE: 1993-10-01  
EARLIER APPLICATION NUMBER: 07/715,196  
EARLIER FILING DATE: 1991-06-14  
EARLIER APPLICATION NUMBER: 07/958,134  
EARLIER FILING DATE: 1992-10-05  
EARLIER APPLICATION NUMBER: 08/007,996  
EARLIER FILING DATE: 1993-01-21  
EARLIER APPLICATION NUMBER: 07/703,619  
EARLIER FILING DATE: 1991-05-21  
EARLIER APPLICATION NUMBER: 08/040,903  
EARLIER FILING DATE: 1993-03-31

EARLIER APPLICATION NUMBER: 07/040,526  
EARLIER FILING DATE: 1987-04-20  
EARLIER APPLICATION NUMBER: 08/174,379  
EARLIER FILING DATE: 1993-12-28  
EARLIER APPLICATION NUMBER: 08/040,933  
EARLIER FILING DATE: 1993-03-31  
EARLIER APPLICATION NUMBER: 08/300,072  
EARLIER FILING DATE: 1994-09-02  
EARLIER APPLICATION NUMBER: 08/039,979  
EARLIER FILING DATE: 1993-03-30  
EARLIER APPLICATION NUMBER: 08/395,168  
EARLIER FILING DATE: 1995-02-27  
EARLIER APPLICATION NUMBER: 07/814,961  
EARLIER FILING DATE: 1991-12-24  
EARLIER APPLICATION NUMBER: 08/244,993  
EARLIER FILING DATE: 1994-06-21  
EARLIER APPLICATION NUMBER: 08/468,037  
EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6359124el Sequence  
US-09-248-386-20

Query Match  
Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GCGCGTCCGCGCGAGCAG 419  
DB 20 GCGCGCGCGCGCGAGCAG 1

RESULT 61  
US-09-517-467B-38/c  
Sequence 38, Application US/09517467B  
Patent No. 6451602  
GENERAL INFORMATION:  
APPLICANT: Ian Popoff  
APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION  
FILE REFERENCE: RTS-0150  
CURRENT APPLICATION NUMBER: US/09/517,467B  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/517,467  
PRIOR FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 345  
SEQ ID NO 38  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-517-467B-38

Query Match  
Best Local Similarity 85.0%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2297 TCTGAGCCACAGTGGATGA 2316  
DB 20 TCTGAGCTTGGTGGATGA 1

RESULT 62  
US-09-706-197-21  
Sequence 21, Application US/09706197  
Patent No. 6475797  
GENERAL INFORMATION:

APPLICANT: C. Frank Bennett  
APPLICANT: David Spector  
TITLE OF INVENTION: Jaqueleine Wyatt  
FILE REFERENCE: RTS-0145  
CURRENT APPLICATION NUMBER: US/09/706,197  
CURRENT FILING DATE: 2000-11-03  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 21  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-706-197-21

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1730 TCATGTGTGTTCACTGC 1749  
DB 1 TCCTTGTGTGTTTACAGC 20

RESULT 63  
US-09-422-978-6860  
Sequence 6860, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marra  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Bisallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET.020C01  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 6860  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..20  
OTHER INFORMATION: upstream amplification primer 99-19860 for SEQ 2926,  
US-09-422-978-6860

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2385 TTACACAGAAATGCTGCTGG 2404  
DB 1 TGACACAGAAATGAGACTGG 20

RESULT 64  
US-09-249-247-151/C  
Sequence 151, Application US/09249247  
Patent No. 6593305  
GENERAL INFORMATION:  
APPLICANT: Wright, Jim A.  
APPLICANT: Young, Aiding H.  
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and  
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase  
FILE REFERENCE: 032396-023

CURRENT APPLICATION NUMBER: US/09/249,247  
CURRENT FILING DATE: 1999-02-11  
EARLIER APPLICATION NUMBER: US 60/023,040  
EARLIER FILING DATE: 1996-08-02  
EARLIER APPLICATION NUMBER: US 60/039,959  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: US 08/904,901  
EARLIER FILING DATE: 1997-08-01  
NUMBER OF SEQ ID NOS: 220  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 151  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Human  
US-09-249-247-151

Query Match 0.6%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAGAGAGGTTGAGACT 1687  
DB 20 GGAGACAGGTTTGAAGACT 1

RESULT 65  
US-08-770-235A-24/C  
Sequence 24, Application US/0870235A  
Patent No. 5839538  
GENERAL INFORMATION:  
APPLICANT: Leavitt, Markley C.  
APPLICANT: Tritz, Richard  
APPLICANT: Feng, Yu  
APPLICANT: Barber, Jack  
APPLICANT: Yu, Mang  
TITLE OF INVENTION: Methods and Compositions for Inhibiting  
TITLE OF INVENTION: HIV Infection of Cells By Cleaving HIV Co-Receptor RNA  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,235A  
FILING DATE: 19-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,875  
FILING DATE: 25-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: QUINE, Jonathan A.  
REGISTRATION NUMBER: P-41,261  
REFERENCE/DOCKET NUMBER: 016556-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-770-235A-24

Query Match 0.6%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 GCGGAGGAGGAGCC 2048  
DB 15 GCGGAGGAGGAGCC 1

RESULT 66

US-09-422-978-8522  
Sequence 8522; Application US/09422978  
Patent No. 6537751

GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marla  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET.0200P1  
CURRENT APPLICATION NUMBER: US/09/422,978  
EARLIER FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 8522

LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..18  
OTHER INFORMATION: downstream amplification primer 99-16140 for SEQ 657, in compleme  
US-09-422-978-8522

Query Match 0.6%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 CCCAGATGAGACAA 878  
DB 3 CCCAGATGAGACAA 17

RESULT 67

US-08-577-081A-20/C  
Sequence 20; Application US/08577081A  
Patent No. 6030775

GENERAL INFORMATION:  
APPLICANT: Yang, Soo Young  
APPLICANT: Cereb, Nezh  
TITLE OF INVENTION: Methods and Reagents for Typing HLA  
TITLE OF INVENTION: Class I Genes  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson  
STREET: 1992 Commerce Street Suite 309  
CITY: Yorktown  
STATE: NY  
COUNTRY: US  
ZIP: 10598

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/577,081A  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: MSK-P-001-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330  
TELEX:

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHEICAL: no

ANTI-SENSE: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE:  
OTHER INFORMATION: sequencing primer for exon 3 of HLA-A, -B  
US-08-577-081A-20

Query Match 0.6%; Score 15; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 55;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 471 CCCGAGCCCGGAGCCG 487  
DB 17 CCCGAGCCCGGAGCCG 1

RESULT 68

US-09-280-805-11/C  
Sequence 11; Application US/09280805  
Patent No. 6184212

GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Neto, Mark J.  
APPLICANT: Graham, Brett P. Monica  
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2  
NUMBER OF SEQUENCES: 271  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 08053

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PC  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,805  
FILING DATE: herewith  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/048,810  
FILING DATE: March 26, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane Massey  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0346  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-810-1515  
TELEFAX: 609-810-1454

; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; ANTI-SENSE: Yes  
 ; US-09-280-805-11

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGTACTACTGATGG 1721  
 DB 19 TGTACTACTGATGG 5

RESULT 69  
 US-09-048-810-11/c  
 ; Sequence 11, Application US/09048810  
 ; Patent No. 6238921  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Law Offices of Jane Massey Licata  
 ; STREET: 66 East Main Street  
 ; CITY: Milton  
 ; STATE: NJ  
 ; COUNTRY: U.S.A.  
 ; ZIP: 08053  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 ; COMPUTER: IBM 486  
 ; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
 ; SOFTWARE: WORDPERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/048,810  
 ; FILING DATE: herewith  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Licata, Jane Massey  
 ; REGISTRATION NUMBER: 32,257  
 ; REFERENCE/DOCKET NUMBER: ISPH-0302  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 609-779-2400  
 ; TELEFAX: 609-810-1454  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; ANTI-SENSE: Yes  
 ; US-09-048-810-11

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGTACTACTGATGG 1721  
 DB 19 TGTACTACTGATGG 5

RESULT 70  
 US-09-300-008B-6/c  
 ; Sequence 6, Application US/09300008B  
 ; Patent No. 6458534

; GENERAL INFORMATION:  
 ; APPLICANT: Concannon et al.  
 ; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE  
 ; FILE REFERENCE: 9924-0003-228  
 ; CURRENT APPLICATION NUMBER: US/09/300,008B  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/083,269  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 ; US-09-300-008B-6

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 GTATGTGAGAGAG 1799  
 DB 15 GTATGTGAGAGAG 1

RESULT 71  
 US-09-342-325C-45/c  
 ; Sequence 45, Application US/09342325C  
 ; Patent No. 650637  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mikoshiba, Katsuhiko  
 ; APPLICANT: Aruga, Jun  
 ; APPLICANT: Nagai, Takeharu  
 ; APPLICANT: Katsunori, Nakata  
 ; TITLE OF INVENTION: Neurogenesis Inducing Gene  
 ; FILE REFERENCE: HIRAKI-03814  
 ; CURRENT APPLICATION NUMBER: US/09/342,325C  
 ; PRIOR FILING DATE: 1999-06-30  
 ; PRIOR APPLICATION NUMBER: JP98/86979  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: JP98/121456  
 ; PRIOR FILING DATE: 1998-04-30  
 ; PRIOR APPLICATION NUMBER: 09/172,045  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 45  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; US-09-342-325C-45

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1106 GCTTGTGAGACCTTC 1120  
 DB 17 GCTTGTGAGACCTTC 3

RESULT 72  
 US-09-780-045-22  
 ; Sequence 22, Application US/09780045  
 ; Patent No. 6602713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B  
 TITLE OF INVENTION: EXPRESSION  
 FILE REFERENCE: RTS-0130  
 CURRENT APPLICATION NUMBER: US/09/780,045  
 CURRENT FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 135  
 SEQ ID NO 22  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-780-045-22

Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 CCGGCCCGCGCGCGC 297  
 DB 2 CCGGCCCGCGCGCGC 16

RESULT 73  
 US-08-849-021-78  
 Sequence 78, Application US/08849021  
 Patent No. 5955276  
 GENERAL INFORMATION:  
 APPLICANT: MORGANTE, MICHELE  
 APPLICANT: VOGEL, JULIE M.  
 TITLE OF INVENTION: COMPOUND MICROSATELLITE  
 TITLE OF INVENTION: PRIMERS FOR THE  
 TITLE OF INVENTION: DETECTION OF GENETIC  
 TITLE OF INVENTION: POLYMORPHISMS  
 NUMBER OF SEQUENCES: 89  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
 ADDRESSEE: COMPANY  
 STREET: 1007 MARKET STREET  
 CITY: WILMINGTON  
 STATE: DELAWARE  
 COUNTRY: U.S.A.  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/849,021  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/346,456  
 FILING DATE: 28 NOVEMBER 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FLOYD, LINDA AARNEY  
 REGISTRATION NUMBER: 33,692  
 REFERENCE/DOCKET NUMBER: BB-1064-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-892-8112  
 TELEFAX: 302-992-7949  
 INFORMATION FOR SEQ ID NO: 78:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-849-021-78

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 54;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1785 GTATGTGAGAGAGAGA 1802  
 DB 1 GTGTGTGTGAGAGAGAGA 18

RESULT 74  
 US-09-205-143-12  
 Sequence 12, Application US/09205143  
 Patent No. 6107091  
 GENERAL INFORMATION:  
 APPLICANT: Lex M. Cowser  
 TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-16 EXPRESSION  
 FILE REFERENCE: RTS-0032  
 CURRENT APPLICATION NUMBER: US/09/205,143  
 CURRENT FILING DATE: 1998-12-03  
 NUMBER OF SEQ ID NOS: 87  
 SEQ ID NO 12  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-205-143-12

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 54;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2149 GACTTCATGCGCTTAAC 2166  
 DB 1 GACTTCCTTCTGTAAC 18

RESULT 75  
 US-09-422-936-37/C  
 Sequence 37, Application US/09422936  
 Patent No. 6465213  
 GENERAL INFORMATION:  
 APPLICANT: Ekstrand, Jonas  
 TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES  
 FILE REFERENCE: 06275-165002  
 CURRENT APPLICATION NUMBER: US/09/422,936  
 CURRENT FILING DATE: 1999-10-22  
 PRIOR APPLICATION NUMBER: US 03/242,608  
 PRIOR FILING DATE: 1999-02-19  
 PRIOR APPLICATION NUMBER: PCT/SE98/01947  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: SWEDEN 9703914-2  
 PRIOR FILING DATE: 1997-10-27  
 PRIOR APPLICATION NUMBER: SWEDEN 9800864-2  
 PRIOR FILING DATE: 1998-03-16  
 PRIOR APPLICATION NUMBER: SWEDEN 9802575-2  
 PRIOR FILING DATE: 1998-07-17  
 NUMBER OF SEQ ID NOS: 85  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 37  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-422-936-37

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 54;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGATGAACCG 2321  
 DB 18 CACATTGGAGAACCG 1

RESULT 76

```
US-09-422-936-40/c
; Sequence 40, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-422-936-40
```

```
Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2304 CACAGTGGAGTGAACCCAG 2321
DB 18 CACATTGGAGGAGAACCCAG 1
```

```
RESULT 77
US-09-422-936-66/c
; Sequence 66, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-422-936-66
```

```
Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2304 CACAGTGGAGTGAACCCAG 2321
DB 18 CACATTGGAGGAGAACCCAG 1
```

```
RESULT 78
US-09-422-936-68/c
; Sequence 68, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-422-936-68
```

```
Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2304 CACAGTGGAGTGAACCCAG 2321
DB 18 CACATTGGAGGAGAACCCAG 1
```

```
RESULT 79
US-09-796-491-2
; Sequence 2, Application US/09796491
; Patent No. 6518416
; GENERAL INFORMATION:
; APPLICANT: Danenberg, K. et al.
; TITLE OF INVENTION: METHOD OF DETERMINING A CHEMOTHERAPEUTIC
; FILE REFERENCE: 11220/999-ERCC1-504F
; CURRENT APPLICATION NUMBER: US/09/796,491
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-796-491-2
```

```
Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 410 GCGGAGGCGAGGAGAGAG 427
DB 1 GCGGAGGCGTGAAGAGACG 18
```

```
RESULT 80
US-09-422-978-6054
; Sequence 6054, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
```



FILE REFERENCE: 11220/145  
CURRENT APPLICATION NUMBER: US/09/988,784  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 09/877,095  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 09/796,491  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide Primer  
US-09-988-784-2

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 54;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 GCGAGGCGAGGAGAG 427  
Db 1 GCGAGGCGTGGAGACAG 18

RESULT 85  
US-08-486-421-26  
Sequence 26, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-421-26

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 50;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 415 GCGAGGAGAGAGGGA 430  
Db 1 GCGAGGAGGAGAGGGA 16

RESULT 86  
US-08-470-911-26  
Sequence 26, Application US/08470911  
Patent No. 5756684  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,911  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-470-911-26

Query Match 0.6%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 50;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GCGAGGAGAGAGGGA 430  
Db 1 GCGAGGAGGAGAGGGA 16  
RESULT 87  
US-08-486-809-26  
Sequence 26, Application US/08486809  
Patent No. 5869622  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-486-803-26

Query Match          0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 50;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      415 GGCAGAGGAGAGGGA 430
Db      1 GGCAGAGGAGAGGGA 16

RESULT 88
US-08-152-313-20
; Sequence 20, Application US/08152313
; Patent No. 5561041
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-152-313-20

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      275 TCCGACACCCGCCG 290
Db      2 TCCACACACCCGCCG 17

RESULT 89
US-08-579-223-20
; Sequence 20, Application US/08579223
; Patent No. 5726019
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,223
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-579-223-20

Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      275 TCCGACACCCGCCG 290
Db      2 TCCACACACCCGCCG 17

```

Mon Sep 20 10:12:25 2004

v1v1emore580-1.rn1

Page 31

RESULT 90

```
US-08-584-040-4263/c
; Sequence 4263, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4263

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 TCTTCATCAGCTTTA 1404
DB 17 TCTTCATCAGCTTTA 2
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-U (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2030
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2030
```

```
Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 TCTTCATCAGCTTTA 1404
DB 17 TCTTCATCAGCTTTA 2
```

RESULT 92

```
US-09-371-772B-5403/c
; Sequence 5403, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-U (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5403
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5403
```

```
Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 163 CGTTGTTGGATTGA 178
DB 17 CTTTGTGTTGATTGA 2
```

RESULT 93

```
PCT-US94-12947A-20
; Sequence 20, Application PC/TUS9412947A
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
```

CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12947A  
FILING DATE: 10-NOV-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Ph.D., Lisa A.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: FD-2912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..17  
PCT-US94-12947A-20

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 275 TCCGCACACCCGCCCG 280  
DB 2 TCCACACACCCGCCCG 17

RESULT 94  
US-08-857-946-23/C  
Sequence 23, Application US/08857946  
Patent No. 5994075  
GENERAL INFORMATION:  
APPLICANT: Goodfellow, P.N.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A  
TITLE OF INVENTION: GENE OF INTEREST  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Inc.  
STREET: 75 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1807  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/857,946  
FILING DATE: 16-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/60/017,824  
FILING DATE: 17-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kathleen M. Williams  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3529/05573

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-857-946-23

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 GATTCCTCGGCCCAT 730  
DB 17 GATTCCTCGGCCCAT 2

RESULT 95  
US-08-970-740-23/C  
Sequence 23, Application US/08970740  
Patent No. 6015670  
GENERAL INFORMATION:  
APPLICANT: Goodfellow, P.N.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A  
TITLE OF INVENTION: GENE OF INTEREST  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Inc.  
STREET: 28 State Street, 28th Floor  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,740  
FILING DATE: 14-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/857,946  
FILING DATE: 16-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017,824  
FILING DATE: 17-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kathleen M. Williams  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3529/59829  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-227-7111  
TELEFAX: 617-227-4399  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-970-740-23

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 GATTCCTCGGCCCAT 730  
DB 17 GATTCCTCGGCCCAT 2

Db 17 GGTTCTCTGGCCAT 2

## RESULT 96

US-08-638-931-2

Sequence 2, Application US/08638931

Patent No. 6194145

GENERAL INFORMATION:

APPLICANT: HEIDRICH, Bjrn

APPLICANT: ROBINSON, Peter-Nicholas

APPLICANT: TIECKE, Frank

APPLICANT: ROLFS, Arndt

TITLE OF INVENTION: Genus and species-specific identification of

TITLE OF INVENTION: Legionella

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nikaido, Marmelstein, Murray &amp; Oram LLP

STREET: 655 Fifteenth Street N.W. Suite 330

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/638,931

FILING DATE: 25-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 15 891.1

FILING DATE: 29-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.

REGISTRATION NUMBER: 22,580

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-5000

TELEFAX: (202)638-4810

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

US-08-638-931-2

Query Match 0.6%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 63;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 CAGATCTCTTGACCA 842

Db 3 CTGATTGCTTGACCA 18

## RESULT 97

US-09-475-947A-340

Sequence 340, Application US/09475947A

Patent No. 6472154

GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

APPLICANT: Wren, Jonathan D.

APPLICANT: Mirna, John D.

TITLE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UTS00667

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 340

US-09-475-947A-340

LENGTH: 18

TYPE: DNA

ORGANISM: human

US-09-475-947A-340

Query Match 0.6%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 63;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2048 CAGCAGCAGCCCAAGC 2063

Db 2 CAGCAGCAGCCCAAGC 17

## RESULT 98

US-09-530-095B-22

Sequence 22, Application US/09530095B

Patent No. 6610515

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, AKIRA

APPLICANT: TUCHITA, KOTARO

APPLICANT: IWATA, AKIRA

APPLICANT: UEDA, SUSUMU

TITLE OF INVENTION: FELINE GRANULOCYTE COLONY STIMULATING FACTOR

FILE REFERENCE: JG-HK-4962

CURRENT APPLICATION NUMBER: US/09/530,095B

PRIOR APPLICATION NUMBER: 2000-04-24

PRIOR FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 22

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HYPOTHETICAL SEQUENCE

US-09-530-095B-22

Query Match 0.6%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 63;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 607 CAGCTGACAGGCTCTGG 622

Db 1 CAGCTGACAGGCTCTGG 16

## RESULT 99

US-09-517-467B-9/c

Sequence 9, Application US/09517467B

Patent No. 6451502

GENERAL INFORMATION:

APPLICANT: Ian Popoff

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION

FILE REFERENCE: RTS-0150

CURRENT APPLICATION NUMBER: US/09/517,467B

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/517,467

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 345

SEQ ID NO 9

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: PCR Primer

US-09-517-467B-9

Query Match 0.6%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 70;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 244 TGCCTGTGGCTGTGG 259  
 DB 16 TGCCTGTGGCTGTGG 1

RESULT 100  
 US-08-287-075-10/c  
 ; Sequence 10, Application US/08287075  
 ; Patent No. 5656462  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keller, Cylla  
 ; APPLICANT: Mitsubishi, Masato  
 ; APPLICANT: Akitaya, Tatsuo  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE IMMOBILIZED SUPPORT  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON, AND BEAR  
 ; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
 ; CITY: NEWPORT BEACH  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/287,075  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/827,975  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Altman, Daniel E  
 ; REGISTRATION NUMBER: 34,115  
 ; REFERENCE/DOCKET NUMBER: HITACHI.002A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 714-760-0404  
 ; TELEFAX: 714-760-9502  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: TAC-AS OLIGONUCLEOTIDE PRIMER  
 ; US-08-287-075-10

Query Match 0.6%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 ATCTGCTGGCTGCC 934  
 DB 15 ATCTGCTGGCTGCC 2

RESULT 101  
 US-08-584-040-2513/c  
 ; Sequence 2513, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Escobedo, Jaime

;; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ;; TREATMENT OF DISEASES OR  
 ;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 ;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
 ;; TITLE OF INVENTION: GROWTH FACTOR  
 ;; NUMBER OF SEQUENCES: 8502  
 ;; CORRESPONDENCE ADDRESS:  
 ;; ADDRESSEE: Lyon & Lyon  
 ;; STREET: 633 West Fifth Street  
 ;; CITY: Los Angeles  
 ;; STATE: California  
 ;; COUNTRY: U.S.A.  
 ;; ZIP: 90071-2066  
 ;; COMPUTER READABLE FORM:  
 ;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ;; COMPUTER: storage  
 ;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ;; SOFTWARE: Word Perfect 5.1  
 ;; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/08/584,040  
 ;; FILING DATE: January 11, 1996  
 ;; CLASSIFICATION: 514  
 ;; PRIORITY APPLICATION DATA:  
 ;; APPLICATION NUMBER: 60/005,974  
 ;; FILING DATE: October 26, 1995  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: Wardburg, Richard J.  
 ;; REGISTRATION NUMBER: 32,327  
 ;; REFERENCE/DOCKET NUMBER: 218/064  
 ;; TELECOMMUNICATION INFORMATION:  
 ;; TELEPHONE: (213) 489-1600  
 ;; TELEFAX: (213) 955-0440  
 ;; TELEX: 67-3510  
 ;; INFORMATION FOR SEQ ID NO: 2513:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 17 base pairs  
 ;; TYPE: nucleic acid  
 ;; STRANDEDNESS: single  
 ;; TOPOLOGY: linear  
 ; US-08-584-040-2513

Query Match 0.6%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTGGATTGA 178  
 DB 17 TTGTGTGGATTGA 4

RESULT 102  
 US-09-371-772B-1037/c  
 ; Sequence 1037, Application US/09371772B  
 ; Patent No. 6566127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Pavco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 ; FILE REFERENCE: MH800,876-J (237/198)  
 ; CURRENT APPLICATION NUMBER: US/09/371,772B  
 ; PRIOR FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: US 60/005,974  
 ; PRIOR FILING DATE: 1995-10-26  
 ; PRIOR APPLICATION NUMBER: US 08/584,040  
 ; PRIOR FILING DATE: 1996-01-08  
 ; NUMBER OF SEQ ID NOS: 14225  
 ; SOFTWARE: Patentin version 3.0

SEQ ID NO 1037  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-1037

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTGA 178  
DB 17 TTGTGTTGATTGA 4

RESULT 103  
US-09-371-772B-5402/c  
Sequence 5402, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00.876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5402  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-5402

Query Match 0.6%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTGTGTTGATTGA 178  
DB 16 TTGTGTTGATTGA 3

RESULT 104  
US-09-358-381-14/c  
Sequence 14, Application US/09358381  
Patent No. 6020199  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION  
FILE REFERENCE: RTS-0079  
CURRENT APPLICATION NUMBER: US/09/358,381  
CURRENT FILING DATE: 1999-07-21  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 14  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-358-381-14

Query Match 0.6%; Score 14; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 573 GTGGCCTGTACCA 586  
DB 15 GTGGCCTGTACCA 2

RESULT 105  
US-09-577-902-14/c  
Sequence 14, Application US/09577902  
Patent No. 6284538  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Lex M. Cowsett  
APPLICANT: Robert McKay  
TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION  
FILE REFERENCE: ISFH-0463  
CURRENT APPLICATION NUMBER: US/09/577,902  
CURRENT FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/358,381  
PRIOR FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: PCT/US99/29594,  
PRIOR FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 51  
SEQ ID NO 14  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-577-902-14

Query Match 0.6%; Score 14; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 GTGGCCTGTACCA 586  
DB 15 GTGGCCTGTACCA 2

RESULT 106  
US-08-390-850-527  
Sequence 527, Application US/08390850  
Patent No. 3612215  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Gustofson, John  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
OF ARTHRITIC CONDITIONS  
NUMBER OF SEQUENCES: 1151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,850  
FILING DATE: February 17, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/354,920

FILING DATE: December 13, 1994  
APPLICATION NUMBER: 08/152,487  
FILING DATE: No. 561221, December 12, 1993  
APPLICATION NUMBER: 07/989,848  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 527:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-390-850-527

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 72;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1062 ACCCCAGTACCTGTGA 1078  
DB 1 ACCCCAGUCAGUGUGA 17

RESULT 107  
US-08-373-124A-196/c  
Sequence 196, Application US/08373124A  
Patent No. 5646042  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
TITLE OF INVENTION: CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 196:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-373-124A-196

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 72;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1318 ACAAGAGGAGGAAG 1334  
DB 17 AGAAGAGGAGGAGG 1

RESULT 108  
US-08-435-634-527  
Sequence 527, Application US/08435634  
Patent No. 5731295  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Gustafson, John  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
OF ARTHRITIC CONDITIONS  
NUMBER OF SEQUENCES: 1151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,634  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,850  
FILING DATE: February 17, 1995  
APPLICATION NUMBER: 08/354,920  
FILING DATE: December 13, 1994  
APPLICATION NUMBER: 08/152,487  
FILING DATE: No. 5731295, September 12, 1993  
APPLICATION NUMBER: 07/989,848  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 527:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-634-527

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 72;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1062 ACCCCAGTCCCTGTGA 1078  
DB 1 ACCCCAGTCCCTGTGA 17

## RESULT 109

US-08-758-306-145/c  
Sequence 145, Application US/08758306  
Patent No. 5807743

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES

TITLE OF INVENTION: ASSOCIATED WITH

TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR

TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION

NUMBER OF SEQUENCES: 1379

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Fastseq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,306

FILING DATE: December 3, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 212/132

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 145:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-758-306-145

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 72;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 643 CTGGAGCTGAAGAACAA 659  
DB 17 CTGGAGCTGAAGAACAA 1

RESULT 110

US-08-435-628-196/c  
Sequence 196, Application US/08435628  
Patent No. 5817796

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTOROSIS AND

TITLE OF INVENTION: CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,628

FILING DATE: 05-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/373,124

FILING DATE: January 13, 1995

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 196:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-435-628-196

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 72;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1318 ACAAGAGAGAGAGAG 1334  
DB 17 AGAAGAGAGAGAGAG 1

## RESULT 111

US-08-584-040-4071/c  
Sequence 4071, Application US/08584040  
Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: McSwigen, James

APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 4071:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-4071  
Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 72;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1472 GAGACTTCTCCAGGGT 1488  
DB 17 GAGTCTTCTACAGGGT 1  
RESULT 112  
US-08-679-645-749  
Sequence 749, Application US/08679645  
Patent No. 6350934  
GENERAL INFORMATION:  
APPLICANT: Zwick, Michael G.  
APPLICANT: Edington, Brent E.  
APPLICANT: McSwigen, James A.  
APPLICANT: Merlo, Patricia Ann Owens  
APPLICANT: Guo, Lining  
APPLICANT: Skokut, Thomas A.  
APPLICANT: Young, Scott A.  
APPLICANT: Folkerts, Otto  
APPLICANT: Merlo, Donald J.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
MODIFICATION OF GENE EXPRESSION  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,645  
FILING DATE: July 12, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 749:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-679-645-749  
Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 72;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 858 CATGACCCGAGTGA 874  
DB 1 CAUGCCUCGAGGAGA 17  
RESULT 113  
US-09-371-772B-1838/c  
Sequence 1838, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ridozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MEH800,878-0 (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
PRIOR FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: 99-005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1838  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-1838

```

OY      2040  GGACGAGCCAGCAGC 2056
      |||||
Db      1  GGCCGAGCCAGCAGC 17

RESULT 115
US-09-371-772B-6442
; Sequence 6442, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Mcswiigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: WMBH00, 8/6-C (1237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6442

```

```

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      416 GCAGAGGAGAGGAGGC 432
      |||||
Db      1 GCAGAGAGAGGAGGAGC 17

RESULT 117
US-09-866-108A-1915
; Sequence 1915, Application US/09866108A
; Patent No. 6686168
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: UT, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.

```

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/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ PCT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1915
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1915

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1356 AGAGTCACTATCCAG 1372
DB      1 AGGTCAACGAACTCCAG 17

RESULT 118
US-09-866-108A-9544
/ Sequence 9544, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ PCT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 9848
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-9848
```

```

/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 9848
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-9848

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      132 CTCCTGCCCGGCTTCTC 148
DB      1 CTCCTCCCTGCTTCTC 17

RESULT 119
US-09-866-108A-9848
/ Sequence 9848, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ PCT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 9848
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-9848
```

Query Match 0.6%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 72;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1528 AATACATCTCTCCAGA 1544  
DB 1 AATGCATCTCTTCAGA 17

## RESULT 120

US-09-178-002-7/c  
Sequence 7, Application US/09178002  
Patent No. H001973  
GENERAL INFORMATION:  
APPLICANT: Hu, Shou-Ih  
TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
FILE REFERENCE: CGC 2048  
CURRENT APPLICATION NUMBER: US/09/178,002  
CURRENT FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-09-178-002-7

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 TGCACATGGAAGAG 1677  
DB 18 TGCACATGGAAGAG 2

## RESULT 121

US-08-436-714-2  
Sequence 2, Application US/08436714  
Patent No. 5602244  
GENERAL INFORMATION:  
APPLICANT: Marvin H. Caruthers et al  
TITLE OF INVENTION: Nucleoside and Polynucleotide  
TITLE OF INVENTION: Thiolphosphoramidite and Phosphorodithioate Compounds and Proce  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,714  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: CU 311 BICGIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-436-714-2

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2033 GCGGCGAGGACGACCA 2049  
DB 1 GCGGCGAGGACGACCA 17

## RESULT 122

US-08-319-492B-715/c  
Sequence 715, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: Two  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Waidburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 715:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-319-492B-715

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2112 AGGAGACAGCTGTGTGA 2128  
| | | | | | | | | |  
Db 17 AGCGACAGCTGTGTCA 1

RESULT 123  
US-08-363-585-79  
; Sequence 79, Application US/08363585  
; Patent No. 5683872

GENERAL INFORMATION:  
APPLICANT: Rudert, William A.  
APPLICANT: Trucco, Massimo  
TITLE OF INVENTION: Polymers of Oligonucleotide Probes  
TITLE OF INVENTION: As The Bound Ligands For Use In Reverse  
TITLE OF INVENTION: Dot Blots  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: University of Pittsburgh  
STREET: Office of Intellectual Property  
STREET: 911 William Pitt Union  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15260

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5-1/4" low density diskette  
COMPUTER: IBM PC or compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,585  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/786,228  
FILING DATE: 31-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frederick H. Coleen; Mary-Elizabeth Buckles  
REGISTRATION NUMBER: 28,061; 31,907  
REFERENCE/DOCKET NUMBER: 92-232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 412/288-4164  
TELEFAX: 412/288-3063  
TELEX: 277871

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
PUBLICATION INFORMATION:  
AUTHORS: Kimura, A.  
AUTHORS: Saezaki, T.  
TITLE: Eleventh International Histocompatibility  
TITLE: Workshop Reference Protocol for the HLA-DNA-Typing  
TITLE: Technique  
JOURNAL: HLA 1991  
VOLUME: 1  
PAGES: 397-419  
DATE: 1992  
RELEVANT RESIDUES IN SEQ ID NO: 79: 1 to 18  
US-08-363-585-79

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2089 TTCTCGAGAGAACTT 2105  
| | | | | | | | | |  
Db 2 TTCTCGAGAGAACTT 18

RESULT 124  
US-08-363-585-80  
; Sequence 80, Application US/08363585  
; Patent No. 5683872

GENERAL INFORMATION:  
APPLICANT: Rudert, William A.  
APPLICANT: Trucco, Massimo  
TITLE OF INVENTION: Polymers of Oligonucleotide Probes  
TITLE OF INVENTION: As The Bound Ligands For Use In Reverse  
TITLE OF INVENTION: Dot Blots  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: University of Pittsburgh  
STREET: Office of Intellectual Property  
STREET: 911 William Pitt Union  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15260

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5-1/4" low density diskette  
COMPUTER: IBM PC or compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,585  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/786,228  
FILING DATE: 31-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frederick H. Coleen; Mary-Elizabeth Buckles  
REGISTRATION NUMBER: 28,061; 31,907  
REFERENCE/DOCKET NUMBER: 92-232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 412/288-4164  
TELEFAX: 412/288-3063  
TELEX: 277871

INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
PUBLICATION INFORMATION:  
AUTHORS: Kimura, A.  
AUTHORS: Saezaki, T.  
TITLE: Eleventh International Histocompatibility  
TITLE: Workshop Reference Protocol for the HLA-DNA-Typing  
TITLE: Technique  
JOURNAL: HLA 1991  
VOLUME: 1  
PAGES: 397-419  
DATE: 1992  
RELEVANT RESIDUES IN SEQ ID NO: 80: 1 to 18  
US-08-363-585-80

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2089 TTCTCGAGAGAACTT 2105  
| | | | | | | | | |  
Db 1 TTCTCGAGAGAACTT 17

RESULT 125  
US-08-363-585-83/C  
; Sequence 83, Application US/08363585  
; Patent No. 5683872

GENERAL INFORMATION:  
APPLICANT: Rudert, William A.  
TITLE OF INVENTION: Polymers of Oligonucleotide Probes  
TITLE OF INVENTION: As the Bound Ligands For Use in Reverse  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESS: University of Pittsburgh  
STREET: Office of Intellectual Property  
STREET: 911 William Pitt Union  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15260  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5-1/4" low density diskette  
COMPUTER: IBM PC or compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,585  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/786,228  
FILING DATE: 31-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frederick H. Cohen, Mary-Elizabeth Buckles  
REGISTRATION NUMBER: 28,061; 31,907  
REFERENCE/DOCKET NUMBER: 92-232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 412/288-4164  
TELEFAX: 412/288-3063  
TELEX: 277871  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
PUBLICATION INFORMATION:  
AUTHORS: Sasazuki, T.  
TITLE: Eleven International Histocompatibility  
TITLE: Workshop Reference Protocol for the HLA-DNA-Typing  
JOURNAL: HLA 1991  
VOLUME: 1  
PAGES: 397-419  
DATE: 1992  
RELEVANT RESIDUES IN SEQ ID NO: 83: 1 to 18  
US-08-363-585-83  
Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2089 TTCCTGCAGAGAACTT 2105  
DB 17 TTCCTGCAGAGAACTT 1  
RESULT 126  
US-08-442-705-2  
Sequence 2, Application US/08442705  
Patent No. 568418  
GENERAL INFORMATION:  
APPLICANT: Marvin H. Caruthers et al  
TITLE OF INVENTION: Nucleoside and Polynucleotide  
TITLE OF INVENTION: Thiophosphoramide and Phosphorodithioate Compounds and Proce  
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,705  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: CU 311 BIGCIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-442-705-2  
Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2033 GCGGCGAGGACGACCA 2049  
DB 1 GCGGCGAGGACGACCA 17  
RESULT 127  
US-08-361-479-45/C  
Sequence 45, Application US/08361479  
Patent No. 3693752  
GENERAL INFORMATION:  
APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,  
APPLICANT: GOTTFRIED; MÜSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; VAIVAL  
APPLICANT: GEORG; STEINDL, FRANZ  
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH  
TITLE OF INVENTION: NEUTRALIZE GENITALLY DIVERGENT HIV-1 ISOLATES.  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,479  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/932,787  
FILING DATE: 29-AUG-1992  
APPLICATION NUMBER: A 987/92  
FILING DATE: 14-MAY-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: CHARLES A. MUSERLIAN  
 REGISTRATION NUMBER: 19,683  
 REFERENCE/DOCKET NUMBER: 366.015  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-661-8000  
 TELEFAX: 212-661-8002  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: POLYNUCLEOTIDE  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: FILAMENTOUS PHAGE FUSES  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 ORGANELLE:  
 FEATURE:  
 NAME/KEY: P3 FUSION PROTEIN GENE  
 LOCATION: RESIDUE 10 TO 27  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION: POLYNUCLEOTIDE FROM RANDOM LIBRARY OF  
 OTHER INFORMATION: GENE CODING THE P3 FUSION PROTEIN  
 US-08-361-479-45

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
 Best Local Similarity 88.2%; Pred. No. 81;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 842 ATGACATCTTCAGCTC 858  
 DB 18 ATGACATTTATCAGCTC 2

RESULT 128  
 US-08-332-829-2  
 Sequence 2, Application US/08332829  
 Patent No. 5750666  
 GENERAL INFORMATION:  
 APPLICANT: Marvin H. Caruthers et al  
 TITLE OF INVENTION: Nucleoside and Polynucleotide  
 TITLE OF INVENTION: Thiophosphoramide and Phosphorodithioate Compounds and Proce  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Yahwak & Associates  
 STREET: 25 Skytop Drive  
 City: Trumbull  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06611  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Microsoft Word 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/332,829  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: George M. Yahwak  
 REGISTRATION NUMBER: 26,824  
 REFERENCE/DOCKET NUMBER: CU 311 BIGCIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-332-829-2

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
 Best Local Similarity 88.2%; Pred. No. 81;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2033 GCGCGAGCAGCAGCA 2049  
 DB 1 GGTGGCAGGTCCAGCCA 17

RESULT 129  
 US-08-473-576-45/c  
 Sequence 45, Application US/08473576  
 Patent No. 5756674  
 GENERAL INFORMATION:  
 APPLICANT: KATZINGER, HERMAN, RUEKER, FLORIAN, HIMMELER  
 APPLICANT: GOTTFRIED, WOSTER, THOMAS, TROILA, ALEXANDRA, PURTSCHER, MARTIN, MAIWAL  
 APPLICANT: GEORG, STEINLE, FRANZ  
 TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH  
 TITLE OF INVENTION: NEUTRALIZE GENITICALLY DIVERGENT HIV-1 ISOLATES.  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BIERMAN & MUSERLIAN  
 STREET: 600 THIRD AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10016

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/473,576  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/361,479  
 FILING DATE: 22-DEC-1994  
 APPLICATION NUMBER: 07/932,787  
 FILING DATE: 29-AUG-1992  
 APPLICATION NUMBER: A 987/92  
 FILING DATE: 14-MAY-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CHARLES A. MUSERLIAN  
 REGISTRATION NUMBER: 19,683  
 REFERENCE/DOCKET NUMBER: 366.015  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-661-8000  
 TELEFAX: 212-661-8002  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: POLYNUCLEOTIDE  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: FILAMENTOUS PHAGE FUSES  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:

HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
FEATURE:  
NAME/KEY: P3 FUSION PROTEIN GENE  
LOCATION: RESIDUE 10 TO 27  
IDENTIFICATION METHOD:  
OTHER INFORMATION: POLYNUCLEOTIDE FROM RANDOM LIBRARY OF  
OTHER INFORMATION: GENE CODING THE P3 FUSION PROTEIN  
US-08-473-576-45

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 842 ATGACATCTTCAGCTC 858  
DB 18 ATGACATTATCAGCTC 2

RESULT 130  
US-08-843-718-45/C  
Sequence 45; Application US/08843718  
Patent No. 586694  
GENERAL INFORMATION:  
APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,  
APPLICANT: GOTTFRIED, MUSTER, THOMAS; TRKOLA, ALEXANDRA; PUTSCHER, MARTIN; MAIWAL  
APPLICANT: GEORG; STEINDL, FRANZ  
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH  
TITLE OF INVENTION: NEUTRALIZE GENITALLY DIVERGENT HIV-1 ISOLATES.  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/843,718  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/932,787  
FILING DATE: 29-AUG-1992  
APPLICATION NUMBER: A 987/92  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 366.015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-661-8002  
TELEFAX: 212-661-8000  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: POLYNUCLEOTIDE  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: FILAMENTOUS PHAGE FUSES  
STRAIN:  
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
FEATURE:  
NAME/KEY: P3 FUSION PROTEIN GENE  
LOCATION: RESIDUE 10 TO 27  
IDENTIFICATION METHOD:  
OTHER INFORMATION: POLYNUCLEOTIDE FROM RANDOM LIBRARY OF  
OTHER INFORMATION: GENE CODING THE P3 FUSION PROTEIN  
US-08-843-718-45

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 842 ATGACATCTTCAGCTC 858  
DB 18 ATGACATTATCAGCTC 2

RESULT 131  
US-08-849-021-77/C  
Sequence 77; Application US/08849021  
Patent No. 595276  
GENERAL INFORMATION:  
APPLICANT: VOGEL, JULIE M.  
APPLICANT: MORGANTE, MICHELE  
TITLE OF INVENTION: COMPOUND MICROSTATELITE  
TITLE OF INVENTION: PRIMERS FOR THE  
TITLE OF INVENTION: DETECTION OF GENETIC  
NUMBER OF SEQUENCES: POLYMORPHISMS  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
ADDRESSEE: COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,021  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,456  
FILING DATE: 28 NOVEMBER 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLOYD, LINDA AXAMETHY  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1064-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-7949  
TELEFAX: 302-992-7949  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-849-021-77

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1785 GTATGTGAGAGAGAG 1801

Db 17 GTGTGTGTGAGAGAG 1

RESULT 132

US-09-205-921-33

Sequence 33, Application US/09205921A

Patent No. 6008048

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: ex M. Cowert

TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION

FILE REFERENCE: RTS-0028

CURRENT APPLICATION NUMBER: US/09/205,921A

CURRENT FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 33

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-205-921-33

Query Match

Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2357 GAGAGGAGAGGAGG 2373

Db 1 GAGAGGAGAGGAGG 17

RESULT 133

US-09-043-085-12

Sequence 12, Application US/09043085

Patent No. 6083685

GENERAL INFORMATION:

APPLICANT: Jura Petrik

TITLE OF INVENTION: SYSTEMATIC EXTRACTION, AMPLIFICATION AND

TITLE OF INVENTION: DETECTION OF RETROVIRAL SEQUENCES, AND OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SALIMANCHIK, LLOYD & SALIMANCHIK

STREET: 2421 NW 41st STREET, SUITE A-1

CITY: GAINESVILLE

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide"

US-09-043-085-12

Query Match

Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1912 TACCGGCCATGCACCA 1928

Db 2 TCCCGGCCATGCACCA 18

RESULT 134

US-09-043-085-36/c

Sequence 36, Application US/09043085

Patent No. 6083685

GENERAL INFORMATION:

APPLICANT: Jura Petrik

TITLE OF INVENTION: SYSTEMATIC EXTRACTION, AMPLIFICATION AND

TITLE OF INVENTION: DETECTION OF RETROVIRAL SEQUENCES, AND OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SALIMANCHIK, LLOYD & SALIMANCHIK

STREET: 2421 NW 41st STREET, SUITE A-1

CITY: GAINESVILLE

STATE: FLORIDA

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/043,085

FILING DATE: 6-MAR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/02196

FILING DATE: 6-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: PACE, DORAN R.

REGISTRATION NUMBER: 38,261

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide"

US-09-043-085-36

Query Match

Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1912 TACCGGCCATGCACCA 1928

Db 2 TCCCGGCCATGCACCA 18

RESULT 134

US-09-043-085-36/c

Sequence 36, Application US/09043085

Patent No. 6083685

GENERAL INFORMATION:

APPLICANT: Jura Petrik

TITLE OF INVENTION: SYSTEMATIC EXTRACTION, AMPLIFICATION AND

TITLE OF INVENTION: DETECTION OF RETROVIRAL SEQUENCES, AND OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SALIMANCHIK, LLOYD & SALIMANCHIK

STREET: 2421 NW 41st STREET, SUITE A-1

CITY: GAINESVILLE

STATE: FLORIDA

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/043,085

FILING DATE: 6-MAR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/02196

FILING DATE: 6-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: PACE, DORAN R.

REGISTRATION NUMBER: 38,261

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide"

US-09-043-085-36

Query Match

Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1912 TACCGGCCATGCACCA 1928

Db 2 TCCCGGCCATGCACCA 18

RESULT 134

US-09-043-085-36/c

Sequence 36, Application US/09043085

Patent No. 6083685

GENERAL INFORMATION:

APPLICANT: Jura Petrik

TITLE OF INVENTION: SYSTEMATIC EXTRACTION, AMPLIFICATION AND

TITLE OF INVENTION: DETECTION OF RETROVIRAL SEQUENCES, AND OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SALIMANCHIK, LLOYD & SALIMANCHIK

STREET: 2421 NW 41st STREET, SUITE A-1

CITY: GAINESVILLE

STATE: FLORIDA

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/043,085

FILING DATE: 6-MAR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/02196

FILING DATE: 6-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: PACE, DORAN R.

REGISTRATION NUMBER: 38,261

RESULT 135  
US-09-487-444-34  
; Sequence 34, Application US/09487444  
; Patent No. 6159697  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Morla  
; APPLICANT: Lex M. Cowert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION  
; FILE REFERENCE: RTS-0133  
; CURRENT APPLICATION NUMBER: US/09/487,444  
; EARLIER FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 34  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-487-444-34

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 GCTTGTTTCTGCTAC 65  
DB 2 GCTTGATTTCTGCTTC 18

RESULT 136  
US-09-358-972-217/c  
; Sequence 217, Application US/09358972  
; Patent No. 6235480  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Leippe, Donna  
; APPLICANT: Mandrekay, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Olson, Ryan J.  
; APPLICANT: Gu, Trent  
; APPLICANT: Wood, Keith W.  
; APPLICANT: Welch, Roy  
; TITLE OF INVENTION: Nucleic Acid Detection  
; FILE REFERENCE: Pro-103 6866/75528  
; CURRENT APPLICATION NUMBER: US/09/358,972  
; EARLIER FILING DATE: 1999-07-22  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 217  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; OTHER INFORMATION: CAH oligo 2 for mutation site 2  
US-09-358-972-217

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 259 GCTGGCGCTGGAGGT 275  
DB 18 GCTGGCGCTGGAGGT 2

RESULT 137  
US-09-406-064-24/c  
; Sequence 24, Application US/09406064  
; Patent No. 6270973  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Leippe, Donna  
; APPLICANT: Mandrekay, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Wood, Keith V.  
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION  
; FILE REFERENCE: PRO-107.0 (6868/75532)  
; CURRENT APPLICATION NUMBER: US/09/406,064  
; EARLIER FILING DATE: 1999-09-27  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-406-064-24

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 259 GCTGGCGCTGGAGGT 275  
DB 18 GCTGGCGCTGGAGGT 2

RESULT 138  
US-09-430-615-53/c  
; Sequence 53, Application US/09430615  
; Patent No. 6277578  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Leippe, Donna  
; APPLICANT: Mandrekay, Michelle  
; APPLICANT: Andrews, Christine Ann  
; APPLICANT: Hartnett, James Robert  
; APPLICANT: Welch, Roy  
; APPLICANT: Shultz, John William  
; TITLE OF INVENTION: Method for Amplified Nucleic Acid Detection  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/430,615  
; EARLIER FILING DATE: 1999-10-29  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1999-02-18  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 53  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-430-615-53

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 259 GCTGGCGCTGGAGGCT 275  
DB 18 GCTGGCGCTGGAGGCT 2

RESULT 139  
US-09-406-065-58/c  
Sequence 58, Application US/09406065  
Patent No. 6312902  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W  
APPLICANT: Lewis, Martin K.  
APPLICANT: Leipzig, Donna  
APPLICANT: Mandrekar, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B  
APPLICANT: Andrews, Christine A  
APPLICANT: Hartnett, James R  
APPLICANT: Gu, Trent  
APPLICANT: Olson, Ryan J  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: Improved Nucleic Acid Detection  
FILE REFERENCE: Improved Nucleic Acid Detection  
CURRENT APPLICATION NUMBER: US/09/406,065  
EARLIER FILING DATE: 1999-09-27/358,972  
EARLIER APPLICATION NUMBER: 09/358,972  
EARLIER FILING DATE: 1999-07-21  
EARLIER APPLICATION NUMBER: 09/252,436  
EARLIER FILING DATE: 1999-02-18  
EARLIER APPLICATION NUMBER: 09/042,287  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 58  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-406-065-58

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 259 GCTGGCGCTGGAGGCT 275  
DB 18 GCTGGCGCTGGAGGCT 2

RESULT 140  
US-08-584-040-8381  
Sequence 8381, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California

COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8381:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-8381

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 GCGCGCGCGCGCGCGC 213  
DB 1 GCGCGCGCGCGCGCGC 17

RESULT 141  
US-08-584-040-8382  
Sequence 8382, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8382:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-8382

```

```

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      202 CCGCCCGCCCGCTGAGCC 218
DB      2 CCGCCCGCCCGCTGAGCC 18

```

```

RESULT 142
US-09-205-995-16
Sequence 16, Application US/09205995
Patent No. 636855
GENERAL INFORMATION:
APPLICANT: Xu, Minzhen
APPLICANT: Qiu, Gang
APPLICANT: Humphreys, Robert
TITLE OF INVENTION: CANCER CELL VACCINE
FILE REFERENCE: U.S. Application 09/205,995, (CIP)
CURRENT APPLICATION NUMBER: US/09/205,995
CURRENT FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 09/036,746
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: 08/661,627
PRIOR FILING DATE: 1996-06-11
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: oligonucleotide corresponding to a specific region
OTHER INFORMATION: of the mouse It gene.
US-09-205-995-16

```

```

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      607 CAGCTGAGGCTGCG 623
DB      1 CAGCTGAGGCTGCG 17

```

```

RESULT 143
US-09-383-316-74/C
Sequence 74, Application US/09383316
Patent No. 639151
GENERAL INFORMATION:
APPLICANT: Shultz, John W
APPLICANT: Lewis, Martin K.
APPLICANT: Liepepe, Donna

```

```

APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: PRO-104 6868/75529
CURRENT APPLICATION NUMBER: US/09/383,316
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/252,436
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: CAH oligo 2 for mutation site 2
US-09-383-316-74

```

```

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      259 GGTGGCGGCTGAGGCT 275
DB      18 GGTGGCGGCTGAGGCT 2

```

```

RESULT 144
US-09-371-772B-4037
Sequence 4037, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHRB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4037
LENGTH: 18
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-4037

```

```

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      197 GGGCGCCCGCCCGCCGC 213
DB      1 GGGCGCCCGCCCGCCGC 17

```

RESULT 145  
US-09-371-772B-4038  
; Sequence 4038, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Rascohedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MH800, 876-C (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4038  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Mus sp.  
US-09-371-772B-4038

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 202 CCGCCGCGCGCGCGCC 218  
DB 2 CCGCCGCGCGCGCGCC 18

RESULT 146  
US-09-788-847-24/C  
; Sequence 24, Application US/09788847  
; Patent No. 6653078  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Leipe, Donna  
; APPLICANT: Mandrekar, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Wood, Keith V.  
; APPLICANT: Welch, Roy  
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION  
; FILE REFERENCE: PRO-107.0 (6868/75532)  
; CURRENT APPLICATION NUMBER: US/09/788, 847  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/406,064  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: 09/252,436  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: 09/042,287  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-788-847-24

Query Match 0.6%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 259 GCTGCGCGCTGAGGCT 275  
DB 18 GCTGCGCGCTGAGGCT 2

RESULT 147  
US-08-334-847-113  
; Sequence 113, Application US/08334847  
; Patent No. 5693532  
; GENERAL INFORMATION:  
; APPLICANT: McSwigen, James  
; APPLICANT: Draper, Kenneth  
; APPLICANT: Pavco, Pam  
; APPLICANT: Woolf, Tod  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING RESPIRATORY  
; TITLE OF INVENTION: SYNCTIAL VIRUS  
; NUMBER OF SEQUENCES: 909  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/334,847  
; FILING DATE: No. 5693532member 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-334-847-113

Query Match 0.6%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 40.0%; Pred. No. 67;  
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 170 TTGATTATATCTTA 184  
DB 1 TUGGATUGAUCUUA 15

RESULT 148  
US-08-363-240A-674/C  
; Sequence 674, Application US/08363240A  
; Patent No. 5705388  
; GENERAL INFORMATION:  
; APPLICANT: Couture, Larry  
; APPLICANT: McSwigen, James  
; APPLICANT: Bisgater, Charles

APPLICANT: Pape, Michael  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: PREVENTION, INHIBITION OF  
 TITLE OF INVENTION: PROGRESSION AND REGRESSION  
 TITLE OF INVENTION: OF VASCULAR DISEASES  
 NUMBER OF SEQUENCES: 1243  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/363,240A  
 FILING DATE: December 23, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 210/096  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ. ID NO: 674:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-363-240A-674  
 Query Match 0.6%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 67;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1174 CTTGTGACAGCTCCT 1188  
 DB 15 CTTGTGAAAGCTCCT 1  
 RESULT 149  
 US-08-363-240A-675/C  
 Sequence 675, Application US/08363240A  
 Patent No. 5705388  
 GENERAL INFORMATION:  
 APPLICANT: Couture, Larry  
 APPLICANT: McSwiggen, James  
 APPLICANT: Bisgaier, Charles  
 APPLICANT: Pape, Michael  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: PREVENTION, INHIBITION OF  
 TITLE OF INVENTION: PROGRESSION AND REGRESSION  
 TITLE OF INVENTION: OF VASCULAR DISEASES  
 NUMBER OF SEQUENCES: 1243  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/363,240A  
 FILING DATE: December 23, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 210/096  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ. ID NO: 675:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-363-240A-675  
 Query Match 0.6%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 67;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1173 CTTGTGACAGCTCCT 1187  
 DB 15 CTTGTGAAAGCTCCT 1  
 RESULT 150  
 US-09-081-646-305  
 Sequence 305, Application US/09081646  
 Patent No. 6333152  
 GENERAL INFORMATION:  
 APPLICANT: Kinzler, Kenneth  
 APPLICANT: Vogelstein, Bert  
 APPLICANT: Zhang, Lin  
 APPLICANT: Zhou, Wei  
 TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and  
 TITLE OF INVENTION: Cancer Cells  
 FILE REFERENCE: 01107.74664  
 CURRENT APPLICATION NUMBER: US/09/081,646  
 CURRENT FILING DATE: 1998-05-20  
 EARLIER APPLICATION NUMBER: 60/047,352  
 EARLIER FILING DATE: 1997-05-21  
 NUMBER OF SEQ. ID NOS: 871  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ. ID NO. 305  
 LENGTH: 15  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-081-646-305  
 Query Match 0.6%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 67;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2349 CATGAGGGAGAGGA 2363  
 DB 1 CATGCGGAGAGGA 15  
 RESULT 151  
 US-08-127-954-44  
 Sequence 44, Application US/08127954

```
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Elich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Peetry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-127-954-44

Query Match          0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 76;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1372 GAGAGCGCCCATGAG 1386
Db      1 GAGAGCGCCCATGAG 15

RESULT 152
; US-09-371-772B-7107/c
; Sequence 7107, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH800, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 06/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7107
; LENGTH: 16
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
; US-09-371-772B-7107

Query Match          0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 76;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1389 TCTTCATCAGTCTT 1403
Db      15 TCTTCATCAGTCTT 1

RESULT 153
; US-09-533-494A-10
; Sequence 10, Application US/09533494A
; Patent No. 6586581
; GENERAL INFORMATION:
; APPLICANT: Bancroft, F. Carter
; APPLICANT: Fliss, Maikiko
; APPLICANT: Taylor Clelland, Catherine L.
; TITLE OF INVENTION: PROLACTIN REGULATORY ELEMENT BINDING
; FILE REFERENCE: AP31818 070165.0497
; CURRENT APPLICATION NUMBER: US/09/533,494A
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Human
; US-09-533-494A-10

Query Match          0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 76;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      388 TCGGCGGCGGCGGCGC 402
Db      1 TCGACGGGCGCGGCGC 15

RESULT 154
; US-08-196-218-25/c
; Sequence 25, Application US/08196218
; Patent No. 5614619
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kamalz Mansouri
; APPLICANT: Disler, Jürgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,218
```

```

ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,916
FILING DATE: 29-JUL-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dadić, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 028750-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-687-916-12

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      873 GAACAAGCAAAATCA 887
|||||
Db      15 GAACAAGCAAAAGG 1

```

```

Sequence 172, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwigen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-172

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY 2148 GGACTTCATGCCTT 2162
DB 3 GGACCCCAUGCCU 17

RESULT 158
US-08-985-162-454/c
Sequence 454, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwigen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

```

```

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 454:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-454

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 789 GCTGTTGGATGAG 803
DB 17 GCTGTTGGATGAG 3

RESULT 159
US-09-138-614-12/c
Sequence 12, Application US/09138614
Patent No. 6245541
GENERAL INFORMATION:
APPLICANT: HOUTZ, Robert L.
TITLE OF INVENTION: ISOLATED SPINACH
TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATTHEW
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916

```

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dadio, Susan M.  
REGISTRATION NUMBER: 40,373  
REFERENCE/DOCKET NUMBER: 028750-138  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ. ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-138-614-12

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 873 GAACAAGAAATGA 887  
DB 15 GAACAAGAAAGA 1

RESULT 160  
US-08-584-040-2495/C  
Sequence 2495, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 2495:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-2495

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 966 TCTCTTACACAGAG 980  
DB 17 TCTCTTACACAGAG 3

RESULT 161  
US-09-371-772B-1019/C  
Sequence 1019, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: M8B00, 876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371, 772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ. ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ. ID NO 1019  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-1019

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 966 TCTCTTACACAGAG 980  
DB 17 TCTCTTACACAGAG 3

RESULT 162  
US-09-401-063-172  
Sequence 172, Application US/09401063  
Patent No. 6623962  
GENERAL INFORMATION:  
APPLICANT: Akhtar, Saghir  
APPLICANT: Felli, Patricia  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT  
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
TITLE OF INVENTION: FACTOR RECEPTORS  
NUMBER OF SEQUENCES: 1877  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB

MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/401,063  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/985,162  
FILING DATE: 04 December 1997  
APPLICATION NUMBER: 60/036,476  
FILING DATE: 31 January 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 230/107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-401-063-172

Query Match 0.6%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 66.7%; Pred. No. 85;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2148 GCACTTCATGCCTT 2162  
DB 3 GGACCCCAUGCCCU 17

RESULT 163  
US-09-401-063-454/c  
Sequence 454, Application US/09401063  
Patent No. 6623962  
GENERAL INFORMATION:  
APPLICANT: Akhtar, Saghir  
APPLICANT: Feil, Patricia  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT  
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
NUMBER OF SEQUENCES: 1877  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/401,063  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/985,162  
FILING DATE: 04 December 1997  
APPLICATION NUMBER: 60/036,476

FILING DATE: 31 January 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 230/107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 454:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-401-063-454

Query Match 0.6%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 789 GCTGTTGGATGTAG 803  
DB 17 GCTGTTGGATGGAG 3

RESULT 164  
US-09-866-108A-548  
Sequence 548, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Jiongqiang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIORITY APPLICATION NUMBER: US 60/207,456  
PRIORITY FILING DATE: 2000-05-26  
PRIORITY APPLICATION NUMBER: GB 24263.6  
PRIORITY FILING DATE: 2000-10-04  
PRIORITY APPLICATION NUMBER: US 60/236,359  
PRIORITY FILING DATE: 2000-09-27  
PRIORITY APPLICATION NUMBER: PCT/US01/00666  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00667  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00664  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00669  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00665  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00668  
PRIORITY FILING DATE: 2001-01-30  
PRIORITY APPLICATION NUMBER: PCT/US01/00663  
PRIORITY FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ. ID NOS: 1575  
SOFTWARE: Acemica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 548  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-548

Query Match 0.6%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1372 GAGAGGCCCATGAG 1386  
DB 3 GAGAGGCCCATGAG 17

## RESULT 165

US-09-866-108A-549

Sequence 549, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2580
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2580
```

```

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      65 CCGGAGCTGGGCAA 79
Db      17 CCGGAGCTGGGCAA 3
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```

RESULT 168
US-09-866-108A-2581/c
; Sequence 2581, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2581
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2581
```

```

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

Qy      65 CCGGAGCTGGGCAA 79
Db      16 CCGGAGCTGGGCAA 2
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RESULT 169
US-09-866-108A-2582/c
; Sequence 2582, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2582
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2582
```

```

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

Qy      65 CCGGAGCTGGGCAA 79
Db      15 CCGGAGCTGGGCAA 1
```

```

RESULT 170
US-09-866-108A-7697/c
; Sequence 7697, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
```

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7697
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7697

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 TGGACGAGCTGCAGG 616
Db 17 TGGGCCAGCTGCAGG 3

RESULT 171
US-09-866-108A-7698/C
; Sequence 7698, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7699
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7699

```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7698
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7698

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 TGGACGAGCTGCAGG 616
Db 16 TGGGCCAGCTGCAGG 2

RESULT 172
US-09-866-108A-7699/C
; Sequence 7699, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7699
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7699

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Query Match 0.6%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 85;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 TGGACGAGCTGCAGG 616  
DB 15 TGGCGCAGCTGCAGG 1

## RESULT 173

US-09-866-108A-8997/c  
Sequence 8997, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: UT, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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PRIOR FILING DATE: 2001-01-30

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PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 8999  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-8999

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 206 CCGCCCGCTGGCCTC 220  
DB 15 CCGCCCGCTGGCCTC 1

RESULT 176  
US-09-866-108A-9307  
Sequence 9307, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AECOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 9307  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-866-108A-9307  
Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2044 CAGCCAGCAGGCC 2058  
DB 3 CAGCCAGCAGGCC 17

RESULT 177  
US-09-866-108A-9308  
Sequence 9308, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AECOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 9308  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-9308  
Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 1; Length 17;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2044 CAGCCAGCAGGCC 2058  
DB 2 CAGCCAGCAGGCC 16

RESULT 178  
US-09-866-108A-9309  
Sequence 9309, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang

/ APPLICANT: PENN, Sharon G.  
 / APPLICANT: RANK, David K.  
 / APPLICANT: CHEN, Wensheng  
 / APPLICANT: SHANNON, Mark  
 / TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 / FILE REFERENCE: AEOMICA-7  
 / CURRENT APPLICATION NUMBER: US/09/866,108A  
 / CURRENT FILING DATE: 2001-05-25  
 / PRIOR APPLICATION NUMBER: US 60/207,456  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: GB 24263.6  
 / PRIOR FILING DATE: 2000-10-04  
 / PRIOR APPLICATION NUMBER: US 60/236,359  
 / PRIOR FILING DATE: 2000-09-27  
 / PRIOR APPLICATION NUMBER: PCT/US01/00666  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00667  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00664  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00669  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00665  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00668  
 / PRIOR FILING DATE: 2001-01-30  
 / PRIOR APPLICATION NUMBER: PCT/US01/00663  
 / PRIOR FILING DATE: 2001-01-30  
 / Remaining Prior Application data removed - See File Wrapper or PALM.  
 / NUMBER OF SEQ ID NOS: 15755  
 / SOFTWARE: Aeomica Sequence Listing Engine  
 / Patent No. 6686188  
 / SEQ ID NO 9309  
 / LENGTH: 17  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / US-09-866-108A-9309  
  
 Query Match 0.6%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 85;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2044 CAGCCAGCAGCAGCC 2058  
 DB 1 CAGCCAGCAGCAGCC 15  
  
 RESULT 179  
 / US-09-371-772B-6025  
 / Sequence 6025, Application US/09371772B  
 / Patent No. 6566127  
 / GENERAL INFORMATION:  
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 / APPLICANT: Pavco, Pam  
 / APPLICANT: McSwiggen, Jim  
 / APPLICANT: Stinchcomb, Dan  
 / APPLICANT: Escobedo, Jaime  
 / TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 / TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 / FILE REFERENCE: MEH800,876-J (237/198)  
 / CURRENT APPLICATION NUMBER: US/09/371,772B  
 / CURRENT FILING DATE: 1999-08-10  
 / PRIOR APPLICATION NUMBER: US 60/005,974  
 / PRIOR FILING DATE: 1995-10-26  
 / PRIOR APPLICATION NUMBER: US 06/584,040  
 / PRIOR FILING DATE: 1996-01-08  
 / NUMBER OF SEQ ID NOS: 14225  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 6025  
 / LENGTH: 16  
 / TYPE: RNA  
 / ORGANISM: Homo sapiens

US-09-371-772B-6025  
 Query Match 0.5%; Score 13; DB 1; Length 16;  
 Best Local Similarity 84.6%; Pred. No. 89;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1070 CACCTGTACAGC 1082  
 DB 4 CACCTGTACAGC 16  
  
 RESULT 180  
 / US-08-292-620A-1760/C  
 / Sequence 1760, Application US/08292620A  
 / Patent No. 5837542  
 / GENERAL INFORMATION:  
 / APPLICANT: Susan Grimm  
 / APPLICANT: Dan T. Stinchcomb  
 / APPLICANT: James McSwiggen  
 / APPLICANT: Sean Sullivan  
 / APPLICANT: Kenneth G. Draper  
 / TITLE OF INVENTION: RIBOZYME TREATMENT OF  
 / TITLE OF INVENTION: DISEASES OR CONDITIONS  
 / TITLE OF INVENTION: RELATED TO LEVELS OF  
 / TITLE OF INVENTION: INTRACELLULAR ADHESION  
 / TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
 / NUMBER OF SEQUENCES: 2390  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Lyon & Lyon  
 / STREET: 633 West Fifth Street  
 / STREET: Suite 4700  
 / CITY: Los Angeles  
 / STATE: California  
 / COUNTRY: U.S.A.  
 / ZIP: 90071-2066  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 / MEDIUM TYPE: Storage  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: IBM P.C. DOS 5.0  
 / SOFTWARE: Word Perfect 5.1  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/292,620A  
 / FILING DATE: August 17, 1994  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / PRIOR APPLICATION DATA: including application  
 / PRIOR APPLICATION DATA: described below:  
 / APPLICATION NUMBER: 08/008,895  
 / FILING DATE: January 19, 1993  
 / APPLICATION NUMBER: 07/989,849  
 / FILING DATE: December 7, 1992  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Wardburg, Richard J.  
 / REGISTRATION NUMBER: 32,327  
 / REFERENCE/DOCKET NUMBER: 208/149  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (213) 489-1600  
 / TELEFAX: (213) 955-0440  
 / TELEX: 67-3510  
 / INFORMATION FOR SEQ ID NO: 1760:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 17 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / US-08-292-620A-1760  
  
 Query Match 0.5%; Score 13; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1072 CCGTGACAGCCA 1084

Db 14 CCTGTGACAGCCA 2

## RESULT 181

US-09-071-845-1760/C

; Sequence 1760, Application US/09071845

; Patent No. 6132967

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Daper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; OPERATING SYSTEM: IBM PC, DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,845

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620

; FILING DATE: August 17, 1994

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEFAX: 67-3510

; INFORMATION FOR SEQ ID NO: 1760:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-071-845-1760

## Query Match

Best local similarity 100.0%; Pred. No. 99;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1072 CCTGTGACAGCCA 1084

Db 14 CCTGTGACAGCCA 2

RESULT 182  
US-08-738-168B-10/C  
; Sequence 10, Application US/08738168B

; Patent No. 6132988

; GENERAL INFORMATION:

; APPLICANT: Sugino, Hiromu

; APPLICANT: Nakamura, Takamori

; APPLICANT: Shouji, Hiroki

; TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/738,168B

; FILING DATE: 25-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 280939/1995

; FILING DATE: 27-OCT-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 174909/1996

; FILING DATE: 04-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Resnick, David S.

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 342/46901

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-738-168B-10

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best local similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 ACAACCTTGACA 1216

Db 17 ACAACCTTGACA 5

RESULT 183  
US-09-017-974-82/C  
; Sequence 82, Application US/09017974  
; Patent No. 6288042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossum, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Conley, Rose & Taylor, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-017-974-82

Query Match          0.5%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      201 CCGCGCGCGCGC 213
DB      16 CCGCGCGCGCGC 4

RESULT 184
; US-08-682-255A-82/c
; Sequence 82, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendegei, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommer, Yves
; APPLICANT: Mazunder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
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; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-682-255A-82

Query Match          0.5%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      201 CCGCGCGCGCGC 213
DB      16 CCGCGCGCGCGC 4

RESULT 185
; US-08-584-040-2055/c
; Sequence 2055, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
```

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2055:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-2055

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 TTGGATGTAGTC 805  
DB 17 TTGGATGTAGTC 5

RESULT 186  
US-08-584-040-2056/c  
Sequence 2056, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
City: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2056:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-584-040-2056  
Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 TTGGATGTAGTC 805  
DB 13 TTGGATGTAGTC 1

RESULT 187  
US-09-429-130-82/c  
Sequence 82, Application US/09429130  
Patent No. 6355785  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennwald, Susan  
APPLICANT: Zendegeui, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
APPLICANT: Pommler, Eyles  
APPLICANT: Mazumder, Abhijit  
60/015,714  
TITLE OF INVENTION: Anti-Viral Guanoxine-Rich  
Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
City: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,130  
FILING DATE: 28-Oct-1999  
CLASSIFICATION: <Unknown>  
19-JULY-95  
25-MARCH-96  
19-MARCH-96  
17-APRIL-96  
23-APRIL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/682,255  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 17-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-429-130-82

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CCGCGCCGCCCGC 213  
DB 16 CCGCGCCGCCCGC 4

RESULT 188  
US-09-371-772B-600/c  
; Sequence 600, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 600  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-600

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 TTGGATGTAGTC 805  
DB 17 TTGGATGTAGTC 5

RESULT 189  
US-09-371-772B-601/c  
; Sequence 601, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 601  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-09-371-772B-601

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 TTGGATGTAGTC 805  
DB 13 TTGGATGTAGTC 1

RESULT 190  
US-09-371-772B-4904/c  
; Sequence 4904, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4904  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-4904

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 TTGGATGTAGTC 805  
DB 15 TTGGATGTAGTC 3

RESULT 191  
US-09-371-772B-5421  
; Sequence 5421, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5421  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-5421

Mon Sep 20 10:12:25 2004

viv1emore580-1.rn1

Page 67

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 84.6%; Pred. No. 99;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1070 CACCTGTGACAGC 1082  
|||:|||||  
Db 5 CACCTGTGACAGC 17

Search completed: September 20, 2004, 10:08:20  
Job time : 6 secs

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108	15.2	0.6	20	1	181	14.4	0.6	17	1	AAA25223	Oestrogen receptor		
109	15.2	0.6	20	1	182	14.4	0.6	17	1	AAO64171	Human KtOmla porin		
110	15.2	0.6	20	1	183	14.4	0.6	17	1	ABO64172	Human KtOmla porin		
111	15.2	0.6	20	1	184	14.4	0.6	17	1	ABV78892	Human HTPL scanrin		
112	15.2	0.6	20	1	185	14.4	0.6	17	1	AAV78891	Human HTPL scanrin		
113	15.2	0.6	20	1	186	14.4	0.6	17	1	ABK19384	Human ERG Ambrzym		
114	15.2	0.6	20	1	187	14.4	0.6	17	1	ABK19385	Human ERG Ambrzym		
115	15.2	0.6	20	1	188	14.4	0.6	17	1	ABK57571	Human CLCA1 gene e		
116	15.2	0.6	20	1	189	14.4	0.6	17	1	ABK57571	Human CLCA1 gene e		
117	15.2	0.6	20	1	190	14.4	0.6	17	1	ABK56508	Human CLCA1 gene e		
118	15.2	0.6	20	1	191	14.4	0.6	17	1	ABK57536	Human CLCA1 gene e		
119	15.2	0.6	20	1	192	14.4	0.6	17	1	ABK57267	Human CLCA1 gene e		
120	15.2	0.6	20	1	193	14.4	0.6	17	1	ACC67338	Murine oligonucleo		
121	15.2	0.6	20	1	194	14.4	0.6	17	1	ADB43111	Tumour suppression		
122	15.2	0.6	20	1	195	14.4	0.6	17	1	ADB43110	Tumour suppression		
123	15.2	0.6	20	1	196	14.4	0.6	17	1	ADB45178	Tumour suppression		
124	15.2	0.6	51	1	197	14.4	0.6	18	1	AAV48252	Primer B for 235 a		
125	15	0.6	15	1	198	14.4	0.6	18	1	AAV76342	Human fibronectin		
126	15	0.6	16	1	199	14.4	0.6	18	1	AAV16023	PCR primer used to		
127	15	0.6	18	1	200	14.4	0.6	18	1	AAV35925	PCR primer for gra		
128	15	0.6	18	1	201	14.4	0.6	18	1	AAV54144	Human fibronectin		
129	15	0.6	19	1	202	14.4	0.6	18	1	AAV33588	Low adenosine anti		
130	15	0.6	20	1	203	14.4	0.6	18	1	AAZ43382	Murine Sox2 gene p		
131	15	0.6	20	1	204	14.4	0.6	18	1	AAAO5267	PCR primer C-F use		
132	15	0.6	20	1	205	14.4	0.6	18	1	AAAF19710	Human fibronectin		
133	15	0.6	20	1	206	14.4	0.6	18	1	ABZ295404	Human fibronectin		
134	15	0.6	20	1	207	14.4	0.6	18	1	ABX80015	EST polymorphic DN		
135	15	0.6	20	1	208	14.4	0.6	19	1	ACG70002	Primer oligo used		
136	15	0.6	20	1	209	14.4	0.6	19	1	AAV59110	Human nuclear rece		
137	15	0.6	20	1	210	14.4	0.6	19	1	AAZ29215	Primer IFW6 used f		
138	15	0.6	20	1	211	14.4	0.6	19	1	AAAB84742	Cyclin F ribozyme		
139	15	0.6	20	1	212	14.4	0.6	19	1	AAAB3615	Cdk-we-hu ribozyme		
140	15	0.6	20	1	213	14.4	0.6	19	1	AA545588	Human PARP-2 RT-PC		
141	15	0.6	20	1	214	14.4	0.6	19	1	AAH58777	Cdk-we-hu ribozyme		
142	15	0.6	20	1	215	14.4	0.6	19	1	AAH59204	Cyclin F ribozyme		
143	14.8	0.6	18	1	216	14.4	0.6	19	1	ABZ97252	Human nucleic acid		
144	14.8	0.6	18	1	217	14.4	0.6	19	1	ABZ9733	Human IL4-R oligon		
145	14.8	0.6	18	1	218	14.4	0.6	19	1	ABZ27352	Stearyl-CoA desat		
146	14.8	0.6	18	1	219	14.4	0.6	19	1	ABZ27062	Stearyl-CoA desat		
147	14.8	0.6	18	1	220	13.8	0.6	18	1	AAV48449	Transforming growt		
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											RESULT 1		
											ABN40154		
											ID	ABN40154	strand; DNA; 60 BP.
											ABN40154;		
											15-JUL-2002	(first entry)	
											Human	spliced transcript	detection oligonucleotide seq ID NO:12902.
											XX	Human;	mouse; rat; splice transcript; detection; RNA transcript;
											KW	splice variant; transcriptome; oligonucleotide library; ss.	
											XX	Homo sapiens.	
											OS	MO200210449-A2.	
											XX	PN	
											PD	07-FEB-2002.	
											PF	20-JUL-2001; 2001WO-IB001903.	
											PR	28-JUL-2000; 2000US-0221607P.	
											PR	02-MAY-2001; 2001US-0287724P.	
											XX	(COMP-) COMPUGEN INC.	
											PA	Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;	
											XX		

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 10:06:47 ; Search time 6 seconds

(without alignments)  
3.497 Million cell updates/sec

Title: US-08-864-955-1

Perfect score: 2419  
Sequence: 1 CGAAGGCCGGCCTTGCTG.....GCTGCCCAATAGCAAGAG 2419

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 217 seqs, 4337 residues

Total number of hits satisfying chosen parameters: 434

Minimum DB seq length: 10  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 220 summaries

Database : rngl.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	2.5	60	1	ABN40154
2	51	2.1	51	1	AAI29294
3	50	2.1	50	1	AAI29295
4	49.4	2.0	51	1	ABU00108
5	39.5	1.6	50	1	AAI29296
6	24	1.0	24	1	ABK66874
7	24	1.0	24	1	ABK66873
8	21	0.9	21	1	AAK25949
9	21	0.9	21	1	AAK6891
10	20	0.8	20	1	AAV06361
11	19.2	0.8	25	1	ACI98767
12	18.8	0.8	25	1	ACI98767
13	18.4	0.8	20	1	ABO65282
14	18.4	0.8	20	1	ABO65414
15	18.4	0.8	20	1	ABK34070
16	18.4	0.8	20	1	ABK28008
17	18.4	0.8	20	1	ABK28008
18	18.4	0.8	20	1	ABK28008
19	18.4	0.8	20	1	ABK28008
20	18.4	0.8	20	1	ABK28008
21	18.2	0.8	23	1	ADK48483
22	18.2	0.8	23	1	ADK48483
23	18.2	0.8	23	1	ADK48483
24	17.8	0.7	21	1	AAV41807
25	17.8	0.7	21	1	AAV41807
26	17.4	0.7	20	1	AAK29188
27	17.4	0.7	20	1	AAK29188
28	17.4	0.7	20	1	AAK29188
29	17.4	0.7	20	1	AAK29188
30	17.4	0.7	20	1	AAK29188
31	16.4	0.7	18	1	ABK10445
32	16.4	0.7	18	1	ABK10445
33	16.4	0.7	18	1	ABK10445

34	16.4	0.7	18	1	ADB84341	Human lymphoid cel
35	16.4	0.7	19	1	AAZ97871	HIV-1 protease gen
36	16.4	0.7	20	1	AAZ58092	Human heat shock p
37	16.4	0.7	20	1	AAZ97870	HIV-1 protease gen
38	16.4	0.7	20	1	AAZ58092	HIV-1 protease gen
39	16.4	0.7	21	1	AAZ58092	HIV-1 protease gen
40	16.4	0.7	21	1	AAZ58092	HIV-1 protease gen
41	16.4	0.7	21	1	AAZ58092	HIV-1 protease gen
42	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
43	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
44	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
45	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
46	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
47	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
48	16.2	0.7	21	1	AAZ58092	HIV-1 protease gen
49	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
50	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
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52	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
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56	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
57	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
58	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
59	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
60	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
61	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
62	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
63	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
64	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
65	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
66	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
67	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
68	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
69	15.8	0.7	19	1	AAZ58092	HIV-1 protease gen
70	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
71	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
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75	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
76	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
77	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
78	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
79	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
80	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
81	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
82	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
83	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
84	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
85	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
86	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
87	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
88	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
89	15.4	0.6	18	1	AAZ58092	HIV-1 protease gen
90	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
91	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
92	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
93	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
94	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
95	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
96	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
97	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
98	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
99	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
100	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
101	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
102	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
103	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
104	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
105	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen
106	15.2	0.6	20	1	AAZ58092	HIV-1 protease gen

```

XX DR WPI; 2002-257383/30.
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of a
XX PT genome, useful for detecting tissue-, pathology-, and developmental-
XX PT specific genes.
XX
XX PS Example 1; SEQ ID NO 12902; 47pp; English.
XX
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX CC )transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises several
XX CC oligonucleotides, each capable of hybridizing selectively to a set of
XX CC messenger RNAs transcribed from a given transcription unit of the genome,
XX CC which encodes one or more messenger RNA splice variants. The
XX CC oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterizing the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcripts. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a particular
XX CC biological or pathological state, and so allowing the detection of tissue
XX CC - and pathology-specific genes such as those genes only expressed in
XX CC specific tissue under a specific pathological condition; to detect
XX CC developmental specific genes; and to detect RNA transcripts and splice
XX CC variants of a transcriptome of a patient suffering from a particular
XX CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX CC rate, humans and mice, which are used in the exemplification of the
XX CC present invention. N.B. The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIP0 at ftp.wip0.int/pub/published_pot_sequences
XX
XX SQ Sequence 60 BP; 15 A; 20 C; 9 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 2.5%; Score 60; DB 1; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1362 AACTATATCCAGAGAGAGCCCATGAGACTCTTCATCATGCTTTATCCCTGACATCTTCCCC 1421
DB 1 AACTATATCCAGAGAGAGCCCATGAGACTCTTCATCATGCTTTATCCCTGACATCTTCCCC 60
XX
XX RESULT 2
XX ID AAL29294
XX XX AAL29294 standard; DNA; 51 BP.
XX
XX AC AAL29294;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE Human SNP oligonucleotide #2502.
XX
XX XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX KW multifactorial disease; autoimmune disease; infection;
XX KW nervous system disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200147944-A2.
XX
XX PD 05-JUL-2001.
XX
XX PF 28-DEC-2000; 2000MO-US035498.
XX
XX PR 28-DEC-1999; 99US-0173419P.
XX
XX PA

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XX PR 27-DEC-2000; 2000US-00173419.
XX
XX PA (CURA-) CURAGEN CORP.
XX
XX PI Shimkets RA, Leach M;
XX
XX DR WPI; 2001-465210/50.
XX
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX PT autoimmune diseases and infections.
XX
XX PS Claim 1; Page 2099; 4143pp; English.
XX
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX CC protein coupled receptors and thioesterases. The present sequence is one
XX CC such oligonucleotide. The oligonucleotides and the peptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of the proteins listed above.
XX CC Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms
XX
XX SQ Sequence 51 BP; 12 A; 19 C; 8 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 51; DB 1; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 0.0003;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 2066 CCCCTCATCCCTCCCTTACCTCTTCTCCTGAGAGAACTTAACCAAGAGG 2116
DB 1 CCCCTCATCCCTCCCTTACCTCTTCTCCTGAGAGAACTTAACCAAGAGG 51
XX
XX RESULT 3
XX ID AAL29295
XX XX AAL29295 standard; DNA; 50 BP.
XX
XX AC AAL29295;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE Human SNP oligonucleotide #2503.
XX
XX XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX KW multifactorial disease; autoimmune disease; infection;
XX KW nervous system disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200147944-A2.
XX
XX PD 05-JUL-2001.
XX
XX PF 28-DEC-2000; 2000MO-US035498.
XX
XX PR 28-DEC-1999; 99US-0173419P.
XX
XX PR 27-DEC-2000; 2000US-00173419.
XX
XX PA (CURA-) CURAGEN CORP.
XX

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XX Shinkets RA, Leach M;  
 PI  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 PS Claim 1; Page 2099; 4143pp; English.  
 XX  
 PS The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one  
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms  
 CC  
 SQ Sequence 50 BP; 11 A; 12 C; 20 G; 7 T; 0 U; 0 Other;  
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 Best Local Similarity 100.0%; Pred. No. 0.00043;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2320 AGCGGCGGCTTATCGGGCTCAGCATCTCATGAGGGAGAGAGACGGA 2359  
 DB 1 AGCGGCGGCTTATCGGGCTCAGCATCTCATGAGGGAGAGAGACGGA 50  
 RESULT 4  
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 ID AB100108 standard; DNA; 51 BP.  
 XX  
 AC AB100108;  
 XX  
 DT 05-MAR-2002 (First entry)  
 XX  
 DE Human silent noncoding SNP oligonucleotide SEQ ID NO:99.  
 XX  
 KM Human; single nucleotide polymorphism; SNP; polymorphism; cytosstatic;  
 KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 KM autoimmune disease; inflammation; cancer; nervous system disease;  
 KM infection; polymorphic protein; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200138586-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 22-NOV-2000; 2000WO-US032311.  
 XX  
 PR 24-NOV-1999; 99US-0167383P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI; 2001-355949/37.  
 XX  
 PT Isolated human nucleic acids comprising one or more single nucleotide  
 PT polymorphisms, useful for treating a subject suffering from a pathology,  
 PT e.g. autoimmune diseases, ascribed to the presence of a sequence

PT polymorphism.  
 XX  
 PS Claim 1; Page 275; 674pp; English.  
 XX  
 PS AB100010 to AB101104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). AB56531  
 CC to AB56503 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytosstatic, antiinflammatory, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterised  
 CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic  
 CC protein within appropriate physiological samples)  
 CC  
 SQ Sequence 51 BP; 11 A; 14 C; 18 G; 8 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 49.4; DB 1; Length 51;  
 Best Local Similarity 98.0%; Pred. No. 0.00055;  
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2278 GAGCACCGTGTCAAGCTGCTGAGCGACAGTGGGATGATACCGCGGGGC 2328  
 DB 1 GAGCACCGTGTCAAGCTGCTGAGTCACAGTGGGATGATACCGCGGGGC 51  
 RESULT 5  
 AAL29296  
 ID AAL29296 standard; DNA; 50 BP.  
 XX  
 AC AAL29296;  
 XX  
 DT 24-JAN-2002 (First entry)  
 XX  
 DE Human SNP oligonucleotide #2504.  
 XX  
 KM Immunosuppressive; immunostimulatory; antiinflammatory; cytosstatic;  
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KM cyclin; polymerase; oncogenes; histone; kinase; colony stimulating factor;  
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KM multifactorial disease; autoimmune disease; infection;  
 KM nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035496.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 XX  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 PS Claim 1; Page 2100; 4143pp; English.

```

XX CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
CC SQ Sequence 50 BP; 18 A; 7 C; 18 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 39.5; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.023; Mismatches 1; Gaps 1;
Matches 50; Conservative 0; Indels 1;
QY 2361 GGAGACGAGCGGAGTAGAGATTACACAGAAATGCTGCTGCCAATA 2411
DB 1 GGAGACGAGCGGAGTAGAGAG-TTACACAGAAATGCTGCTGCCAATA 50
RESULT 6
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ID ABK66874 standard; DNA; 24 BP.
XX AC ABK66874;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #962.
XX KM Primer; ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-00225928.
XX PR 21-MAY-1997; 97US-00859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Johndaze G, Bibilashvilli R;
XX DR WPI; 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analyzing
XX differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers.
XX PS Example 3; SEQ ID NO 962; 11bp; English.
XX CC The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where each
XX gene specific primer has a sequence complementary to a distinct mRNA, and
XX each labeled NA is generated using a single gene specific primer. The
XX method is useful for producing a sub-population of labeled NAs which is
XX useful for analysing the differences in the RNA profiles between several
XX different physiological sources, where the method comprises producing
XX subpopulation of labeled NAs for the different physiological sources,

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CC comprising the populations for each physiological source to identify
CC differences in the population, where the comparison is preferably
CC performed by hybridising the labeled NAs for each of the distinct
CC physiological sources to an array of probe NAs stably associated with the
CC surface of a substrate to produce a hybridisation pattern for each of the
CC sources, and comparing the patterns for each of the sources, where
CC differential gene expression assays are utilised in differential
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC tissue, or different tissue or sub-tissue types. The present sequence is a
CC human gene specific PCR primer used in the method of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at http://ipo.segdata.uspto.gov/sequence.html?docid=635282981
XX SQ Sequence 24 BP; 2 A; 6 C; 9 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1954 AAGTTCGACCAAGACCGGACC 1977
DB 24 AAGTTCGACCAAGACCGGACC 1
RESULT 7
ABK66873
ID ABK66873 standard; DNA; 24 BP.
XX AC ABK66873;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #961.
XX KM Primer; ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-00225928.
XX PR 21-MAY-1997; 97US-00859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Johndaze G, Bibilashvilli R;
XX DR WPI; 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analyzing
XX differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers.
XX PS Example 3; SEQ ID NO 961; 11bp; English.
XX CC The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where each
XX gene specific primer has a sequence complementary to a distinct mRNA, and
XX each labeled NA is generated using a single gene specific primer. The
XX method is useful for producing a sub-population of labeled NAs which is
XX useful for analysing the differences in the RNA profiles between several
XX different physiological sources, where the method comprises producing
XX subpopulation of labeled NAs for the different physiological sources,
XX comprising the populations for each physiological source to identify
XX differences in the population, where the comparison is preferably
XX performed by hybridising the labeled NAs for each of the distinct
XX physiological sources to an array of probe NAs stably associated with the

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CC surface of a substrate to produce a hybridisation pattern for each of the  
CC sources, and comparing the patterns for each of the sources, where  
CC differential gene expression assays are utilised in differential  
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal  
CC tissue, or different tissue or subtypes. The present sequence is a  
CC human gene specific PCR primer used in the method of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at <http://wipo.segdata.uspto.gov/sequence.html?DocID=6355282931>

CC Sequence 24 BP, 6 A, 5 C, 10 G, 3 T, 0 U, 0 Other;

Query Match 1.0%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1632 GGGAGGCCACATCAAGGTCAGT 1655  
1 GGGAGGCCACATCAAGGTCAGT 24

RESULT 8  
AAZ25949  
ID AAZ25949 standard; DNA; 21 BP.

AC AAZ25949;

DT 30-NOV-1999 (first entry)

DE Human polymorphic region 138.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX cell viability; loss of heterozygosity; precancerous condition; ASI;  
XX allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX graft versus host disease; malignant cell removal; bone marrow; ss.

OS Homo sapiens.

PN WO9841648-A2.

PD 24-SEP-1998.

PF 19-MAR-1998; 98MO-US005419.

PR 20-MAR-1997; 97US-0041057P.

PA (VARI-) VARIAGENICS INC.

PI Housman D, Ledley FD, Stanton VP;

DR WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for diagnosis,  
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
XX dysplastic lesions, endometriosis or graft versus host disease.

PS Disclosure; Fig 7; 605bp; English.

XX This invention describes a novel method for identifying an inhibitor  
XX potentially useful for treatment of cancer, where the inhibitor is active  
XX on a gene vital for cell growth or viability, and where the gene is  
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
XX used for preventing the development of cancer in a patient having a  
XX precancerous condition, by administering to the patient a first allele  
XX specific inhibitor (ASI) targeted to an allele of a first essential gene  
XX present in cells of the precancerous condition, where the normal somatic  
XX cells of the patient are heterozygous for the first gene, the inhibitor  
XX is active on at least one but less than all allelic forms of the gene  
XX present in a population and targets only one allelic form present in the  
XX normal somatic cells, and the first gene. The products and methods can be  
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.

CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25912-226825 represent  
CC human polymorphic sites described in the method of the invention

CC Sequence 21 BP, 6 A, 7 C, 4 G, 4 T, 0 U, 0 Other;

Query Match 0.9%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1919 CCATGCACACAGAGACTTTA 1939  
1 CCATGCACACAGAGACTTTA 21

RESULT 9  
AAF66891  
ID AAF66891 standard; DNA; 21 BP.

AC AAF66891;

DT 06-JUN-2001 (first entry)

DE Human gene single nucleotide polymorphism #1652.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
XX polymorphism; vascular disease; coronary artery disease; forensics;  
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
XX pulmonary embolism; paternity test; de.

OS Homo sapiens.

PN WO200118250-A2.

PD 15-MAR-2001.

PF 07-SEP-2000; 2000WO-US024503.

PR 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.

PI (MILL-) MILLENNIUM PHARM INC.

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JI;

DR WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
XX applications such as forensics, paternity testing, medicine, genetic  
XX analysis and phenotype correlations to diseases such as diabetes and  
XX atherosclerosis.

PS Example; Page 159; 242bp; English.

XX The present invention provides a method of diagnosing a vascular disease  
XX in an individual, involving determining the sequence at various  
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
XX genes. The sequences at a number of polymorphic sites are also provided  
XX in the specification. In particular, the method can be used in the  
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart  
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and  
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
XX useful in forensics, paternity testing, genetic analysis and phenotype  
XX correlations to diseases. The present sequence is an example of one of

CC the human gene SNPS shown in the specification  
 XX  
 SQ Sequence 21 BP; 5 A; 7 C; 7 G; 2 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1339 TCTGGGGCCAGCCCAAGAG 1359  
 Db 1 TCTGGGGCCAGCCCAAGAG 21  
 RESULT 10  
 AAV06361/C  
 ID AAV06361 standard; DNA; 20 BP.  
 XX  
 AC AAV06361;  
 XX  
 DT 01-MAY-1998 (first entry)  
 DE cdc25A antisense S-oligonucleotide.  
 XX  
 KM cdc25; MYC; apoptosis; mitosis; inhibitor; treatment; tumour; retroviral;  
 KM autoimmune; neurodegenerative; diagnosis; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9740379-A2.  
 XX  
 PD 30-OCT-1997.  
 XX  
 PF 16-APR-1997; 97WO-US006189.  
 XX  
 PR 23-APR-1996; 96US-00636597.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Beach DH;  
 DR WPI; 1997-536002/49.  
 XX  
 PT Identifying inhibitors of cdc25-induced apoptosis or myc-mediated  
 PT transcriptional activation - useful for treating retroviral, autoimmune,  
 PT neurodegenerative diseases etc. and for maintenance of in vitro cultures,  
 PT also for diagnosis.  
 XX  
 PS Example 6; Page 35; 48pp; English.  
 XX  
 CC This is a cdc25A antisense S-oligonucleotide. This is used in a method  
 CC for investigating the role of cdc25A in myc-driven apoptosis. Methods for  
 CC identifying an inhibitor of cdc25-mediated cell cycle progression/  
 CC mitotic activation are provided. One method for identifying modulators of  
 CC cdc25-mediated mitosis in which levels of a protein, preferably p53,  
 CC which are modulated by apoptosis, rather than cell death is compared in  
 CC presence and absence of test compound. The inhibitor is identified by  
 CC comparing levels of expression of a reporter gene (RG) under control of a  
 CC p53-responsive element in a cell that includes a recombinant cdc25 gene.  
 CC A decrease in RG expression indicates an inhibitor. Another assay for  
 CC identifying an inhibitor of myc-mediated transcriptional activation is by  
 CC comparing the binding of myc to an isolated nucleic acid that has the  
 CC consensus binding site CAYGTG. Any decrease in binding indicates an  
 CC inhibitor. The inhibitor is identified by measuring expression of RG in  
 CC cells transfected with myc and regulatory sequence including the  
 CC consensus sequence for control of RG. A similar method for identifying an  
 CC inhibitor comprises treating test cells, having a recombinant cdc25  
 CC phosphatase gene that can be expressed at a level sufficient to cause  
 CC apoptosis, with a test compound. The level of cell death is then compared  
 CC with that in similar cells not treated with test compound and a  
 CC significant reduction in cell death indicates an inhibitor of cdc25-  
 CC mediated mitotic activation. The inhibitors are used to reduce apoptosis.  
 CC They can be used for treating retroviral infections (e.g. acquired immune

CC deficiency syndrome, adult T cell or hairy cell leukaemia, uveitis,  
 CC hepatitis C), autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC rheumatoid arthritis, ulcerative colitis, insulin-dependent diabetes),  
 CC disease associated with thrombocytopaenia (e.g. aplastic anaemia or  
 CC disseminated intravascular coagulation), liver disease (e.g. hepatitis or  
 CC cirrhosis); neurodegenerative diseases (e.g. Alzheimer's, Parkinson's or  
 CC Huntington's diseases), myocarditis, adult respiratory distress syndrome,  
 CC prostatic hypertrophy, bronchial asthma, congenital deformations;  
 CC nephritis, senile cataracts, chronic fatigue syndrome and myotonic  
 CC dystrophy. They may also be used in vitro, e.g. to increase survival in  
 CC cultures and to maintain differentiation of e.g. glial cells. These  
 CC applications are based on the discovery that cdc25, already known as a  
 CC mitotic activator, also induces apoptosis (probably acting as a  
 CC downstream target for myc). Measurement of the levels of cdc25 can be  
 CC used diagnostically, e.g. to distinguish between apoptosis and necrosis,  
 CC while detecting presence/absence of wild-type myc can be used for  
 CC diagnosis/prognosis of tumours  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 458 CCATGGAACCTGGGCCGAGC 477  
 Db 20 CCATGGAACCTGGGCCGAGC 1  
 RESULT 11  
 AC198767/C  
 ID AC198767 standard; DNA; 25 BP.  
 XX  
 AC AC198767;  
 XX  
 DT 14-OCT-2003 (first entry)  
 DE Human microarray DNA oligonucleotide SEQ ID NO 98758.  
 XX  
 KM EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KM genetic variation; diallelic marker; polymorphism; human;  
 KM cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Miltmann MP;  
 XX  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 98758; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises

hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 4 A; 5 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.8%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 24;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1511 GGAACATCAGAGTTTAAATCA 1534  
DB 24 GGAACATCAGAGTATATACACA 1

RESULT 12  
ACT99882/C  
ID ACT99882 standard; DNA; 25 BP.

ACT99882;  
14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 99873.

EST; ss; probe; expressed sequence tag; microarray; gene expression;  
genetic variation; diallelic marker; polymorphism; human;  
cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFRY-) AFFYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 99873; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid

probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 8 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 28;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1290 TTCTCAGAGAGTCTCCACT 1311  
DB 25 TTCTCAGAGAGTATCTCTCT 4

RESULT 13  
ABQ65282/C  
ID ABQ65282 standard; DNA; 20 BP.

ABQ65282;

20-AUG-2002 (first entry)

Human gene methylation status determination method PCR primer #22.

Toxicological diagnosis; DNA methylation; methylation status;

Toxic response; human; PCR; primer; ss.

Homo sapiens.

WO200240710-A2.

23-MAY-2002.

08-NOV-2001; 2001WO-EP012951.

14-NOV-2000; 2000DE-01056802.

(EPIC-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2002-463571/49.

Toxicological diagnosis, useful for diagnosis and prognosis of adverse reactions, based on effect of test compounds on methylation status of selected genes, involves determining changes in DNA methylation status.

Example 2; Page 102; 113pp; German.

The present invention relates to a method of toxicological diagnosis, involving taking a DNA-containing sample from an organism or cell culture that has been treated with a test compound and determining any changes in the DNA methylation status or pattern caused by said test compound. The method is used for diagnosis and prognosis of adverse toxic responses in individuals. The present sequence is a PCR primer used to demonstrate the method of the invention

Sequence 20 BP; 13 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 26;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 164 GTTGTGGATTATTCCT 183
   |||||||
Db 20 GTTGTGGATTATTTT 1

RESULT 14
ID ABO65414/c
AC ABO65414 standard; DNA; 20 BP.
XX
XX ABO65414;
AC
DT 20-AUG-2002 (first entry)
XX
XX Human gene methylation status determination oligo SEQ ID NO: 26.
DE
XX Toxicological diagnosis; DNA methylation; methylation status;
KM toxic response; human; ds.
OS Homo sapiens.
XX
XX WO200240710-A2.
XX
XX 23-MAY-2002.
XX
XX 08-NOV-2001; 2001WO-EP012951.
XX
XX 14-NOV-2000; 2000DE-01056802.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-463571/49.
XX
XX Toxicological diagnosis; useful for diagnosis and prognosis of adverse
XX reactions, based on effect of test compounds on methylation status of
XX selected genes, involves determining changes in DNA methylation status.
XX
XX Disclousre; Page 111; 113pp; German.
XX
XX The present invention relates to a method of toxicological diagnosis,
XX involving taking a DNA-containing sample from an organism or cell culture
XX that has been treated with a test compound and determining any changes in
XX the DNA methylation status or pattern caused by said test compound. The
XX method is used for diagnosis and prognosis of adverse toxic responses in
XX individuals. The present sequence is a human sequence used to demonstrate
XX the method of the invention
XX
XX Sequence 20 BP; 13 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
S0

Query Match 0.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0,

Oy 164 GTTGTGGATTATTCCT 183
   |||||||
Db 20 GTTGTGGATTATTTT 1

RESULT 15
ID ABRK34070/c
AC ABRK34070 standard; DNA; 20 BP.
XX
XX ABRK34070;
AC
DT 18-JUN-2002 (first entry)
XX
XX Human CDC25A PCR primer #2.
XX
XX Human; ss; astrocytoma; cytostatic; staging; cysteine methylation; CpG;
XX bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
XX matrix assisted laser desorption/ionization mass spectrometry; primer.
KM

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XX Homo sapiens.  
XX WO200202808-A2.  
XX  
XX 10-JAN-2002.  
XX  
XX 02-JUN-2001; 2001WO-EP007538.  
XX  
XX 30-JUN-2000; 2000DE-01032529.  
XX 01-SEP-2000; 2000DE-01043826.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A. Piepenbrock C, Berlin K;  
XX  
XX WPI; 2002-171649/22.  
XX  
XX Novel chemically modified genomic DNA sequences, useful in the  
XX characterization, classification, differentiation, grading, staging,  
XX treatment and/or diagnosis of astrocytomas or predisposition to  
XX astrocytomas.  
XX  
XX Example; Page 24; 37pp; English.  
XX  
XX The invention relates to a nucleic acid comprising a sequence (I) of at  
XX least 18 bases in length of a segment of chemically pre-treated genomic  
XX DNA which has any one of the sequences of (ABK33919-ABK34032) or its  
XX complement. Also included are an oligonucleotide or peptide nucleic acid  
XX (or set thereof) of at least 9 nucleotides which hybridises to (I),  
XX primers for (I), probes for detecting cytosine methylation or single-  
XX nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide  
XX nucleic acids for analysing diseases associated with the methylation  
XX states of the CpG dinucleotides of (I). The array is useful for  
XX determining genetic and/or epigenetic parameters, classification,  
XX differentiation, grading, staging, treatment and/or diagnosis of  
XX astrocytomas, or the predisposition to astrocytomas by analysing cytosine  
XX methylations, involves obtaining a biological sample containing genomic  
XX DNA, extracting the genomic DNA, converting cytosine bases which are  
XX unmethylated at the 5-position, in the genomic DNA sample, to uracil or  
XX another base which is dissimilar to cytosine in terms of hybridisation  
XX behaviour by chemical treatment and amplifying chemically pre-treated  
XX genomic DNA fragments using the array and a polymerase, where the  
XX amplicates carry a detectable label. The method further involves  
XX identifying methylation status of one or more cytosine positions, and  
XX analysing methylation status of the cytosine positions by reference to  
XX one or more data sets. The genomic DNA is chemically treated by using a  
XX biophiles, hydrogen sulphate or disphilete. The amplification step  
XX amplifies DNA which is of particular interest in astrocytoma or brain  
XX tissue, based on the specific genomic methylation status of brain  
XX tissues, as opposed to background DNA. The amplicates carry a  
XX fluorescent label or radionucleide. Optionally, the labels of the  
XX amplicates are detachable molecule fragments having a typical mass  
XX which are detected in a mass spectrometer. The fragments of chemically  
XX pre-treated genomic DNA to be amplified, have a single positive or  
XX negative charge for a better detectability in the mass spectrometer.  
XX Preferably, the amplicates or fragments of the amplicates are  
XX detected by matrix assisted laser desorption/ionization mass spectrometry  
XX (MALDI) or using electron spray mass spectrometry (ESI). The present  
XX sequence is a PCR primer used to amplify a region containing a methylated  
XX cytosine from one of the chemically pre-treated reference DNA samples of  
XX the invention. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences

XX  
XX Sequence 20 BP; 13 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

XX Query Match            0.8%;   Score 18.4; DB 1; Length 20;  
XX Best Local Similarity   95.0%;   Pred. No. 26;  
XX Matches   19; Conservative   0; Mismatches   1; Indels   0; Gaps   0.

XX 164 GTTTGGATTTCCTT 193



```

RESULT 18
ADA20482/C
ID ADA20482 standard; DNA; 20 BP.
XX
AC ADA20482;
XX
DT 20-NOV-2003 (first entry)
XX
DE Prostate tumour related gene CRIP1 PCR primer #1.
XX
KM cytosinatic; Gene therapy; genetic marker; epigenetic parameter;
KM classification; differentiation; diagnosis; prostate tumour;
KM prostate cancer; cytosine methylation; uracil;
KM single nucleotide polymorphism; SNP; prostate carcinoma; ss; primer; PCR.
XX
OS Homo sapiens.
XX
PN WO2002103042-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-EP006605.
XX
PR 14-JUN-2001; 2001DE-01028508.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Distler J, Model F, Adorjan P;
XX
DR WPI; 2003-167536/16.
XX
PT Determining genetic and/or epigenetic parameters, useful for the
PT classification, differentiation and/or diagnosis of prostate tumors or a
PT predisposition to prostate cancer, comprises analyzing cytosine
PT methylation.
XX
PS Example 2; Page 16; 376pp; English.
XX
CC The invention relates to a method of determining genetic and/or
CC epigenetic parameters for the classification, differentiation and/or
CC diagnosis of prostate tumors or the predisposition to prostate cancer,
CC by analysing cytosine methylation in a sample of genomic DNA. The method
CC comprises chemically treating unmethylated cytosine bases at the 5-
CC position to uracil or another base, which is dissimilar to cytosine in
CC terms of hybridization behaviour; followed by amplifying at least one
CC fragment of the chemically pre-treated genomic DNA using sets of primer
CC oligonucleotides and a polymerase. The oligomers or probes derived from
CC them are useful for detecting the methylation state of all Cps
CC dinucleotides and/or single nucleotide polymorphisms (SNPs) in a
CC chemically pre-treated genomic DNA. They are all useful for treating
CC prostate carcinoma. This sequence represents an oligonucleotide used to
CC amplify a gene possibly involved in predisposition to prostate cancer
CC which may contain methylated or unmethylated CpG dinucleotides.
XX
SQ Sequence 20 BP; 13 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 164 GTTGTGATTGAATTAATCTT 183
DB 20 GTTGTGATTGAATTAATTTT 1
XX
RESULT 19
ADA84283/C
ID ADA84283 standard; DNA; 20 BP.
XX
AC ADA84283;
XX
DT 20-NOV-2003 (first entry)
XX

```

```

DE Human CDC25A PCR primer 2.
XX
KM renal cancer; prostate cancer; cytosine methylation;
KM single nucleotide polymorphism; histological; cytological; ss; primer;
KM PCR.
XX
OS Homo sapiens.
XX
PN WO2002103041-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-EP006603.
XX
PR 14-JUN-2001; 2001DE-01028509.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Distler J, Model F, Adorjan P;
XX
DR WPI; 2003-183991/18.
XX
PT Method for characterizing, classifying and/or differentiating renal and
PT prostate cancers, by analyzing the genetic and/or epigenetic parameters
PT of genomic DNA, particularly by determining its cytosine methylation
PT status.
XX
PS Example 2; Page 16; 211pp; English.
XX
CC The invention relates to a novel method for characterizing, classifying
CC and/or differentiating renal and prostate cancer. The method comprises
CC extracting genomic DNA from a biological sample, converting cytosine
CC bases (by chemical treatment) that are unmethylated at the 5-position to
CC uracil or another base, and amplifying at least one fragment of the
CC chemically pre-treated genomic DNA using sets of primer oligonucleotides
CC and a polymerase. The method is useful for detecting the cytosine
CC methylation state and/or single nucleotide polymorphisms in genomic DNA,
CC particularly for characterizing, classifying and/or differentiating renal
CC and prostate cancers. The oligomers are useful as primer oligonucleotides
CC for the amplification of any of the 112 DNA sequences of the invention.
CC The set of oligomer probes is useful for detecting the cytosine
CC methylation state and/or single nucleotide polymorphisms in any of the
CC 112 chemically pre-treated genomic DNA sequences. The method is also
CC useful for identifying the tissue of origin of cancer cells. The method
CC allows the classification, differentiation and/or diagnosis of cancer
CC tissues using minute samples which would be inadequate for histological
CC or cytological analysis. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 20 BP; 13 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 164 GTTGTGATTGAATTAATCTT 183
DB 20 GTTGTGATTGAATTAATTTT 1
XX
RESULT 20
AAV41807/C
ID AAV41807 standard; DNA; 23 BP.
XX
AC AAV41807;
XX
DT 20-NOV-1998 (first entry)
XX
DE Human pancreatic carboxypeptidase B primer (v).
XX
KM ss; primer; PCR; amplification; human; pancreatic carboxypeptidase B;
KM insulin; protein sequencing; prodrug therapy.
XX

```

OS Synthetic.  
 OS Homo sapiens.  
 XX WO9835388-A1.  
 XX 20-AUG-1998.  
 PD  
 XX 10-FEB-1998; 98WO-GB000415.  
 PF  
 XX 14-FEB-1997; 97GB-00003104.  
 PR 18-OCT-1997; 97GB-00022003.  
 PR 29-OCT-1997; 97GB-00022727.  
 XX  
 PA (ZENEC) ZENEC LTD.  
 XX  
 PI Edge MD;  
 XX  
 DR WPI; 1998-467168/40.  
 XX  
 PT New modified pro-domain of carboxy-peptidase B - enhances expression of  
 PT co-expressed proteins for production of recombinant carboxy-peptidase or  
 PT its fusions with antibodies, used, e.g. in enzyme prodn therapy.  
 CC  
 XX Example 4; Page 59; 83pp; English.  
 XX  
 CC The primers AAV41796-V41809 were used in the expression of human  
 CC pancreatic carboxypeptidase B (CPB). The co-expression of a modified pro-  
 CC domain of CPB from a separate gene enhances recombinant expression. This  
 CC process can be used to produce recombinant CPB in eukaryotic cells, or  
 CC fusions of CPB with antibody chains. CPB is used in insulin production  
 CC and protein sequencing, while its fusions with antibody are useful in  
 CC antibody-directed enzyme prodn therapy. The Modified pro-domain  
 CC provide increased yields of recombinant CPB, possibly by protecting the C  
 CC terminus against enzymatic degradation or by increasing intracellular  
 CC trafficking  
 CC  
 SQ Sequence 23 BP; 6 A; 8 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.8%; Score 18.2; DB 1; Length 23;  
 Best Local Similarity 87.0%; Pred. No. 32;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 599 CTATGACCACTGCGAGGCTGTG 621  
 DB 23 CTGTGACCTGTGCGAGGCTGTG 1  
 XX  
 XX  
 RESULT 21  
 AAV41790/C  
 ID AAV41790 standard; DNA; 23 BP.  
 XX  
 XX AAV41790;  
 AC  
 XX 20-NOV-1998 (first entry)  
 DT  
 XX Human pancreatic carboxypeptidase B primer 679.  
 DE  
 XX ss; primer; PCR; amplification; human; pancreatic carboxypeptidase B;  
 KW insulin; protein sequencing; prodn therapy.  
 KW  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX WO9835388-A1.  
 PN  
 XX 20-AUG-1998.  
 PD  
 XX 10-FEB-1998; 98WO-GB000415.  
 PF  
 XX 14-FEB-1997; 97GB-00003104.  
 PR 18-OCT-1997; 97GB-00022003.  
 PR 29-OCT-1997; 97GB-00022727.  
 XX

PA (ZENEC) ZENEC LTD.  
 XX  
 XX Edge MD;  
 XX  
 DR WPI; 1998-467168/40.  
 XX  
 PT New modified pro-domain of carboxy-peptidase B - enhances expression of  
 PT co-expressed proteins for production of recombinant carboxy-peptidase or  
 PT its fusions with antibodies, used, e.g. in enzyme prodn therapy.  
 CC  
 XX Example 1; Page 51; 83pp; English.  
 XX  
 CC The primers AAV41785-V41794 were used in the cloning of human pancreatic  
 CC carboxypeptidase B (CPB). The co-expression of a modified pro-domain of  
 CC CPB from a separate gene enhances recombinant expression. This process  
 CC can be used to produce recombinant CPB in eukaryotic cells, or fusions of  
 CC CPB with antibody chains. CPB is used in insulin production and protein  
 CC sequencing, while its fusions with antibody are useful in antibody-  
 CC directed enzyme prodn therapy. The Modified pro-domain provide  
 CC increased yields of recombinant CPB, possibly by protecting the C-  
 CC terminus against enzymatic degradation or by increasing intracellular  
 CC trafficking  
 CC  
 SQ Sequence 23 BP; 6 A; 8 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.8%; Score 18.2; DB 1; Length 23;  
 Best Local Similarity 87.0%; Pred. No. 32;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 599 CTATGACCACTGCGAGGCTGTG 621  
 DB 23 CTGTGACCTGTGCGAGGCTGTG 1  
 XX  
 XX  
 RESULT 22  
 AAX90750  
 ID AAX90750 standard; DNA; 21 BP.  
 XX  
 XX AAX90750;  
 AC  
 XX 11-OCT-1999 (first entry)  
 DT  
 XX PCR primer 1 for 5' end of Hm2 clone.  
 DE  
 XX PCR primer; Hm2 cDNA; RT-PCR; express sequence tag; CUSAB95R; CNAMK28R;  
 KW cyclic tetrapeptide toxin; disease resistance; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9936543-A1.  
 PN  
 XX 22-JUL-1999.  
 PD  
 XX 15-JAN-1999; 99WO-US000939.  
 PF  
 XX 16-JAN-1998; 98US-0071684P.  
 PR  
 XX (PION-) PIONEER HI-BRED INT INC.  
 PA (UMOR) UNIV MISSOURI.  
 PA  
 XX Briggs SP, Johal G, Multani DS;  
 PI  
 XX WPI; 1999-444399/37.  
 DR  
 XX Maize Hm2 polynucleotides and products, useful for imparting disease  
 PT resistance against cyclic tetrapeptide toxins.  
 PT  
 XX Example 1; Page 79; 84pp; English.  
 PS  
 XX The present sequence is a PCR primer which is used with its primer pair  
 CC for Hm2 cDNA. The 5' end of the Hm2 cDNA was PCR amplified using an RT-PCR  
 CC approach. These primers were designed based on information obtained from  
 CC two Pioneer express sequence tags. These tags were CUSAB95R and CNAMK28R.

CC The polypeptide encoded by the Hm2 cDNA will degrade cyclic tetrapeptide  
 CC toxins, and confer disease resistance in transformed plants

XX Sequence 21 BP, 8 A, 1 C, 11 G, 1 T, 0 U, 0 Other;

Query Match 0.7%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 34;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1980 GGCAGGGGAGAGAGAGAG 2000

DB 1 GGAAGGGGAGAGAGAGAG 21

# RESULT 23

AB299188/c  
 ID AB299188 standard; DNA, 20 BP.

XX AB299188;

DT 17-OCT-2003 (first entry)

XX Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX antiinflammatory; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200265308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Disclosure; SEQ ID NO 14430; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP, 1 A, 11 C, 1 G, 7 T, 0 U, 0 Other;

Query Match 0.7%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 38;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 409 GCGAGGCGAGAGAGAG 427

DB 19 GAGAGGCGAGAGAGAG 1

# RESULT 24

AA92434  
 ID AA92434 standard; DNA, 20 BP.

XX AA92434;

DT 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

XX neutralising epitope; PCR primer; ss.

XX Synthetic.

XX Chlamydia pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014573.

XX 04-NOV-1998; 98US-0107078P.

XX (GIST ) GENSET.

XX Griffiths R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1511; Disclosure; 1912pp; English.

CC AA91991-97517 represent PCR primers used to amplify open reading frames  
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
 CC (see AA91990). C. pneumoniae causes respiratory disease such as  
 CC pneumonia and bronchitis and is thought to be a contributing factor in  
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
 CC frames of the C. pneumoniae genome (see AA934584- AA935879) can be used  
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
 CC nucleotide sequences can also be used as immunogenic compositions,  
 CC especially where the vector directs the expression of a neutralising  
 CC epitope of C. pneumoniae

XX Sequence 20 BP, 4 A, 6 C, 3 G, 7 T, 0 U, 0 Other;

Query Match 0.7%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1386 GACTCTTCATCAGTCTT 1402

DB 1 GACTCTTCATCAGTCTT 17

XX	AD36447	standard; DNA; 20 BP.	
XX	AD36447		
XX	AD36447		
DT	09-AUG-2002	(first entry)	
XX			
DE	Mouse L66 intron 4/exon 5 junction sequence #4.		
XX			
KM	Mouse; nuclear receptor; L66 protein; FXR-beta; physiological response;		
XX	drug screening; ds.		
XX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	intron	1..10	
FT		/*tag= a	
FT		/number= 4	
FT		/partial	
FT	exon	11..20	
FT		/*tag= b	
FT		/number= 5	
FT		/partial	
XX			
PN	W020022817-A2.		
PD			
PD	21-MAR-2002.		
XX			
PF	07-SEP-2001; 2001MO-EF010323.		
XX			
PR	16-SEP-2000; 2000EP-00120370.		
PR	14-MAY-2001; 2001EP-00111658.		
XX			
PA	(LION-) LION BIOSCIENCE AG.		
XX			
PI	Casati G, Hoefler M, Jackson D, Kranz H, Otte K, Remmel B;		
EI	Suckow U;		
DR	WPI; 2002-393967/42.		
XX			
PT	Novel mammalian nuclear receptor polypeptide, L66, useful for screening		
PT	for agents which inhibit cellular function of the polypeptide and for		
PT	construction of multiple nuclear receptor specific sequence alignments.		
XX			
XX	Disclosure; Fig 18a; 136pp; English.		
XX			
PS			
CC	The present invention relates to mammalian nuclear receptor proteins, L66		
CC	(also referred as FXR-beta) and polynucleotides encoding such proteins.		
CC	Sequences of the are useful for screening for agents which are capable of		
CC	inhibiting the cellular function of L66. They are useful for the		
CC	construction of multiple nuclear receptor specific sequence alignments		
CC	and for the construction of protein sequence alignments. L66 proteins are		
CC	useful for screening drugs for agonist and antagonist activity, for		
CC	developing antibodies for detection of L66, for screening for drugs		
CC	useful in regulating physiological responses associated with L66, in cell		
CC	free screening assays for isolating compounds which affect the activity		
CC	of L66, for in silico, i.e., computer analyses, for identifying domains		
CC	and new receptors and for modelling the 3-dimensional structure of L66.		
CC	L66 nucleic acid sequences are useful for making vectors, for determining		
CC	L66 expression levels, for transforming cells, as scientific research		
CC	tools for developing nucleic acid probes and primers and for developing		
CC	analytical tools for selectively inhibiting expression of the L66 gene to		
CC	determine physiological responses. The present DNA sequence is an intron		
CC	4/exon 5 junction sequence of mouse L66 gene		
XX			
SQ	Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;		
XX			
Query Match	0.7%; Score 17; DB 1; Length 20;		
Best Local Similarity	100.0%; Pred. No. 44;		
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX			
600	TATGACCACTGCAGG 616		
XX			

	Db	1 TATGACCGACTGCAGC 17       
	RESULT_26	
	AHA73497/c	
Xx	ID	AHA73497 standard; DNA; 20 BP.
Xx	Ac	AHA73497;
Xx	Dt	19-OCT-2001 (first entry)
Xx	Df	Human depressed growth rate protein DEGI cDNA PCR primer #1.
Xx	Dk	Human; depressed growth rate protein; DEGI; mitochondrial dysfunction;
Kw	Km	immunological disease; cancer; gene therapy; PCR primer; ss.
Xx	Os	Homo sapiens.
Xn	Pn	CN196014-A.
Xx	Pd	23-MAY-2001.
Xx	Bf	11-NOV-1999; 99CN-00119986.
Xx	Rr	11-NOV-1999; 99CN-00119986.
Pa	(SHAN--)	SHANGHAI SHENGYUAN GENE DEV CO LTD.
Xx	Mao Y,	Xie Y;
Xx	WPI;	2001-483838/53.
Xx	Noel	human growth arrestin and coding sequence thereof.
Ps	Example 3;	Page 12(Disclosure); 22pp; Chinese.
Xc	The present invention provides the protein and coding sequences of human	
Cc	depressed growth rate protein DEGI. The sequences can be used in the	
Cc	treatment of cancer, immunological diseases and diseases related to	
Cc	mitochondrial dysfunction. The present sequence is a PCR primer for the	
Cc	coding sequence of the invention	
SQ	Sequence 20 BP; 3 A; 6 C; 11 G; 0 T; 0 U; 0 Other;	
	Query Match	0.7%; Score 16.8; DB 1; Length 20;
	Best Local Similarity	90.0%; Pred.No. 47;
	Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	288 CGGGCCGCCGCTTGCCC 307 	
DB	20 CCggccgcgccgctttccc 1	
	RESULT_27	
	AHA20643	
Xx	ID	AHA20643 standard; DNA; 20 BP.
Xx	Ac	AHA20643;
Xx	Dt	13-AUG-2001 (first entry)
Xx	Df	Human telomeric repeat binding factor 2 oligonucleotide 111371.
Kw	Km	Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
Kw	Km	inhibitor; premature aging; hyperproliferative disorder; cancer;
Xx	Os	cytosolic; ss.
Xx	Hom	sapiens.
Ft	Key	Location/Qualifiers
FT	modified_base	1..20
T	/tag= b	

```

FT      /mod_base= OTHER
FT      /note= "phosphorochioate backbone"
FT      modified_base
FT      1..3
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "2-O-methoxyethyl"
FT      modified_base
FT      13..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2-O-methoxyethyl"
XX      WO200143752-A1.
XX      21-JUN-2001.
XX      14-DEC-2000; 2000WO-US033954.
XX      17-DEC-1999; 99US-00467642.
XX      (ISIS-) ISIS PHARM INC.
XX      Monia BP, Cowsett LM;
XX      WPI; 2001-398071/42.
XX      Antisense compounds targeted to nucleic acid encoding telomeric repeat
XX      binding factor 2 useful for treating conditions such as premature aging
XX      and diseases such as cancer.
XX      Claim 3; Page 80; 108bp; English.
XX      This invention describes a novel antisense compound (I) 8-30 nucleobases
XX      in length targeted to a polynucleotide encoding human telomeric repeat
XX      binding factor 2 (II) which specifically hybridizes with, and inhibits
XX      the expression of (II). (I) is useful for treating a human having a
XX      disease or condition associated with (II) such as premature aging or a
XX      hyperproliferative disorder especially cancer, by inhibiting the
XX      expression of (II) in human cells or tissues. (I) is useful for
XX      diagnostics, therapeutic, prophylaxis and as research reagents and kits.
XX      The products of the invention have cytostatic activity. This sequence
XX      represents an antisense oligonucleotide used to illustrate the method of
XX      the invention
XX      Sequence 20 BP; 0 A; 11 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match      0.7%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      283 CCGCGCGCGCGCGCGCTT 302
DB      1 CCGTCCGCGCGCGCGCTT 20

```

## RESULT 28

AAZ75813

ID AAZ75813 standard; DNA; 21 BP.

AAZ75813;

10-SEP-2001 (first entry)

Human biallelic marker downstream amplification primer SEQ ID NO:10169.

Human genome; biallelic marker; high density disequilibrium map;  
 genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 haplotyping; hybridisation; identification; characterisation;  
 amplification; single nucleotide polymorphism; SNP; PCR primer;  
 diagnosis; ss.

Homo sapiens.  
 WO954500-A2.

```

XX      28-OCT-1999.
XX      21-APR-1999; 99WO-IB000822.
XX      21-APR-1998; 98US-0082614P.
XX      23-NOV-1998; 98US-0109732P.
XX      (GEST ) GENSET.
XX      Cohen D, Blumenfeld M, Chumakov I;
XX      WPI; 2000-013267/01.
XX      Novel biallelic markers used to construct a high density disequilibrium
XX      map of the human genome.
XX      Claim 9; Page 2398; 2745bp; English.
XX      AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX      invention, which contain a polymorphic base at position 24 of their
XX      nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX      primers for the biallelic markers. The biallelic markers of the invention
XX      have a variety of uses; they can be used for high density mapping of the
XX      human genome, and in complex association studies and haplotyping studies
XX      which are useful in determining the genetic basis for disease states.
XX      CC Identification of the targets for the development of pharmaceutical
XX      agents and diagnostic methods, as well as the characterisation of the
XX      differential efficacious responses to and side effects from
XX      CC pharmaceutical agents acting on a disease as well as other treatment.
XX      N.B. The SEQ ID NOS 2832, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX      3367, are not actually given a sequence in the Sequence Listing from the
XX      present invention
XX      Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match      0.7%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1037 CAGGGAATTCATTCCTCTT 1056
DB      1 CAGGACTTCATTCATCTT 20

```

## RESULT 29

AAT00061

ID AAT00061 standard; DNA; 22 BP.

AAT00061;

02-JUL-1996 (first entry)

Hepatitis GB virus (HGBV) clone 18 PCR primer.

Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A;  
 non-B; non-C; non-D; non-E; clone; tamara; infected plasma;  
 lambda phage; cDNA library; PCR primer; ss.

Synthetic.

WO9521922-A2.

17-AUG-1995.

14-FEB-1995; 95WO-US002118.

14-FEB-1994; 94US-00196030.

13-MAY-1994; 94US-00242654.

29-JUL-1994; 94US-00283314.

23-NOV-1994; 94US-00344185.

23-NOV-1994; 94US-00344190.

```

PR 27-JAN-1995; 95US-00344557.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Simons JN, Pilot-Matias TJ, Dawson GJ, Schlauder GG, Desai SM;
PI Leary TP, Muerhoff AS, Erker JC, Buljk SL, Mushahwar IK;
XX WPI; 1995-293133/38.
XX
XX Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for
PT diagnosis and therapy of hepatitis GB virus.
XX
XX Example 6; Page 267; 661pp; English.
XX
XX Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected
CC tamatin plasma, using standard procedures, was used to prepare a lambda
CC phage HGBV cDNA library. cDNA clones rescued from the lambda phage and
CC amplified using the PCR primers AAT0053-66, were searched against a
CC sequence database and found to be unique HGBV sequences. Reagents which
CC comprise the HGBV DNA, or its protein prods. can be used for the
CC diagnosis, therapy or in a vaccine to prevent HGBV infection
XX
XX Sequence 22 BP; 7 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
SO
Query Match 0.7%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 834 TCTTGACATGACATCTTC 853
DB 3 TCTTGACATGACATCTTC 22
RESULT 30
AAAS5307
ID AAAS5307 standard; DNA; 22 BP.
XX
XX AAAS5307;
AC
XX 06-AUG-2003 (revised)
DT 30-AUG-2003 (first entry)
XX
XX Hepatitis GB virus PCR primer SEQ ID NO:95.
DE
XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
KW detection; characterisation; hepatitis; PCR primer; ss.
XX
XX Hepatitis GB virus.
OS
XX US6051374-A.
PN
XX 18-APR-2000.
PD
XX
XX 07-JUN-1995; 95US-00488445.
PF
XX
XX 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 30-JAN-1995; 95US-00377557.
XX
XX (ABBO ) ABBOTT LAB.
PA
XX Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buljk SL,
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX WPI; 2000-338307/29.
XX
XX Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the HGBV
PT polynucleotide probe and detecting the complex that contains target HGBV.
XX

```

```

PS Example 6; Col 255; 369pp; English.
XX
XX The present invention describe a method for detecting target hepatitis GB
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
CC containing HGBV. The method involves reacting (T) with a HGBV
CC polynucleotide probe (1) containing 15 contiguous nucleotides, and which
CC selectively hybridises to the HGBV genome or its full complement, and
CC detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid in
CC the test sample suspected of containing HGBV and for characterisation of
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
CC AAAS5270 to AAAS5489 and AAB08985 to AAB09480 represent nucleotide and
CC protein sequences used in the exemplification of the present invention.
XX
XX Sequence 22 BP; 7 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
SO
Query Match 0.7%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 834 TCTTGACATGACATCTTC 853
DB 3 TCTTGACATGACATCTTC 22
RESULT 31
ABZ11019
ID ABZ11019 standard; DNA; 18 BP.
XX
XX ABZ11019;
AC
XX 16-JAN-2003 (first entry)
DT
XX
XX Haematopoietic cell proliferation disorder related oligonucleotide #1159.
DE
XX
XX Human, haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200277272-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002MO-EP003401.
PF
XX
XX 26-MAR-2001; 2001US-0278333P.
PR
XX
XX (EPig-) EPIDENOMICS AG.
PA
XX
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX WPI; 2003-018942/01.
XX
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 44; 117pp; English.
XX
XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG

```

CC dinucleotides within the target nucleic acid. AB209861 to AB21118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used, for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 CC  
 SQ Sequence 18 BP; 1 A; 1 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 39 GTGTAGGTCGGCTTGTT 56  
 1 GTGTAGGTCGGCTTGTT 18

OY 39 GTGTAGGTCGGCTTGTT 56  
 1 GTGTAGGTCGGCTTGTT 18

Db

CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB21118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used, for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 CC  
 SQ Sequence 18 BP; 1 A; 1 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 39 GTGTAGGTCGGCTTGTT 56  
 1 GTGTAGGTCGGCTTGTT 18

Db

RESULT 32  
 AB210445  
 ID AB210445 standard; DNA; 18 BP.

RESULT 33  
 AB211021/C  
 ID AB211021 standard; DNA; 18 BP.

AC AB210445;

AC AB211021;

DT 16-JAN-2003 (first entry)

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related oligonucleotide #585.

DE Haematopoietic cell proliferation disorder related oligonucleotide #1161.

KW Human; haematopoietic cell proliferation disorder; cytostatic;

KW Human; haematopoietic cell proliferation disorder; cytostatic;

KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KM cytosine methylation state; probe; primer; ss.

KM cytosine methylation state; probe; primer; ss.

OS Homo sapiens.

OS Homo sapiens.

OS Synthetic.

OS Synthetic.

PN WO200277272-A2.

PN WO200277272-A2.

PD 03-OCT-2002.

PD 03-OCT-2002.

PF 26-MAR-2002; 2002WO-EP003401.

PF 26-MAR-2002; 2002WO-EP003401.

PR 26-MAR-2001; 2001US-0278333P.

PR 26-MAR-2001; 2001US-0278333P.

XX (EPIC-) EPIGENOMICS AG.

XX (EPIC-) EPIGENOMICS AG.

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

XX PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;

XX PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;

XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;

XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;

XX PI Schwope I, Ziebarth H;

XX PI Schwope I, Ziebarth H;

XX WPI; 2003-018942/01.

XX WPI; 2003-018942/01.

XX Detecting and differentiating between haematopoietic cell proliferative

XX Detecting and differentiating between haematopoietic cell proliferative

XX PT disorders, comprises contacting a target nucleic acid with a reagent that

XX PT disorders, comprises contacting a target nucleic acid with a reagent that

XX PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX Claim 15; SEQ ID NO 585; 117PP; English.

XX Claim 15; Page 76; 117PP; English.

XX The present invention describes a method for detecting and

XX The present invention describes a method for detecting and

XX CC differentiating between haematopoietic cell proliferative disorders

XX CC differentiating between haematopoietic cell proliferative disorders

XX CC associated with at least 1 gene and/or their regulatory regions in a

XX CC associated with at least 1 gene and/or their regulatory regions in a

XX CC subject. The method comprises contacting a target nucleic acid in a

XX CC subject. The method comprises contacting a target nucleic acid in a

XX CC biological sample obtained from the subject with at least 1 reagent,

XX CC biological sample obtained from the subject with at least 1 reagent,

CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB21118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclases, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 CC  
 XX Sequence 18 BP; 8 A; 8 C; 1 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.7%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 39 GTGTAGTCGCGCTTGCTT 56  
 18 GTGTAGTCGCGCTTGCTT 1  
 DB  
 RESULT 34  
 ADE84341  
 ID ADE84341 standard; DNA; 18 BP.  
 XX  
 AC ADE84341;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human lymphoid cell proliferative disorder gene Cpg analysis oligo #47.  
 XX  
 KW Lymphoid cell proliferative disorder; methylation;  
 KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
 KW diffuse large B-cell lymphoma; mantle cell lymphoma;  
 KW chronic lymphocytic leukaemia; small lymphocytic lymphoma;  
 KW follicular lymphoma; diagnosis; prognosis; primer; ss.  
 XX  
 OS Homo sapiens;  
 XX  
 PN WO2003044226-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-EP013265.  
 XX  
 PR 23-NOV-2001; 2001DE-01057491.  
 XX  
 PR 28-DEC-2001; 2001DE-01064501.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;  
 XX  
 DR WPI; 2003-457621/43.  
 XX  
 PT Detecting and differentiating between lymphoid cell proliferative  
 PT disorders comprises contacting a target nucleic acid with at least one  
 PT reagent that distinguishes between methylated and non-methylated CpG  
 PT dinucleotides.  
 XX  
 PS Claim 30; SEQ ID NO 337; 448bp; English.  
 CC The invention relates to a method of detecting and differentiating  
 CC between lymphoid cell proliferative disorders associated with at least  
 CC one gene and/or their regulatory regions in a subject by contacting a

CC target nucleic acid in a biological sample obtained from the subject with  
 CC at least one reagent or series of reagents that distinguish between  
 CC methylated and non-methylated CpG dinucleotides within the target nucleic  
 CC acid. The genes and/or their regulatory regions are preferably selected  
 CC from MDRL, CSNK2B, EGFR, AR, CDK4, RB2, CCR25A, GPR beta, MPOD1, CDH3,  
 CC MYCL1, ELK1, ABL1, APC, BCL2, CHL1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,  
 CC GSTRP1, HIC-1, MGMT, MSH1, MOS, MTC, PTEN, RB2, TGFBR2, TP73, CDKN1C,  
 CC GSK3beta, ESR1, APAF1, BAX1, BAX or HOXA5. Oligomers, peptide nucleic  
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences  
 CC of the genes are useful for detecting the methylation state of all the  
 CC CpG dinucleotides within one or more the sequences, or their complements,  
 CC for determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs), and for differentiating at least two of the medical  
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
 CC chronic lymphocytic leukaemia, small lymphocytic lymphoma and follicular  
 CC lymphoma. They are also useful for detecting of a predisposition to,  
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or  
 CC monitoring of lymphoid cell proliferative disorder. This sequence  
 CC represents an oligonucleotide used to analyse of CpG positions within the  
 CC above mentioned genes.  
 CC  
 XX Sequence 18 BP; 1 A; 1 C; 8 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.7%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 39 GTGTAGTCGCGCTTGCTT 56  
 1 GTGTAGTCGCGCTTGCTT 18  
 DB  
 RESULT 35  
 AA297871/C  
 ID AA297871 standard; DNA; 19 BP.  
 XX  
 AC AA297871;  
 XX  
 DT 15-SEP-2003 (revised)  
 XX  
 DT 26-APR-2000 (first entry)  
 XX  
 DE HIV-1 protease gene probe SEQ ID NO:361.  
 XX  
 KW Human immunodeficiency virus; HIV; protease; probe; detection;  
 KW drug selected mutation; hybridisation; genotyping; infection;  
 KW drug resistance; ss.  
 XX  
 OS Homo immunodeficiency virus 1.  
 XX  
 PN WO967428-A2.  
 XX  
 PD 29-DEC-1999.  
 XX  
 PF 22-JUN-1999; 99WC-EP004317.  
 XX  
 PR 24-JUN-1998; 98EP-00870143.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Stuyver L;  
 XX  
 DR WPI; 2000-147219/13.  
 XX  
 PT Detection of drug-selected mutations in the HIV protease gene used to  
 PT treat HIV infections.  
 XX  
 PS Claim 3; Page 42; 76pp; English.  
 CC The present invention describes the detection of drug-selected mutations  
 CC in the HIV protease gene. The method of detection allows the simultaneous  
 CC characterisation of a range of codons involved in drug resistance using  
 CC sets of probes optimised to function together in a reverse-hybridisation  
 CC assay. AA297517 to AA297997 represent specifically claimed probes for use

in the assay, and AA297479 to AA297501 represent specifically claimed HIV protease gene polymorphic nucleotide sequences. AA297502 to AA297515, and AA298004 to AA298007, represent PCR primers for the HIV protease gene. CC and AA297516 represents an HIV protease probe used in an example from the present invention. The method, probes and primers can be used for the detection of drug-selected mutations in the HIV protease gene. The method allows the simultaneous characterisation of a range of codons involved in drug resistance. The method may also be used for HIV protease genotyping assays. The probes are able to discriminate between wild type and mutated protease sequences. The method allows rapid and reliable detection of drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS field)

Sequence 19 BP; 6 A; 3 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.7%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

683 CCTCCGAGTCAACAGATT 700  
19 CCTCTGAGTCAACAGATT 2

RESULT 36  
AAT58092/C  
ID AAT58092 standard; DNA; 20 BP.

24-OCT-1997 (first entry)  
Human heat shock protein 70 primer 70-3R (1755-1736).  
Human; heat shock protein 70; HSP70; primer; PCR; detection;  
intracellular; abnormal transcription; acute; chronic; sustained; stress;  
polymerase chain reaction; amplification; ss.

Synthetic.

JP08322577-A.

10-DEC-1996.

01-JUN-1995; 95JP-00158581.

01-JUN-1995; 95JP-00158581.

(HOKI-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 1997-081088/08.

Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific  
PT primer or probe, used in detection of human acute and chronic sustained  
stress load.

Disclosure; Page 4; 13pp; Japanese.

The present sequence is a primer for the PCR amplification of a human  
heat shock protein 70 (HSP70) cDNA coding sequence. The HSP70 gene is  
located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and  
probes based on the HSP70 cDNA coding sequence can be used to detect the  
abnormal transcription of intracellular HSP70 mRNA in human acute and  
chronic sustained stress load

Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 54;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1313 GAAGTACAAAGAGAGA 1330

Db 18 GAAGTACAAAGAGAGA 1  
AA297870/C  
ID AA297870 standard; DNA; 20 BP.

AA297870;  
15-SEP-2003 (revised)  
26-APR-2000 (first entry)  
HIV-1 protease gene probe SEQ ID NO:360.

Human immunodeficiency virus; HIV; protease; probe; detection;  
drug selected mutation; hybridisation; genotyping; infection;  
drug resistance; ss.

Human immunodeficiency virus 1.

WO9967428-A2.

29-DEC-1999.

22-JUN-1999; 99WO-EP004317.

24-JUN-1998; 98EP-00870143.

(INNO-) INNOGENETICS NV.

Stuyver L;

WPI; 2000-147219/13.

Detection of drug-selected mutations in the HIV protease gene used to  
treat HIV infections.

Claim 3; Page 42; 76pp; English.

The present invention describes the detection of drug-selected mutations  
in the HIV protease gene. The method of detection allows the simultaneous  
characterisation of a range of codons involved in drug resistance using  
sets of probes optimised to function together in a reverse-hybridisation  
assay. AA297517 to AA297997 represent specifically claimed HIV  
in the assay, and AA297479 to AA297501 represent specifically claimed HIV  
protease gene polymorphic nucleotide sequences. AA297502 to AA297515, and  
AA298004 to AA298007, represent PCR primers for the HIV protease gene,  
and AA297516 represents an HIV protease probe used in an example from the  
present invention. The method, probes and primers can be used for the  
detection of drug-selected mutations in the HIV protease gene. The method  
allows the simultaneous characterisation of a range of codons involved in  
drug resistance. The method may also be used for HIV protease genotyping  
assays. The probes are able to discriminate between wild type and mutated  
protease sequences. The method allows rapid and reliable detection of  
drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS  
field)

Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 54;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

683 CCTCCGAGTCAACAGATT 700  
20 CCTCTGAGTCAACAGATT 3

RESULT 38  
AAA15628/C  
ID AAA15628 standard; DNA; 20 BP.

AAA15628;

```

XX 31-JUL-2000 (first entry)
DT PCR primer 108c for heat shock protein LHSPP70/SHSPP70 amplification.
DE
XX Human, heat shock protein, HSP70; chromosome 6p21.3-22; stress;
KM chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome; PCR primer; ss.
XX
XX Synthetic.
OS
XX JP2000069999-A.
PN
XX 07-MAR-2000.
PD
XX 01-JUN-1995; 99JP-00257146.
PF
XX 01-JUN-1995; 95JP-00158581.
PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
PA
XX WPI; 2000-264458/23.
DR
XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
PT continuous load of stress in a human being and its application.
PS
XX Disclosure; Page 3; 11pp; Japanese.
XX
XX This sequence represents a PCR primer used to amplify the human
CC LHSPP70/SHSPP70 heat shock protein nucleotide sequences. Human heat shock
CC proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention
CC relates to the abnormal transcription of intracellular HSP70mRNA under
CC acute and chronic stress load in a human. The abnormal transcription of
CC HSP70 can be used in the improvement of stress and response and diagnosis
CC of stress diseases including rheumatism, schizophrenia, depression and
CC nephrotic syndrome
XX
SQ Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1313 GAAGTACAAAGCGAGGA 1330
Db 18 GAAGTACAAAGCGAGGA 1
RESULT 39
AA297872/C
ID AA297872 standard; DNA; 21 BP.
XX
XX AA297872;
AC
XX 15-SEP-2003 (revised)
DT 26-APR-2000 (first entry)
DE HIV-1 protease gene probe SEQ ID NO:362.
XX
XX Human immunodeficiency virus; HIV; protease; probe; detection;
KM drug selected mutation; hybridisation; genotyping; infection;
KW drug resistance; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX WO9967428-A2.
PN
XX 29-DEC-1999.
PD
XX 22-JUN-1999; 99WO-EP004317.
PF
XX 24-JUN-1998; 98EP-00870143.
PR
XX
XX

```

```

PA (INNO-) INNOBENTICS NV.
XX
XX Stuyver L;
PI
XX WPI; 2000-147216/13.
DR
XX Detection of drug-selected mutations in the HIV protease gene used to
PT treat HIV infections.
XX
XX Claim 3; Page 42; 76pp; English.
XX
XX The present invention describes the detection of drug-selected mutations
CC in the HIV protease gene. The method of detection allows the simultaneous
CC characterisation of a range of codons involved in drug resistance using
CC sets of probes optimised to function together in a reverse-hybridisation
CC assay. AA297517 to AA297997 represent specifically claimed probes for use
CC in the assay, and AA297479 to AA297501 represent specifically claimed HIV
CC protease gene polymorphic nucleotide sequences. AA297502 to AA297515, and
CC AA298004 to AA298007, represent PCR primers for the HIV protease gene,
CC and AA297516 represents an HIV protease probe used in an example from the
CC present invention. The method, probes and primers can be used for the
CC detection of drug-selected mutations in the HIV protease gene. The method
CC allows the simultaneous characterisation of a range of codons involved in
CC drug resistance. The method may also be used for HIV protease genotyping
CC assays. The probes are able to discriminate between wild type and mutated
CC protease sequences. The method allows rapid and reliable detection of
CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 21 BP; 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 683 CCTCCGAGTCAACAGATT 700
Db 21 CCTCTGAGTCAACAGATT 4
RESULT 40
AAH62400
ID AAH62400 standard; DNA; 21 BP.
XX
XX AAH62400;
AC
XX 12-SEP-2001 (first entry)
DT
DE Inwardly rectifying K+ channel polymorphism containing DNA fragment #301.
XX
XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KM heart disease; paternity testing; forensic science; ds.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Variation replace(11,A)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200138576-A2.
PN
XX 31-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-US031639.
PF
XX 24-NOV-1999; 99US-0167334P.
PR
XX (WHD) WHITEHEAD INST BIOLOGICAL RES.
PA
XX Cargill M, Ireland JS, Lander ES;
PI
XX WPI; 2001-367705/38.
DR

```

XX New nucleic acid segments of the human genome, particularly from genes  
PT including polymorphic sites for phenotype correlation, forensics,  
PT paternity testing, medicine and genetic analysis.  
PS Claim 1, Page 54; 80pp; English.  
XX  
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
CC contain single nucleotide polymorphisms (SNPs). A method is included in  
CC the invention for analysing a nucleic acid sample, which consists of  
CC determining the base occupying any one of the polymorphic sites given in  
CC the SNP containing sequences. The nucleotide sequences can be used in the  
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
CC diseases, diseases of the cardiovascular system, and infection by  
CC microorganisms. The oligonucleotides are also useful in the manufacture  
CC of a medicament for the treatment or prophylaxis of the diseases, and as  
CC a pharmaceutical. SNP containing oligonucleotides are useful in  
CC applications such as phenotype correlation, forensics, paternity testing,  
CC medicine and genetic analysis  
CC  
SQ Sequence 21 BP; 1 A; 9 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 16.4; DB 1; Length 21;  
XX Best Local Similarity 94.4%; Pred. No. 56;  
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1104 TGGCTTGTGGACCTTCT 1121  
Db 4 TGGCTTGTGGACCTTCT 21  
XX  
XX RESULT 41  
XX AAH88914  
XX ID AAH88914 standard; DNA; 21 BP.  
XX AC AAH88914;  
XX DT 27-FEB-2002 (first entry)  
XX DE Human polymorphic oligonucleotide AL031274 fragment #8.  
XX  
XX Human; single nucleotide polymorphic; SNP; forensic science;  
XX paternity testing; phenotypic trait; genetic mapping; animal breeding;  
XX plant breeding; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Variation replace(11,a)  
XX /tag=a  
XX /standard\_name="single nucleotide polymorphism"  
XX  
XX WO200134840-A2.  
XX  
XX 17-MAY-2001.  
XX  
XX 10-NOV-2000; 2000WO-US030766.  
XX  
XX 10-NOV-1999; 99US-0164596P.  
XX  
XX (GLAX) GLAXO GROUP LTD.  
XX (AFHY-) AFFYMETRIX INC.  
XX  
XX Au K, Chen J, Patil N, Thomas D;  
XX  
XX WPI, 2001-335945/35.  
XX  
XX New polymorphic sites derived from the human genome are useful to  
XX determine sites correlating with phenotypic traits, particularly disease,  
XX and also in forensics and paternity testing.  
XX  
XX Claim 38; Page 9; 43pp; English.  
XX

CC The present invention relates to human oligonucleotides comprising a  
CC single nucleotide polymorphic site (SNP: AAH88914-AAH89219). The present  
CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
CC forensics, paternity testing, correlation of polymorphisms with  
CC phenotypic traits, genetic mapping of phenotypic traits and marker  
CC assisted breeding of animals and crop plants  
XX  
XX SQ Sequence 21 BP; 7 A; 4 C; 9 G; 1 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 16.4; DB 1; Length 21;  
XX Best Local Similarity 94.4%; Pred. No. 56;  
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1976 CCTGGCCAGGAGAGAGA 1993  
Db 3 CCTGGCCAGGAGAGAGA 20  
XX  
XX RESULT 42  
XX AAT96894  
XX ID AAT96894 standard; DNA; 21 BP.  
XX AC AAT96894;  
XX DT 27-APR-1998 (first entry)  
XX DE Human pRB2/p130 tumour suppressor gene exon 13(rev) PCR primer.  
XX  
XX Retinoblastoma susceptibility gene; pRB2; p130; pRB2/p130 gene;  
XX cell cycle; tumour suppressor gene; cancer; molecular marker; diagnosis;  
XX prognosis; predisposition; endometrial carcinoma; ovary cancer;  
XX lung squamous cell carcinoma; lung adenocarcinoma; human; primer; PCR;  
XX ss.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX PN WO9738125-A1.  
XX PD 16-OCT-1997.  
XX  
XX 03-APR-1997; 97WO-US005598.  
XX  
XX 05-APR-1996; 96US-0014943P.  
XX 05-JUN-1996; 96US-0019372P.  
XX 21-JUN-1996; 96US-0020196P.  
XX 03-MAR-1997; 97US-0039532P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Giordano A, Baldi A;  
XX  
XX WPI; 1997-512731/47.  
XX  
XX Tumour suppressor pRB2/p130 gene intron and promoter sequences - used for  
XX the diagnosis and prognosis of cancer and predicting pre-disposition to  
XX cancer.  
XX  
XX Claim 85; Page 69; 169pp; English.  
XX  
XX A PCR primer pair (AAT96893 and AAT96894) is designed to amplify exon 13  
XX of the human pRB2/p130 tumour suppressor gene. The size of the PCR  
XX product is 378 bp. The relative level of pRB2/p130 expression correlates  
XX with the presence of cancer, tumour grade, and patient prognosis. Claimed  
XX methods for identifying polymorphisms and mutations in an exon of the  
XX pRB2/p130 gene use claimed amplification primers (see AAT96853-96) that  
XX are complementary to the pRB2/p130 gene promoter region (see AAT96831-51)  
XX 3' non-coding region, or to a segment of an intron (see AAT96852). The  
XX exclusive of the splice signal dinucleotides of the intron. The methods  
XX can be used for the diagnosis and prognosis of cancer and for prediction  
XX of predisposition to cancer, particularly endometrial carcinoma, ovarian  
XX cancer, a squamous cell carcinoma of the lung, or adenocarcinoma of the  
XX lung  
XX

XX Sequence 21 BP; 6 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2161 TTTAACTTACCTCCCACTC 2161  
DB 1 TTTAACTTACCTCCCACTC 21

RESULT 43  
AAT93175/C  
ID AAT93175 standard; DNA; 21 BP.  
XX AAT93175;  
AC AAT93175;

DT 08-MAY-1998 (first entry)

DE PCR analysis of a novel recombinant retroviral vector using primer 2.

KW Recombinant retroviral vector; replication defective; gene therapy;  
leukaemia; haematopoietic; PCR primer; ss.

OS Synthetic.

OS Moloney murine leukemia virus.

PN W09742336-A1.

PD 13-NOV-1997.

PF 06-MAY-1997; 97WO-AU000280.

PR 06-MAY-1996; 96AU-00009701.

XX (UNIX) UNISEARCH LTD.

PA Mackenzie KL, Symonds GP;

PI WPI; 1997-558991/51.

PT Replication defective recombinant retroviral vector - useful in gene  
therapy e.g. of leukaemia.

PS Disclosure; Page 7; 48pp; English.

CC This provirus specific primer is used for the PCR analysis of a novel  
CC recombinant retroviral vector. The novel recombinant retroviral vector of  
CC this invention is replication defective and includes a long terminal  
CC repeat (LTR) for expressing a heterologous nucleic acid. The vector does  
CC not contain a heterologous promoter or a heterologous gene that imparts  
CC antibiotic or other drug resistance. The recombinant retroviral vector  
CC includes sequences from Moloney murine leukaemia virus, particularly  
CC those that encode a packaging region and/or the gag protein, or parts of  
CC them. Specifically, the vector is LK and may include a gene for N-ras;  
CC p53 (wild-type or mutant), v-myc or WAF1. The recombinant retroviral  
CC vectors are used to infect mammalian cells, specifically haematopoietic  
CC cells or their progenitors, from human, rat or mouse, to introduce the  
CC heterologous nucleic acid. The introduced gene is, particularly a gene  
CC involved in tumorigenesis or its reversion. Gene transfer is used to  
CC study tumorigenesis or therapeutically (e.g. in cases of leukaemia),  
CC where the heterologous nucleic acid is a tumour suppressor or antisense  
CC sequence. The recombinant retroviral vectors stably integrate into target  
CC cells in vivo resulting in reliable, long-term expression of the gene

XX Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 60;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2387 ACACAGAAATGCTGCGCCA 2407

DB 21 ACACAGATAAGTGTGCGCCA 1

RESULT 44  
AAT93179/C  
ID AAT93179 standard; DNA; 21 BP.

XX AAT93179;

DT 08-MAY-1998 (first entry)

DE PCR analysis of a novel recombinant retroviral vector using primer 6.

KW Recombinant retroviral vector; replication defective; gene therapy;  
leukaemia; haematopoietic; PCR primer; ss.

OS Synthetic.

OS Moloney murine leukemia virus.

PN W09742336-A1.

PD 13-NOV-1997.

PF 06-MAY-1997; 97WO-AU000280.

PR 06-MAY-1996; 96AU-00009701.

XX (UNIX) UNISEARCH LTD.

PA Mackenzie KL, Symonds GP;

PI WPI; 1997-558991/51.

PT Replication defective recombinant retroviral vector - useful in gene  
therapy e.g. of leukaemia.

PS Disclosure; Page 7; 48pp; English.

CC This primer is used for the PCR analysis of a novel recombinant  
CC retroviral vector. The novel recombinant retroviral vector of this  
CC invention is replication defective and includes a long terminal repeat  
CC (LTR) for expressing a heterologous nucleic acid. The vector does not  
CC contain a heterologous promoter or a heterologous gene that imparts  
CC antibiotic or other drug resistance. The recombinant retroviral vector  
CC includes sequences from Moloney murine leukaemia virus, particularly  
CC those that encode a packaging region and/or the gag protein, or parts of  
CC them. Specifically, the vector is LK and may include a gene for N-ras;  
CC p53 (wild-type or mutant), v-myc or WAF1. The recombinant retroviral  
CC vectors are used to infect mammalian cells, specifically haematopoietic  
CC cells or their progenitors, from human, rat or mouse, to introduce the  
CC heterologous nucleic acid. The introduced gene is, particularly a gene  
CC involved in tumorigenesis or its reversion. Gene transfer is used to  
CC study tumorigenesis or therapeutically (e.g. in cases of leukaemia),  
CC where the heterologous nucleic acid is a tumour suppressor or antisense  
CC sequence. The recombinant retroviral vectors stably integrate into target  
CC cells in vivo resulting in reliable, long-term expression of the gene

XX Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2387 ACACAGAAATGCTGCGCCA 2407  
DB 21 ACACAGATAAGTGTGCGCCA 1

RESULT 45

AAZ26629

XX AAZ26629 standard; DNA; 21 BP.

AA226629;  
 30-NOV-1999 (first entry)  
 Human polymorphic region 818.  
 polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
 cell viability; loss of heterozygosity; precancerous condition; ASI;  
 allele specific inhibitor; somatic cell; diagnosis; prevention;  
 atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
 dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
 graft versus host disease; malignant cell removal; bone marrow; ss.  
 Homo sapiens.  
 WO9841648-A2.  
 24-SEP-1998.  
 19-MAR-1998; 98WO-US005419.  
 20-MAR-1997; 97US-0041057P.  
 (VARI-) VARIAGENICS INC.  
 Housman D, Ledley FD, Stanton VP;  
 WPI; 1998-521232/44.  
 Identifying target genes for allele-specific drugs - used for diagnosis,  
 prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 dysplastic lesions, endometriosis or graft versus host disease.  
 Disclosure: Fig 7; 605pp; English.  
 This invention describes a novel method for identifying an inhibitor  
 potentially useful for treatment of cancer, where the inhibitor is active  
 on a gene vital for cell growth or viability, and where the gene is  
 subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 used for preventing the development of cancer in a patient having a  
 precancerous condition by administering to the patient a first allele  
 specific inhibitor (ASI) targeted to an allele of a first essential gene  
 present in cells of the precancerous condition, where the normal somatic  
 cells of the patient are heterozygous for the first gene, the inhibitor  
 is active on at least one but less than all allelic forms of the gene  
 present in a population and targets only one allelic form present in the  
 normal somatic cells, and the first gene. The products and methods can be  
 used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 graft versus host disease. The method can also be used to remove  
 malignant cells from bone marrow transplants. AA25812-Z26825 represent  
 human polymorphic sites described in the method of the invention  
 Sequence 21 BP; 8 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1315 AGTACAAAGAGGAGAGAGC 1335  
 1 ATTACGATGAGGAGAGAGC 21

Db 1  
 1315 AGTACAAAGAGGAGAGAGC 1335  
 1 ATTACGATGAGGAGAGAGC 21

RESULT 46  
 ADE34531/C  
 ID ADE34531 standard; DNA; 21 BP.  
 AC ADE34531;  
 XX 29-JAN-2004 (first entry)  
 DT XX

Human G-protein coupled receptor related primer #SEQ ID 151.  
 Cytostatic; antiinflammatory; hepatocarcinoma; nephrotropic; dermatological;  
 antiarrhythmic; antidiabetic; hypotensive; antitumor;  
 antileukemic; antiatherosclerotic; neurotropic; neuroprotective; anorectic;  
 immunomodulator; uterotropic; antiinfectivity; G-protein coupled receptor;  
 GPCR; GPCR185; GPCR186; GPCR187; GPCR189; GPCR222; GPCR223;  
 hepatitis; nephritis; dermatitis; pancreatitis; rheumatoid arthritis;  
 osteoarthritis; atopic dermatitis; asthma; diabetes; hypertension;  
 inflammatory bowel disease; gastric ulcer; arteriosclerosis;  
 hyperlipemia; Alzheimer's disease; dementia; obesity; pulmonary fibrosis;  
 renal fibrosis; immune deficiency; infertility; urinary blockage; cancer;  
 PCR; primer; ss.  
 Homo sapiens.  
 WO2003078632-A1.  
 25-SEP-2003.  
 14-MAR-2003; 2003WO-JP003050.  
 15-MAR-2002; 2002JP-00071567.  
 14-MAY-2002; 2002JP-00138013.  
 28-FEB-2003; 2003JP-00054663.  
 (NISB) JAPAN TOBACCO INC.  
 Watanabe H, Nozaki Y;  
 WPI; 2003-722435/68.  
 G-protein coupled receptor proteins, genes encoding them and antibodies  
 recognizing them for treatment and diagnosis of cancer, inflammatory and  
 gastrointestinal disorders.  
 Example; SEQ ID NO 151; 274pp; Japanese.  
 The invention relates to G-protein coupled receptor proteins of human  
 origin. These proteins include GPCR185, GPCR186, GPCR187, GPCR189,  
 GPCR189, GPCR222 and GPCR223. Proteins of the invention are used in the  
 treatment and prevention of diseases associated with inflammation,  
 angiogenesis and tissue neogenesis, including hepatitis, nephritis,  
 dermatitis, pancreatitis, rheumatoid arthritis, osteoarthritis, atopic  
 dermatitis, asthma, diabetes, hypertension, inflammatory bowel disease,  
 gastric ulcer, arteriosclerosis, hyperlipemia, Alzheimer's disease,  
 dementia, obesity, pulmonary fibrosis, renal fibrosis, immune deficiency,  
 infertility, urinary blockage and cancer (such as cancer of the brain,  
 neck, tongue, lung, breast, pancreas, stomach, colon, duodenum, prostate,  
 bladder, ovary, womb or rectum). Primers of the invention are devised and  
 synthesized based on G-protein coupled receptor consensus sequences and  
 used for 5'-RACE (rapid amplification of cDNA ends) and 3'-RACE  
 amplification of human cDNA derived from adrenal and visual cortex RNA.  
 Sequences given in ADE34534-ADE34533 represent human G-protein coupled  
 receptor proteins, genes encoding them, and primers for the amplification  
 of these sequences.  
 Sequence 21 BP; 4 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1763 AGAGAGTCCCGCATGTGCC 1783  
 21 AGAGAGTCCCGCATGTGCC 1

Db 1  
 1763 AGAGAGTCCCGCATGTGCC 1783  
 21 AGAGAGTCCCGCATGTGCC 1

RESULT 47  
 AA236455/C  
 ID AA236455 standard; DNA; 20 BP.  
 AC AA236455;  
 XX

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XX 22-FEB-2000 (first entry)
XX PCR primer 9BP-1 R4 used to amplify a 509 bp fragment of MMS2 cDNA.
DE
XX
XX Human; MMS2; MMS2, PDZ domain; tumour suppressor; tyrosine phosphatase;
XX scalding protein; cancer; PCR primer; ss.
OS Synthetic.
OS Homo sapiens.
XX
XX WO958548-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-US00969.
XX
XX 08-MAY-1998; 98US-0084740P.
XX
XX (MRI-) MYRIAD GENETICS INC.
XX
XX Bartel PL, Tavtigian SV;
XX
XX WPI; 2000-053077/04.
XX
XX Nucleic acids and polypeptides representing human MMS2, useful for
XX detecting, diagnosing a predisposition to, and treating cancer.
XX
XX Example 1; Page 50; 112pp; English.
XX
XX PCR primers AA236454-55 were used to amplify a fragment of human MMS2
XX cDNA. The amplified fragment was used as a probe to isolate the full
XX length sequence. The MMS2 protein has 11 post-synaptic density protein,
XX disc-large, 20-1 (PDZ) domains and one or more of these domains interacts
XX specifically with the carboxyl terminal amino acids of MMS2 (see
XX AA553754). Specifically, it appears that domain 7, 10 and 13 interact
XX with MMS2. Since MMS2 contains 11 PDZ domains and interacts with MMS2,
XX a known tumour suppressor having a region of homology with protein
XX tyrosine phosphatases, MMS2 acts as a scaffolding protein in a common
XX biological pathway with MMS2. It is believed that the interaction
XX between MMS2 and MMS2 is required for the tumour suppressor activity of
XX MMS2. The MMS2 polypeptides, polynucleotides, fragments and specific
XX complex specific antibodies may be used for detecting cancer or a
XX predisposition to cancer and screening for agents that may be used to
XX treat MMS2 and/or MMS2 related cancer. The polypeptides and
XX polynucleotides may also be used to treat cancer.
XX
XX Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 16; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 62;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1317 TACAAAGAGGAGAG 1332
XX
XX Db 16 TACAAAGAGGAGAG 1
XX
XX RESULT 48
XX AAT99882/c
XX ID AAT99882 standard; DNA; 19 BP.
XX
XX AC AAT99882;
XX
XX DT 07-MAY-1998 (first entry)
XX
XX DE 5' vglbwp5 primer for exon 3 of HLA-B gene.
XX
XX KW PCR primer; amplify; pathogen identification; mutation detection;
XX nucleic acid analysis; microorganism characterisation; human;
XX HLA type determination; HLA-B gene exon 3; ss.
XX
XX OS Synthetic.

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```

OS Homo sapiens.
XX
XX WO9741259-A1.
XX
XX 06-NOV-1997.
XX
XX 23-APR-1997; 97WO-US007135.
XX
XX
XX 01-MAY-1996; 96US-00640672.
XX
XX 19-JUL-1996; 96US-00684498.
XX
XX 27-FEB-1997; 97US-00807138.
XX
XX (VISI-) VISIBLE GENETICS INC.
XX
XX Leushner J, Hui M, Dunn DM, Larson MT, Lacroix J, Shipman R;
XX
XX WPI; 1997-549755/50.
XX
XX Nucleic acid sequence determination - comprising synthesising chain
XX extension products, which are indicative of positions of selected species
XX of nucleotide in nucleotide sequence.
XX
XX Example 6; Page 23; 69pp; English.
XX
XX This sequence represents a primer for exon 3 of the HLA-B gene. This
XX sequence can be used in the method of the invention for determining the
XX position of at least one selected species of nucleotide, in a region of
XX interest, in a target nucleic acid polymer, in a sample. The method
XX comprises combining the sample with a reaction mixture to synthesise
XX chain extension products indicative of the positions of the species of
XX nucleotide in the region of interest and evaluating the products
XX produced, characterised in that the sample, which is combined with the
XX reaction mixture, and contains target and non-target nucleic acid
XX polymers in natural abundance. The method can be used to detect
XX mutations, particularly mutations of medical significance, in samples
XX derived from a human patient, animal, plant or microorganism, determine
XX HLA type auxiliary to transplant procedures, detect and identify
XX microorganisms, particularly pathogenic microorganisms, in a sample and
XX in situ sequencing reactions to produce sequencing fragments in a
XX histological specimen
XX
XX Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 64;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 471 CCCGAGCCCGCAGCCGC 489
XX
XX Db 19 CCCGAGCCCGCAGCCGC 1
XX
XX RESULT 49
XX AAT99878/c
XX ID AAT99878 standard; DNA; 19 BP.
XX
XX AC AAT99878;
XX
XX DT 07-MAY-1998 (first entry)
XX
XX DE 5' vglawsp3 primer for exon 3 of HLA-A gene.
XX
XX KW PCR primer; amplify; pathogen identification; mutation detection;
XX nucleic acid analysis; microorganism characterisation; human;
XX HLA type determination; HLA-A gene exon 3; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN WO9741259-A1.
XX
XX PD 06-NOV-1997.
XX

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PF 29-APR-1997; 97WO-08007135.  
 XX  
 PR 01-MAY-1996; 96US-00640672.  
 PR 19-JUN-1996; 96US-00684498.  
 PR 27-FEB-1997; 97US-00807138.  
 XX  
 PA (VIST-) VISIBLE GENETICS INC.  
 XX  
 PI Leushner J, Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R;  
 XX WPI; 1997-549755/50.  
 DR  
 XX Nucleic acid sequence determination - comprising synthesising chain  
 PT extension products, which are indicative of positions of selected species  
 PT of nucleotide in nucleotide sequence.  
 XX  
 PS Example 6; Page 23; 69pp; English.  
 XX  
 CC This sequence represents a primer for exon 3 of the HLA-A gene. This  
 CC sequence can be used in the method of the invention for determining the  
 CC position of at least one selected species of nucleotide, in a region of  
 CC interest, in a target nucleic acid polymer, in a sample. The method  
 CC comprises combining the sample with a reaction mixture to synthesise  
 CC chain extension products indicative of the positions of the species of  
 CC nucleotide in the region of interest and evaluating the products of  
 CC produced, characterised in that the sample, which is combined with the  
 CC reaction mixture, and contains target and non-target nucleic acid  
 CC polymers in natural abundance. The method can be used to detect  
 CC mutations, particularly mutations of medical significance, in samples  
 CC derived from a human patient, animal, plant or microorganism, determine  
 CC HLA type ancillary to transplant procedures, detect and identify  
 CC microorganisms, particularly pathogenic microorganisms, in a sample and  
 CC in situ sequencing reactions to produce sequencing fragments in a  
 CC histological specimen  
 CC  
 SO Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 471 CCCGAGCCCCGACCGCGC 469  
 19 CCCGAGCCCCCGCCGCC 1  
 XX  
 RESULT 50  
 AAV17327  
 ID AAV17327 standard; DNA; 19 BP.  
 AC AAV17327;  
 XX  
 DT 02-JUN-1998 (first entry)  
 DE Primer used in construction of antibody of the invention.  
 XX  
 KM Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 KM cancer diagnosis; complementarity determining region; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9742329-A1.  
 PS 13-NOV-1997.  
 PD 29-APR-1997; 97WO-GB001165.  
 PF 04-MAY-1996; 96GB-00009405.  
 PR 14-FEB-1997; 97GB-00003103.  
 XX  
 PA (ZENB) ZENECA LTD.  
 XX  
 PI Copley CG, Edge MD, Emery SC;

XX  
 DR WPI; 1997-558987/51.  
 XX  
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis  
 PT and therapy of cancer.  
 XX  
 PS Example 48; Page 170; 208pp; English.  
 XX  
 CC This sequence is a primer that was used to construct the antibody of the  
 CC invention. The antibody is an anti-CEA (carcinoembryonic antigen)  
 CC antibody (806.077 Ab). Host cells or transgenic organisms transformed  
 CC with DNA encoding the antibody, are used to make the antibody or  
 CC conjugate. The conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The antibody can be used for in vivo or in vitro  
 CC diagnosis of cancer  
 CC  
 SO Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 603 GGACCACTGTCAGAGCTTG 621  
 1 GGACCTGTCGACAGCTTG 19  
 XX  
 RESULT 51  
 AAV46261/c  
 ID AAV46261 standard; DNA; 19 BP.  
 AC AAV46261;  
 XX  
 DT 16-OCT-1998 (first entry)  
 DE Human HLA-A primer Ex3 #2.  
 XX  
 KM Histocompatibility locus antigen; HLA-A class I; human; class typing;  
 KM donor; host; tissue transplantation; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9826091-A2.  
 PD 18-JUN-1998.  
 XX  
 PF 12-DEC-1997; 97WO-CA000955.  
 XX  
 PR 12-DEC-1996; 96US-00766189.  
 XX  
 PA (VIST-) VISIBLE GENETICS INC.  
 XX  
 PI Blaszyk RH, Leushner J;  
 XX  
 DR WPI; 1998-348544/30.  
 XX  
 PT HLA Class I typing - by primer-based amplification of target DNA using  
 PT group-specific untranslated region primer pair.  
 XX  
 PS Claim 26; Page 141; 185pp; English.  
 XX  
 CC AAV46054 and AAV46200-V46264 are primers used in isolating human  
 CC histocompatibility locus antigen (HLA-A) Class I alleles which are used  
 CC in a novel method of HLA Class I typing. The method involves combining a  
 CC group-specific untranslated region primer pair with a target DNA to allow  
 CC primer-based amplification of the DNA, and determining whether a nucleic  
 CC acid product is produced by the amplification. The ability of the primer  
 CC pair to produce a product is associated with a particular HLA group type.  
 CC The methods can be used for typing the 3 classical HLA Class I genes  
 CC (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g. donors and hosts  
 CC for tissue transplantation. The initial group specific amplification

CC allows a PCR based separation of haplotypes in 95% of patient samples.  
 CC The subsequent sequencing can provide for high-resolution typing  
 XX  
 SQ Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 471 CCCGAGCCCCGACCGCGC 489  
 DB 19 CCCGAGCCCCGACCGCGC 1  
 RESULT 52  
 AAV41791  
 ID AAV41791 standard; DNA; 19 BP.  
 AC AAV41791;  
 XX  
 DT 20-NOV-1998 (first entry)  
 XX  
 DE Human pancreatic carboxypeptidase B primer 677.  
 XX  
 KM ss; primer; PCR; amplification; human; pancreatic carboxypeptidase B;  
 KM Insulin; protein sequencing; prodng therapy.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 EN WO9835988-A1.  
 XX  
 PD 20-AUG-1998.  
 XX  
 PF 10-FEB-1998; 98WO-GB000415.  
 XX  
 PR 14-FEB-1997; 97GB-00003104.  
 PR 18-OCT-1997; 97GB-00022003.  
 PR 29-OCT-1997; 97GB-00022727.  
 XX  
 PA (ZENEC) ZENECA LTD.  
 XX  
 PI Edge MD;  
 XX  
 DR WPI; 1998-467168/40.  
 XX  
 PT New modified pro-domain of carboxy-peptidase B - enhances expression of  
 PT co-expressed proteins for production of recombinant carboxy-peptidase or  
 PT its fusions with antibodies, used, e.g. in enzyme prodng therapy.  
 XX  
 PS Example 1; Page 51; 83pp; English.  
 XX  
 CC The primers AAV41785-V41794 were used in the cloning of human pancreatic  
 CC carboxypeptidase B (CPB). The co-expression of a modified pro-domain of  
 CC CPB from a separate gene enhances recombinant expression. This process  
 CC can be used to produce recombinant CPB in eukaryotic cells, or fusions of  
 CC CPB with antibody chains. CPB is used in insulin production and protein  
 CC sequencing, while its fusions with antibody are useful in antibody-  
 CC directed enzyme prodng therapy. The Modified pro-domain provide  
 CC increased yields of recombinant CPB, possibly by protecting the C-  
 CC terminus against enzymatic degradation or by increasing intracellular  
 CC trafficking  
 XX  
 SQ Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 603 GGACCACTGCAGGCTCG 621  
 DB 1 GGACCTGCTCAGAGTCTG 19

RESULT 53  
 AAX38086/C  
 ID AAX38086 standard; DNA; 19 BP.  
 XX  
 AC AAX38086;  
 XX  
 DT 04-JUN-1999 (first entry)  
 XX  
 DE Histocompatibility locus antigen primer SEQ ID NO:242.  
 XX  
 KM Human; histocompatibility locus antigen; HLA; determination; allele;  
 KM HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 EN WO907883-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 11-AUG-1998; 98WO-CA000768.  
 XX  
 PR 11-AUG-1997; 97US-00909290.  
 XX  
 PA (VISI-) VISIBLE GENETICS INC.  
 PA (BLAS/) BLASCTYK R H.  
 XX  
 PI Blasczyk RH, Leushner J;  
 XX  
 DR WPI; 1999-167446/14.  
 XX  
 PT Determination of HLA class I group type of a subject - using group  
 PT specific untranslated region primer pair.  
 XX  
 PS Disclosure; Page 24; 195pp; English.  
 XX  
 CC The present invention describes a method using novel primers involving  
 CC the PCR-based determination of histocompatibility locus antigen B (HLA-B)  
 CC Class I group type. Determining the HLA-B Class I group type of a subject  
 CC comprises: (i) combining a group-specific untranslated region primer pair  
 CC with a target DNA sample from the subject under conditions such that  
 CC primer-based amplification of the target DNA may occur; and (ii)  
 CC determining whether a nucleic acid product is produced by the  
 CC amplification; where the ability of the primer pair to produce a nucleic  
 CC acid product is associated with a particular HLA group type. The method  
 CC can be used for HLA-B typing. In the method, the initial group specific  
 CC amplification allows a PCR based separation of haplotypes in 95% of  
 CC patient samples. It permits the resolution of cis/trans linkages of  
 CC heterozygote sequencing results which cannot be achieved with other  
 CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 471 CCCGAGCCCCGACCGCGC 489  
 DB 19 CCCGAGCCCCGACCGCGC 1  
 RESULT 54  
 AAZ39654  
 ID AAZ39654 standard; DNA; 19 BP.  
 XX  
 AC AAZ39654;  
 XX  
 DT 28-FEB-2000 (first entry)  
 XX  
 DE Human Vth aggregation factor gene specific PCR-SSCP primer.

XX Gene polymorphism; human; Vth aggregation factor; genetic diagnosis;  
 KW diabetes; FPCR; SSCP; fluorescence-based polymerase chain reaction;  
 KM single strand conformation polymorphism; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX JPL1313676-A.  
 PN 16-NOV-1999.  
 PD 30-APR-1998; 98JP-00120217.  
 PF 30-APR-1998; 98JP-00120217.  
 PR 30-APR-1998; 98JP-00120217.  
 XX (SAXA) OTSUKA PHARM CO LTD.  
 PA WPI; 2000-057352/05.  
 DR Discrimination of human V aggregation factor gene polymorphism.  
 PT Disclosure; Page 9; 34pp; Japanese.  
 PS The invention provides a method for the discrimination of the gene  
 CC polymorphism of human Vth aggregation factor, where one of the following  
 CC (1) to (6) residues/nucleotides in the aggregation gene is discriminated  
 CC in the patient to be tested: (1) residue 495: guanine (G) or adenine (A),  
 CC (2) residue 642: (G) or thymine (T), (3) residue 2663: (G) or (A), (4)  
 CC residue 2763: (G) or (A), (5) residue 2863: (A) or (G), (6) residue 5112:  
 CC (A) or (G). The method is useful in the genetic diagnosis of a diabetes  
 CC patient. The method uses FPCR-SSCP (fluorescence-based polymerase chain  
 CC reaction-single strand conformation polymorphism) for analyzing DNA  
 CC samples for polymorphisms. Sequences AA239632-717 represent primers used  
 CC for the FPCR-SSCP analysis of the human Vth aggregation factor gene  
 CC  
 SQ Sequence 19 BP; 7 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 961 AAAGATCTCTCACACAGA 979  
 Db 1 AAACATCTCTCCACAGA 19  
 RESULT 55  
 AA272309/c  
 ID AA272309 standard; DNA; 19 BP.  
 XX  
 AC AA272309;  
 XX  
 XX 10-SEP-2001 (first entry)  
 DT  
 XX  
 XX Human biallelic marker upstream amplification primer SEQ ID NO:6665.  
 DE  
 XX  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 XX  
 PR 23-NOV-1998; 98US-0109732P.

XX (BEST) GENSET.  
 PA Cohen D, Blumenfeld M, Chumakov I,  
 XX  
 PI WPI; 2000-013267/01.  
 DR  
 XX  
 XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 PS Claim 9; Page 1652; 2745pp; English.  
 XX  
 CC AA265654 to AA269578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AA269579 to AA277440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses; they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 CC  
 SQ Sequence 19 BP; 2 A; 4 C; 3 G; 10 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2095 CAGGAAACTTAAGCAAG 2113  
 Db 19 CAGGAAACTTAAGCAAG 1  
 RESULT 56  
 AAA65784/c  
 ID AAA65784 standard; DNA; 19 BP.  
 XX  
 AC AAA65784;  
 XX  
 XX 22-NOV-2000 (first entry)  
 DT  
 XX  
 XX Human leukocyte antigen A exon 3 sequencing primer SEQ ID NO:5.  
 DE  
 XX  
 KW Human; VHL gene; sequencing; mutation; human leukocyte antigen; HLA;  
 KW transplantation surgery; detection; identification; primer;  
 KW pathogenic microorganism; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6083699-A.  
 XX  
 PD 04-JUL-2000.  
 XX  
 PF 20-JAN-1998; 98US-00009483.  
 XX  
 PR 01-MAY-1996; 96US-00640672.  
 XX  
 PR 19-JUL-1996; 96US-00684498.  
 XX  
 PR 27-FEB-1997; 97US-00807138.  
 XX  
 PR 29-APR-1997; 97WO-US007134.  
 XX  
 PA (VIST-) VISIBLE GENETICS INC.  
 XX  
 XX Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R, Leusner J;  
 PT WPI; 2000-464336/40.  
 Bi-directional sequencing of nucleic acid polymers for identifying

PT pathogens or detecting mutations by using a single reaction mixture  
 PT having first and second primers with different, spectroscopically-  
 PT distinguishable labels.  
 XX  
 PS Example 2; Col 11; 27pp; English.  
 CC The present invention describes a method for simultaneously determining  
 CC the position of a nucleotide base in a target region of both strands of a  
 CC denatured duplex nucleic acid polymer. The method comprises using a  
 CC single set of reaction mixture that is combined with the nucleic acid  
 CC polymer. The reaction mixture contains first and second oligonucleotide  
 CC primers, each with different, spectroscopically-distinguishable  
 CC fluorescent labels. The method is used to detect mutations, especially  
 CC medically significant mutations, in samples derived from a human patient,  
 CC animal, plant or microorganism, and for the determination of human  
 CC leukocyte antigen (HLA) type prior to transplantation surgery. The method  
 CC can also be used to detect and identify microorganisms, especially  
 CC pathogenic microorganisms, in a sample, and in situ sequencing  
 CC reactions to produce sequencing fragments within a histological specimen,  
 CC which are then removed from a selected location on the tissue preparation  
 CC and loaded onto a gel for sequence analysis. The sequencing reaction is  
 CC useful for evaluating archived samples in retrospective studies where the  
 CC outcome of a disease condition is known, but the causative mutation is  
 CC not. The present sequence represents a sequencing primer for the human  
 CC HLA-A gene, which is used in an example from the present invention  
 CC  
 SQ Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 471 CCCGAGCCCCGACCGCCG 489  
 Db 19 CCCGAGCCCCGACCGCCG 1  
 RESULT 57  
 AAA65788/c  
 ID AAA65788 standard; DNA; 19 BP.  
 AC AAA65788;  
 XX  
 DT 22-NOV-2000 (first entry)  
 XX  
 DE Human leukocyte antigen B exon 3 sequencing primer SEQ ID NO:9.  
 XX  
 KM Human; VHL gene; sequencing; mutation; human leukocyte antigen; HLA;  
 KM transplantation surgery; detection; identification; primer;  
 KM pathogenic microorganism; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US608369-A.  
 XX  
 PD 04-JUL-2000.  
 XX  
 PF 20-JAN-1998; 98US-00009463.  
 XX  
 PR 01-MAY-1996; 96US-00640672.  
 PR 19-JUL-1996; 96US-00684498.  
 PR 27-FEB-1997; 97US-00807138.  
 PR 29-APR-1997; 97WO-US007134.  
 XX  
 PA (VIST-) VISIBLE GENETICS INC.  
 XX  
 PI Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R, Leushner J;  
 DR WPI; 2000-46436/40.  
 XX  
 PT Bi-directional sequencing of nucleic acid polymers for identifying  
 PT pathogens or detecting mutations by using a single reaction mixture  
 PT having first and second primers with different, spectroscopically-

PT distinguishable labels.  
 XX  
 PS Example 2; Col 11; 27pp; English.  
 CC The present invention describes a method for simultaneously determining  
 CC the position of a nucleotide base in a target region of both strands of a  
 CC denatured duplex nucleic acid polymer. The method comprises using a  
 CC single set of reaction mixture that is combined with the nucleic acid  
 CC polymer. The reaction mixture contains first and second oligonucleotide  
 CC primers, each with different, spectroscopically-distinguishable  
 CC fluorescent labels. The method is used to detect mutations, especially  
 CC medically significant mutations, in samples derived from a human patient,  
 CC animal, plant or microorganism, and for the determination of human  
 CC leukocyte antigen (HLA) type prior to transplantation surgery. The method  
 CC can also be used to detect and identify microorganisms, especially  
 CC pathogenic microorganisms, in a sample, and in situ sequencing  
 CC reactions to produce sequencing fragments within a histological specimen,  
 CC which are then removed from a selected location on the tissue preparation  
 CC and loaded onto a gel for sequence analysis. The sequencing reaction is  
 CC useful for evaluating archived samples in retrospective studies where the  
 CC outcome of a disease condition is known, but the causative mutation is  
 CC not. The present sequence represents a sequencing primer for the human  
 CC HLA-B gene, which is used in an example from the present invention  
 CC  
 SQ Sequence 19 BP; 0 A; 4 C; 14 G; 1 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 471 CCCGAGCCCCGACCGCCG 489  
 Db 19 CCCGAGCCCCGACCGCCG 1  
 RESULT 58  
 AAT47370/c  
 ID AAT47370 standard; DNA; 20 BP.  
 AC AAT47370;  
 XX  
 DT 10-SEP-1997 (first entry)  
 XX  
 DE Variant #26 of universal primer sequence for M13mp18.  
 XX  
 KM PCR; primer; amplify; polymerase chain reaction; bacteriophage; M13mp18;  
 KM cystic fibrosis transmembrane conductance regulator gene; multiplex PCR;  
 KM chimeric primer; genetic screening; mutation detection; CPTB;  
 KM Wilms Tumour gene; beta-thalassaemia gene; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9641012-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US009637.  
 XX  
 PR 07-JUN-1995; 95US-00474450.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Shuber AP;  
 XX  
 DR WPI; 1997-052372/05.  
 XX  
 PT Universal primer used for multiplex DNA amplification - allows  
 PT simultaneous amplification of multiple DNA target sequences for high  
 PT through-put genetic screening.  
 XX  
 PS Claim 28; Page 10; 38pp; English.  
 CC AAT47345-T47374 represent variants of a universal primer sequence (see

CC AAT47344) derived from the bacteriophage vector M13mp18. This sequence  
CC can be used as half of the DNA primer of the invention. The primers are  
CC used for amplification of a target DNA sequence, and can be used in a  
CC multiplex PCR amplification. The primers have the sequence 5'-XY-3',  
CC where X is a sequence that does not hybridise to the target sequence  
CC (such as this sequence), and Y is a sequence contained within or flanking  
CC the target sequence. The melting temperature of a hybrid between X and  
CC its complement (in the absence of other sequences) is 60 degrees C.  
CC During early cycles of amplification, products are synthesised that  
CC contain the chimeric primers on either end. The primers then serve as  
CC high stringency recognition sequences for subsequent rounds of  
CC amplification. As a result, the annealing efficiency of different primers  
CC and their targets in a multiplex amplification reaction is normalised,  
CC thereby reducing preferential amplification of certain targets. The  
CC chimeric primer comprise a 5' universal domain and a 3' target-specific  
CC domain. They are used for the simultaneous PCR amplification of multiple  
CC DNA targets in a sample. The primer containing AAT47344 is particularly  
CC useful in high-throughput genetic screening for detecting the presence of  
CC multiple defined targets e.g. to detect mutations in genes like the  
CC cystic fibrosis transmembrane conductance regulator (CFTR), the Wilms  
CC Tumour, and the beta-thalassaemia genes

XX SQ Sequence 20 BP; 3 A; 6 C; 10 G; 1 T; 0 U; 0 Other;  
XX  
XX

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 67;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 205 CCCGCCGCTGGCCTCGCG 223  
Db 19 CTCGACCGCTGGCCTCGCG 1

RESULT 59  
AAT47369/c  
ID AAT47369 standard; DNA; 20 BP.  
XX  
XX AAT47369;  
AC  
XX  
DT 10-SEP-1997 (first entry)  
XX  
DE Variant #25 of universal primer sequence for M13mp18.  
XX  
KM PCR; primer; amplify; polymerase chain reaction; bacteriophage; M13mp18;  
KM cystic fibrosis transmembrane conductance regulator gene; multiplex PCR;  
KM chimeric primer; genetic screening; mutation detection; CFTR;  
KM Wilms Tumour gene; beta-thalassaemia gene; ss.  
XX  
OS Synthetic.  
XX  
PN WO9641012-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009637.  
XX  
PR 07-JUN-1995; 95US-00474450.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Shuber AP;  
XX  
DR WPI; 1997-052372/05.  
XX  
PT Universal primer used for multiplex DNA amplification - allows  
PT simultaneous amplification of multiple DNA target sequences for high  
PT through-put genetic screening.  
XX  
PS Claim 27, Page 10; 38pp; English.  
XX  
XX AAT47345-T47374 represent variants of a universal primer sequence (see  
CC AAT47344) derived from the bacteriophage vector M13mp18. This sequence  
CC can be used as half of the DNA primer of the invention. The primers are

CC used for amplification of a target DNA sequence, and can be used in a  
CC multiplex PCR amplification. The primers have the sequence 5'-XY-3',  
CC where X is a sequence that does not hybridise to the target sequence  
CC (such as this sequence), and Y is a sequence contained within or flanking  
CC the target sequence. The melting temperature of a hybrid between X and  
CC its complement (in the absence of other sequences) is 60 degrees C.  
CC During early cycles of amplification, products are synthesised that  
CC contain the chimeric primers on either end. The primers then serve as  
CC high stringency recognition sequences for subsequent rounds of  
CC amplification. As a result, the annealing efficiency of different primers  
CC and their targets in a multiplex amplification reaction is normalised,  
CC thereby reducing preferential amplification of certain targets. The  
CC chimeric primer comprise a 5' universal domain and a 3' target-specific  
CC domain. They are used for the simultaneous PCR amplification of multiple  
CC DNA targets in a sample. The primer containing AAT47344 is particularly  
CC useful in high-throughput genetic screening for detecting the presence of  
CC multiple defined targets e.g. to detect mutations in genes like the  
CC cystic fibrosis transmembrane conductance regulator (CFTR), the Wilms  
CC Tumour, and the beta-thalassaemia genes

XX SQ Sequence 20 BP; 3 A; 7 C; 10 G; 0 T; 0 U; 0 Other;  
XX  
XX

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 67;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 205 CCCGCCGCTGGCCTCGCG 223  
Db 19 CTCGACCGCTGGCCTCGCG 1

RESULT 60  
AAT47371/c  
ID AAT47371 standard; DNA; 20 BP.  
XX  
XX AAT47371;  
AC  
XX  
DT 10-SEP-1997 (first entry)  
XX  
DE Variant #27 of universal primer sequence for M13mp18.  
XX  
KM PCR; primer; amplify; polymerase chain reaction; bacteriophage; M13mp18;  
KM cystic fibrosis transmembrane conductance regulator gene; multiplex PCR;  
KM chimeric primer; genetic screening; mutation detection; CFTR;  
KM Wilms Tumour gene; beta-thalassaemia gene; ss.  
XX  
OS Synthetic.  
XX  
PN WO9641012-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009637.  
XX  
PR 07-JUN-1995; 95US-00474450.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Shuber AP;  
XX  
DR WPI; 1997-052372/05.  
XX  
PT Universal primer used for multiplex DNA amplification - allows  
PT simultaneous amplification of multiple DNA target sequences for high  
PT through-put genetic screening.  
XX  
PS Claim 29, Page 10; 38pp; English.  
XX  
XX AAT47345-T47374 represent variants of a universal primer sequence (see  
CC AAT47344) derived from the bacteriophage vector M13mp18. This sequence  
CC can be used as half of the DNA primer of the invention. The primers are  
CC used for amplification of a target DNA sequence, and can be used in a  
CC multiplex PCR amplification. The primers have the sequence 5'-XY-3',

CC where X is a sequence that does not hybridise to the target sequence  
 CC (such as this sequence), and Y is a sequence contained within or flanking  
 CC the target sequence. The melting temperature of a hybrid between X and  
 CC its complement (in the absence of other sequences) is 60 degrees C.  
 CC During early cycles of amplification, products are synthesised that  
 CC contain the chimeric primers on either end. The primers then serve as  
 CC high stringency recognition sequences for subsequent rounds of  
 CC amplification. As a result, the annealing efficiency of different primers  
 CC and their targets in a multiplex amplification reaction is normalised,  
 CC thereby reducing preferential amplification of certain targets. The  
 CC chimeric primer comprise a 5' universal domain and a 3' target-specific  
 CC domain. They are used for the simultaneous PCR amplification of multiple  
 CC DNA targets in a sample. The primer containing AAT7344 is particularly  
 CC useful in high-throughput genetic screening for detecting the presence of  
 CC multiple defined targets e.g. to detect mutations in genes like the  
 CC cystic fibrosis transmembrane conductance regulator (CFTR), the Wilms  
 CC tumour, and the beta-thalassaemia genes

SQ Sequence 20 BP; 3 A; 6 G; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
 Best Local Similarity 89.5%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 205 CCCGCCCGCTGGCGCTGCG 223  
 DB 19 CTCGACCGCTGGCGCTGCG 1

RESULT 61  
 AAV35212  
 ID AAV35212 standard; DNA; 20 BP.

XX AAV35212;  
 AC AAV35212;  
 DT 10-SEP-1998 (first entry)

DE Hepatitis C virus type 1b PCR primer #15.

KW Nonstructural viral protein; hepatocyte; detection; replication;  
 inhibition; RNA polymerase; PCR primer; ss.

OS Synthetic.  
 OS Hepatitis C virus.

PN CP10165186-A.

PD 23-JUN-1998.

PF 13-DEC-1996; 96UP-00352920.

PR 13-DEC-1996; 96UP-00352920.

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 1998-406110/35.

XX Hepatitis C virus-sensitive recombinant hepatocyte - useful for, e.g.  
 PT replicating HCV and producing its non-structural protein.

PS Example 4; Page 9; 11p; Japanese.

XX AAV5197-V35200, AAV5202 and AAV35215 are primers used in a method for  
 CC producing a nonstructural protein of hepatitis C virus (HCV) type 1b from  
 CC a recombinant hepatocyte. Also described is a method for the replication  
 CC of HCV which involves contacting HCV with the sensitive recombinant  
 CC hepatocyte, and culturing the hepatocyte. The method may also be used for  
 CC detecting a substance capable of inhibiting replication of HCV. The  
 CC method can prepare HCV-sensitive recombinant hepatocyte capable of  
 CC producing HCV RNA polymerase constitutively, and replicating HCV  
 CC efficiently for a long period

SQ Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
 Best Local Similarity 89.5%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1092 TGATGAGATGATGGCTTC 1110  
 DB 2 TGAGAGATGATGGCTTC 20

RESULT 62  
 AA204239/C  
 ID AA204239 standard; DNA; 20 BP.

XX AA204239;

DT 07-OCT-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

KW Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;  
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihypertitis;  
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

OS Synthetic.  
 OS Chlamydia trachomatis.

PN M09928475-A2.

PD 10-JUN-1999.

PF 27-NOV-1998; 98MO-IB001939.

PR 28-NOV-1997; 97RR-00015041.

PR 17-DEC-1997; 97RR-00015034.

PR 04-NOV-1998; 98US-0107077P.

XX (BEST ) GENSET.

XX Griffais R;

DR WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

PS Disclosure; Page 1672; 1755pp; English.

XX PCR primers AA201426-206209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs  
 CC encode polypeptides (see AA136754-Y37949) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
 CC be used to control growth of the microorganism. Chlamydia trachomatis is  
 CC responsible for a large number of diseases, e.g. eye diseases such as  
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;  
 CC epididymitis; cervicitis; salpingitis; perihypertitis; Bartholinitis;  
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
 CC The polypeptides of the invention may be of use in treating these  
 CC diseases

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 15.8; DB 1; Length 20;  
 Best Local Similarity 89.5%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 913 AGACCTGATCTGCTGCT 931  
 DB 20 AGACCTGATCTGCTGCT 2

RESULT 63

PN WO2003075934-A1.  
 XX 18-SEP-2003.  
 XX 13-MAR-2003; 2003WO-IL000218.  
 PF 13-MAR-2002; 2002IL-00148668.  
 XX 13-MAR-2002; 2002IL-00148668.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA Shintzky M, Haimovitz R;  
 PI WPI; 2003-812460/76.  
 DR WPI; 2003-812460/76.  
 XX New cyclic 1,3-propanediol phosphate derivatives useful for treating  
 PT disorder and diseases, which can be created by promoting cell  
 PT differentiation, e.g. tumor growth.  
 XX  
 XX Example 20; Page 21; 43pp; English.  
 CC The present sequence is that of a PCR primer for human oestrogen receptor  
 CC alpha. PCR was used to show that expression of oestrogen receptor alpha  
 CC mRNA was promoted in human breast cancer MCF-7 cells treated with novel  
 CC cyclic 1,3-propanediol phosphate (CPP) derivatives of the invention. The  
 CC invention relates to the use of the CPP derivatives to promote cell  
 CC differentiation and enhance expression of various proteins, including the  
 CC oestrogen receptor alpha and progesterone receptor, in target cells.  
 CC Promotion of cancer cell differentiation and promotion of protein  
 CC expression within such cells suppresses their growth, thus effectively  
 CC fighting cancer. Expression of both oestrogen receptor alpha and  
 CC progesterone receptor correlate with better prognosis of breast cancer.  
 CC CPP compounds of the invention demonstrated effective antitumor ability  
 CC against tumors in cancerous breast cells. Acute toxicity testing of the  
 CC compounds did not show any pharmacotoxic effects in doses as high as 5  
 CC g/kg.  
 CC  
 CC Sequence 20 BP; 1 A; 6 C; 2 G; 11 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 0.7%; Score 15.8; DB 1; Length 20;  
 XX Best Local Similarity 89.5%; Pred. No. 67;  
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1317 TACAAAGAGAGAGAGAGC 1335  
 DB 19 TAAAAACAGAGAGAGAGC 1  
 RESULT 66  
 AAQ26030/c  
 ID AAQ26030 standard; DNA; 21 bp  
 XX  
 XX AAQ26030;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 05-JAN-1993 (first entry)  
 XX  
 XX Primer SP2.  
 DE  
 XX Semliki forest virus; SFV; sequencing primers; M13mpl8; mpl9; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9210578-A1.  
 XX  
 XX 25-JUN-1992.  
 PD  
 XX 12-DEC-1991; 91WO-S0000855.  
 PF  
 XX 13-DEC-1990; 90SE-00003978.  
 PR  
 XX (BIOP-) BIOPITION AB.  
 PA  
 XX Garoff H, Liljestrom P;  
 PI

No (date) date

XX WPI; 1992-234633/28.  
 DR RNA mol. derived from alphavirus RNA genome - chimeric alphavirus antigen  
 XX and vaccine for immunisation against viral infections.  
 PT  
 XX Disclosure; Page 24; 94pp; English.  
 PS  
 XX The sequences given in AAQ26029-30 are sequencing primers which were used  
 CC within the scope of the invention to determine the inclusion of a linker  
 CC sequence in a Semliki forest virus (SFV) cDNA clone. The SFV clone was  
 CC contained within plasmids M13mpl8 or mpl9. The insertion of the linker  
 CC sequence allowed deletion of the 6x region of the SFV cDNA. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 CC  
 CC Sequence 21 BP; 1 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 0.7%; Score 15.8; DB 1; Length 21;  
 XX Best Local Similarity 89.5%; Pred. No. 69;  
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 356 CGGCGCGCGGTGGCGCGC 374  
 DB 21 CGGCGCGCGGTGGCGCGC 3  
 RESULT 67  
 AAZ61424  
 ID AAZ61424 standard; DNA; 21 BP.  
 AC  
 XX AAZ61424;  
 DT 19-JUN-2000 (first entry)  
 XX  
 XX PCR primer for DNA encoding short extracellular form of human B7-1.  
 DE  
 XX Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;  
 KW CD28; CTLA4; T cell surface receptor; cytokine production;  
 KW cell proliferation; T cell; infection; autoimmune disease; inflammation;  
 KW quality assurance; cancer; PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200008057-A2.  
 PN  
 XX 17-FEB-2000.  
 PD  
 XX 05-AUG-1999; 99WO-US017906.  
 PF  
 XX 07-AUG-1998; 98US-0095663P.  
 PR  
 XX (IMMUNEX ) IMMUNEX CORP.  
 PA  
 XX Baum PR;  
 PI  
 XX WPI; 2000-205674/18.  
 DR  
 XX Novel B7-1 polypeptide and nucleotides encoding them useful as T cell  
 PT costimulatory molecules for therapeutics against infections, autoimmune  
 PT diseases and inflammation.  
 PT  
 XX Example-3; Page 49; 57pp; English.  
 PS  
 XX PCR primers AAZ61424-25 were used to amplify DNA encoding the short  
 CC extracellular form of human B7-1 (CD80). B7-1 is a T-cell costimulatory  
 CC molecule that is found on the surface of antigen presenting cells (APCs).  
 CC CD28 and CTLA4 are its T cell surface receptors. B7-1 interacts with CD28  
 CC to signal cytokine production, cell proliferation, and the generation of  
 CC effector and memory T cells. Disorders mediated by interaction of B7-1  
 CC and its binding partner, such as infections, autoimmune diseases and  
 CC inflammation, are treated by administering B7-1 to the disordered  
 CC mammal. B7L-1 polypeptides are useful to separate cells expressing a

AA97009  
ID AAX97009 standard; DNA; 20 BP.  
XX  
AC AAX97009;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
XX  
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
KW neutralising epitope; PCR primer; ss.  
XX  
OS Synthetic.  
XX Chlamydia pneumoniae.  
XX  
PN MO9927105-A2.  
XX  
PD 03-JUN-1999.  
XX  
PF 20-NOV-1998; 98WC-IB001890.  
XX  
PR 21-NOV-1997; 97FR-00014673.  
PR 04-NOV-1998; 98US-0107078P.  
XX  
PA (GENSET) GENSET.  
XX  
PI Griffrals R;  
XX  
DR WPI; 1999-357842/30.  
XX  
PT Genome sequence of Chlamydia pneumoniae.  
PS Page 1870; Disclosure; 1912pp; English.  
XX  
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames  
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
CC pneumonia and bronchitis and is thought to be a contributing factor in  
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used  
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
CC nucleotide sequences can also be used as immunogenic compositions,  
CC especially where the vector directs the expression of a neutralising  
CC epitope of C. pneumoniae  
XX  
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 67;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2297 TCTGAGCCCACTGGGAGT 2315  
DB 2 TCTGAGCCCACTGTGGAGG 20  
RESULT 64  
AB299238  
ID AB299238 standard; DNA; 20 BP.  
XX  
AC AB299238;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human PDE4C oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX

KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WC-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPICGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan U, Aguilar D;  
PI Miller S, Tang L, Shahbuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 14480; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' and genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 67;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1335 CATGCTGTGGGCGCAGCC 1353  
DB 2 CATGCTGTGGCGCAGCAC 20  
RESULT 65  
ADD89884/C  
ID ADD89884 standard; DNA; 20 BP.  
XX  
AC ADD89884;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Oestrogen receptor alpha PCR primer.  
XX  
KW Human; oestrogen receptor alpha; receptor; cyclic propanediol phosphate;  
KW cytostatic; cell differentiation; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX

protein to which it binds and to measure the biological activity of LDCAM  
CC polypeptides. They can also be used as reagents for conducting quality  
CC assurance studies e.g., to monitor shelf life and stability of proteins  
CC to which it binds, and as carriers for delivering agents attached to  
CC cells bearing its counter structure, LDCAM or other cell receptors. They  
CC are also useful as a research tool for studying T-cell signalling and  
CC proliferation. They are employed in *in vitro* assays for detecting  
CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic  
CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes  
CC which catalyse a colorimetric or fluorometric reaction, may be attached  
CC to a B7-1 polypeptide, e.g. nitrogen mustards are attached to the B7-1  
CC and used to treat various forms of cancer  
CC  
SQ Sequence 21 BP; 0 A; 8 C; 6 G; 7 T; 0 U; 0 Other;  
QY Query Match 0.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 492 CCTGCTCTTCGCGCTGCAGC 510  
1 CCTGCTCTTCGCGCTGCAGC 19  
RESULT 68  
ABS97428/C  
ID ABS97428 standard; DNA; 21 BP.  
AC ABS97428;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human cyclooxygenase 2 (COX2) polymorphic sequence #15.  
XX  
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTP;  
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
KW HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMMT;  
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxtransferase themlabile; STM;  
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uronkinase receptor; UPA;  
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KW multidrug resistance associated protein 3; cancer; prostate;  
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
KW altered drug metabolism; cardiovascular function; colorectal tumour;  
KW central nervous system; pulmonary; immunological; SNP;  
KW single nucleotide polymorphism.  
XX  
OS Homo sapiens.  
XX  
PN WO200257410-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 28-NOV-2001; 2001WO-US044838.  
XX  
PR 28-NOV-2000; 2000US-00724389.  
XX  
PA (DNAS-) DNA SCI LAB INC.  
XX  
PI Guida M, Hall J;  
XX  
DR WPI, 2002-698522/75.  
XX  
PT Isolated nucleic acid molecules having polymorphisms in known human genes  
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers  
PT for locating, identifying and characterizing the genes responsible for  
PT disorder-related traits.  
XX

Example 8; Page 113; 714pp; English.  
XX  
CC This invention relates to the sequence of an isolated nucleic acid  
CC molecule comprising at least one base variation from that of a known  
CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
CC transferase (HMMT), (kallikrein 2) KLK2, nicotinamide-N-methyl  
CC transferase (NMMT), NADPH quinone oxidoreductase 2 (NQO2),  
CC sulfoxtransferase themlabile (STM), UDP-glucuronosyl transferase 2B4  
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
CC transferase (UGT2B15), uronkinase receptor (UPA), multidrug resistance 1  
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
CC Genetic linkage markers for locating and characterizing the genes that  
CC are responsible for specific traits within the genome and eventually  
CC identifying the genes responsible for a variety of disorder-related  
CC traits as a result of their e.g., overexpression, constitutive  
CC expression, mutation or underexpression, which may be used in diagnosing  
CC and/or treating the disorders. The nucleic acid molecules comprising the  
CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1, AHR,  
CC ARNT, EPHX2, GST12, NMMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
CC used to screen for altered cardiovascular function, in COX2 for altered  
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
CC nervous system function, in FLAP and HMMT for altered pulmonary,  
CC immunological or haematological function, in KLK2 for altered serine  
CC protease activity or in the prostate, in LTP for altered immunological or  
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
CC peripheral nervous system function. The present sequence represents a  
CC polymorphic DNA sequence of the invention  
CC  
SQ Sequence 21 BP; 8 A; 0 C; 7 G; 6 T; 0 U; 0 Other;  
QY Query Match 0.7%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 1532 ACATCTCTCCAGAAATTAT 1550  
21 ACATCTCTCCATCAATTAT 3  
RESULT 69  
ABL00108/C  
ID ABL00108 standard; DNA; 51 BP.  
AC ABL00108;  
XX  
DT 05-MAR-2002 (first entry)  
XX  
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:99.  
XX  
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
KW autoimmune disease; inflammation; cancer; nervous system disease;  
KW infection; polymorphic protein; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200138586-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-US032311.  
XX

XX	PR	24-NOV-1999:	99US-0167383P.	
XX	XX			
XX	PA	(CURA-) CURAGEN CORP.		
XX	P1	Shinkets RA, Leach M;		
XX	DR	WPI; 2001-355949/37.		
XX	PT	Isolated human nucleic acids comprising one or more single nucleotide		
XX	PT	polymorphisms, useful for treating a subject suffering from a pathology,		
XX	PT	e.g. autoimmune diseases, ascribed to the presence of a sequence		
XX	PT	polymorphism.		
PS	Claim 1; Page 275; 674pp; English.			
XX	XX			
CC	CC	ABU00010 to ABU01104 represent human nucleic acid oligonucleotides		
CC	CC	comprising one or more single nucleotide polymorphisms (SNPs). ABB56531		
CC	CC	to ABB56503 represent human peptides encoded by some of the SNP		
CC	CC	oligonucleotides. The sequences from the present invention can have		
CC	CC	immunosuppressive, cytostatic, antiinflammatory, neuroprotective and		
CC	CC	antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides		
CC	CC	and antibodies from the present invention can be used for treating a		
CC	CC	subject suffering from, at risk for, or suspected of, suffering from a		
CC	CC	pathology ascribed to the presence of a sequence polymorphism. The		
CC	CC	pathology may be autoimmune diseases, inflammation, cancer, diseases of		
CC	CC	the nervous system, and infection by pathogenic microorganisms. The SNPs		
CC	CC	are also useful for determining which forms of a characterised		
CC	CC	polymorphism are present in individuals. The antibodies may be used in		
CC	CC	the detection, quantitation and/or cellular or tissue localisation of a		
CC	CC	polymorphic protein (e.g., for use in measuring levels of the polymorphic		
CC	CC	protein within appropriate physiological samples)		
XX	XX			
XX	XX	Sequence 51 BP; 11 A; 14 C; 18 G; 8 T; 0 U; 0 Other;		
XX	XX			
XX	XX	Query March	0.7%; Score 15.8; DB 1; Length 51;	
XX	XX	Best Local Similarity	65.7%; P-adj. No. 1.1e+02;	
XX	XX	Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0		
QY	2264	CACAAATGCAATTCTTGAGCACCCTGTCAAGTGTCTC	2298	
DB	35	CCCACTGTGACTCAGAGCAGCTTGACACGGTGTCTC	1	
XX	XX			
XX	XX	RESULT 70		
XX	XX	AAX36722		
XX	XX	AAX36722 standard; DNA; 18 BP.		
XX	XX	AAX36722;		
XX	XX	14-JUL-1999 (first entry)		
XX	XX	PCR primer for Human phosphodiesterase, PD58, coding sequence.		
XX	XX	Phosphodiesterase 8; PD58; human; cyclic nucleotide pathway; therapy;		
XX	XX	intracellular cyclic nucleotide level modulation; cAMP; cGMP; PCR primer;		
XX	XX	ss.		
XX	XX	Synthetic.		
XX	XX	Homo sapiens.		
XX	XX	MO9919495-A1.		
XX	XX	22-APR-1999.		
XX	XX	16-OCT-1998; 98WO-US021955.		
XX	XX	16-OCT-1997; 97US-00951648.		
XX	XX	(ICOS-) ICOS CORP.		
XX	XX	Loughney K;		
XX	XX			

DR	WPI; 1999-277645/23.
XX	
PT	New isolated phosphodiesterase genes and polypeptides for identifying specific binding partners.
XX	
PS	Example 3; Page 15; 80pp; English.
XX	
CC	This sequence is a PCR primer for DNA encoding the human phosphodiesterase 8 (PDE8) of the invention. The phosphodiesterase genes and polypeptides are used to develop products for treating conditions in which cyclic nucleotide pathways are aberrant and for modulation of intracellular cyclic nucleotide levels. The PDE8 polypeptides exhibit high affinity for hydrolysis of both cAMP and cGMP but relatively low sensitivity to enzyme inhibitors specific for other PDE families. The PDE8A polypeptides and polynucleotides can be used for identifying their specific binding partners. The products can provide approaches for treating conditions in which cyclic nucleotide pathways are aberrant as well as conditions in which modulation of intracellular cAMP and/or cGMP levels in certain cell types is desirable
CC	
CC	
SQ	Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
DB	
QY	Query Match                      0.6%; Score 15.4; DB 1; Length 18; Best Local Similarity    94.1%; Pred No. 71; Matches    16; Conservative    0; Mismatches    1; Indels        0; Gaps        0  2399 TGCTGGCCCAATAGCAA 2415       1 TGCTGGCCCAATAGCAA 17
Db	
RESULT 71	
ID	AAA53107/c
ID	AAA53107 standard; DNA; 18 BP.
XX	
AC	AAA53107;
XX	
DT	15-SEP-2000 (first entry)
XX	
DE	Phage DNA primer Tagl SEQ ID NO:31.
XX	
KM	Genome analysis; tag; chromosomal location; integration site; insertion element; identification; polymorphism; PCR; primer; ss.
XX	
OS	Enterobacteria phage M13.
OS	Synthetic.
XX	
PN	MO200024937-A2.
PD	
PD	04-MAY-2000.
XX	
PF	27-OCT-1999; 99WO-US025037.
XX	
PR	28-OCT-1998; 98US-0105914P.
PR	26-OCT-1999; 99US-00427834.
XX	
PA	(STRA/) STRATHMANN M.
XX	
FI	Strathmann M;
XX	
DR	WPI; 2000-350769/30.
PT	Parallel methods of genomic analysis useful for determining polymorphisms, chromosome rearrangements and generating physical maps.
XX	
PS	Example 2; Page 97; 153pp; English.
XX	
CC	The present invention describes parallel methods of genomic analysis using polynucleotides associated with sample tags. The parallel methods are used for the following claimed procedures: (1) constructing a recombinant molecule consisting of a sequence element from a homologue of a sequenced polynucleotide joined to a vector; (2) producing a polypeptide, preferably of known sequence, from a recombinant molecule as



CC PDB8 coding sequence may be used in hybridisation assays to detect the  
CC capacity of cells to express PDB8, and as a basis for diagnostic methods  
CC useful for identifying a genetic alteration in a PDB8 locus that  
CC underlies a disease state or states. The human PDB8 gene has been  
CC localised to chromosome 6p26-27. The present sequence is a PCR primer  
CC used to isolate the coding sequence of human PDB8  
CC  
SQ Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 71;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2399 TCCTGGCCCAATAGCAA 2415  
DB 1 TCCTGGCCCAATAGCAA 17

## RESULT 74

AAD60000 standard; DNA; 18 BP.

AC AAD60000;  
XX  
XX AAD60000; (first entry)  
DT 18-DEC-2003  
XX  
XX Human FB66a DNA sequencing primer; M4857.  
DE  
XX Phosphodiesterase 8; PDB8; human; FB66a; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX US6566087-B1.  
PN  
XX 20-MAY-2003.  
PD  
XX  
XX 11-OCT-2000; 2000US-00686055.  
PF  
XX  
XX 16-OCT-1997; 97US-00951648.  
PR 16-OCT-1996; 96US-00174437.  
XX  
XX (ICOS-) ICOS CORP.  
PA  
XX  
XX Loughney K;  
PI  
XX WPI; 2003-719642/68.  
DR  
XX  
XX Identifying a specific binding partner of phosphodiesterase 8 (PDB8)  
PT useful for purifying PDB8 products in fluid samples comprises contacting  
PT PDB8 with a compound and detecting binding.  
PT  
XX  
XX Example 3; Col 10; 37pp; English.  
PS  
XX The invention relates to a method for identifying a specific binding  
CC partner of phosphodiesterase 8 (PDB8). The method is useful for  
CC identifying a specific binding partner of PDB8, which inhibits or  
CC enhances activity of PDB8. The binding partners of PDB8 are useful for  
CC purification, detection or quantification of PDB8 products in fluid and  
CC tissue samples using immunological procedures. Modulators of PDB8  
CC activity are useful in treating a wide range of diseases and  
CC physiological conditions in which PDB8 activity is known to be involved.  
CC The present sequence is a primer used for sequencing human PDB8 A2 splice  
CC variant DNA (FB66a)  
CC  
XX

SQ Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 71;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2399 TCCTGGCCCAATAGCAA 2415  
DB 1 TCCTGGCCCAATAGCAA 17

## RESULT 75

ABK33463/C  
ID ABK33463 standard; DNA; 19 BP.

AC ABK33463;  
XX

DT 23-APR-2002 (first entry)  
XX

DE Human TNF-receptor II 3' UNT nt 1690 (T/C) forward PCR primer.  
XX

XX Human; anti-tumour necrosis factor receptor II; TNF receptor II;  
XX TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder;  
XX inflammatory disorder; chronic disease; receptor; primer; ss.  
XX

OS Homo sapiens.  
XX

PN EP1172444-A1.  
XX

PD 16-JAN-2002.  
XX

PF 10-JUL-2000; 2000EP-00114786.  
XX

PR 10-JUL-2000; 2000EP-00114786.  
XX

PA (CONA-) CONNARIS RES INST GMBH.  
XX

PI Schreiber S, Hampe J, Mascheretti S;  
XX

DR WPI; 2002-156651/21.  
XX

PT Detecting non-responders to anti-human necrosis factor therapy, comprises  
PT testing an individual for homozygosity for a single nucleotide  
PT polymorphism in the gene coding for the tumor necrosis factor receptor  
PT II.  
XX

PS Disclosure; Page 8; 45pp; English.  
XX

XX The present invention relates to a method for detecting non-responders to  
CC anti-tumour necrosis factor (TNF) therapy. The method involves testing an  
CC individual for homozygosity for at least one single nucleotide  
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is  
CC located on chromosome 19p36. Two novel SNPs, one in exon 2 (position 168  
CC A/G) and one in exon 6 (position 587 T/G) which result in 15651ys and  
CC Met196Arg respectively, are also described. The method of the invention  
CC is useful for detecting non-responders to anti-TNF therapy such as  
CC infliximab therapy, or therapy of Crohn's disease. The genes containing  
CC the 2 novel polymorphisms are useful for diagnostic purposes in  
CC inflammatory, malignant or other chronic diseases. The present sequence  
CC represents a Tagman primer used in the methods of the present invention  
XX

SQ Sequence 19 BP; 6 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 493 CTGCTCTGGCCCTGAG 509  
DB 17 CTGCTCTGGCCCTGAG 1

## RESULT 76

AAQ43822  
ID AAQ43822 standard; DNA; 20 BP.

AC AAQ43822;  
XX

DT 25-MAR-2003 (revised)  
XX

DT 14-OCT-1993 (first entry)  
XX

DE Tumour cell proliferation inhibition factor PCR primer.  
XX

```
XX
KM Leukaemia; leukemia; uterine cancer; treatment;
KM polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9311233-A1.
XX
PD 10-JUN-1993.
XX
PF 03-DEC-1992; 92WO-JP001580.
XX
PR 05-DEC-1991; 91JP-00321929.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
PI Komurasaki T, Toyoda H, Yoshimoto M, Hanada K;
DR WPI; 1993-197052/24.
XX
XX New DNA fragment which codes for tumour cell proliferation inhibiting
PT factor - useful in treatment of leukemia and uterine cancer, and is
PT easily expressed in large amts. using Escherichia coli.
XX
PS Example; Fig 3; 42pp; Japanese.
XX
CC The sequence is that of a PCR primer #7 which was used in the
CC amplification and isolation of DNA encoding a tumour cell proliferation
CC inhibiting factor which can be used in the treatment of leukemia and
CC uterine cancer. The factors can be expressed easily in large amts. using
CC conventional techniques with E. coli. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
XX
QY
Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
2243 CCGTCCATATCAGAACT 2259
DB 3 CCGTCCATGTCAGAACT 19
XX
RESULT 77
AAQ43819/c
ID AAQ43819 standard; DNA; 20 BP.
XX
AC AAQ43819;
XX
DT 25-MAR-2003 (revised)
DT 14-OCT-1993 (first entry)
XX
DE Tumour cell proliferation inhibition factor PCR primer.
XX
KM Leukaemia; leukemia; uterine cancer; treatment;
KM polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9311233-A1.
XX
PD 10-JUN-1993.
XX
PF 03-DEC-1992; 92WO-JP001580.
XX
PR 05-DEC-1991; 91JP-00321929.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
PI Komurasaki T, Toyoda H, Yoshimoto M, Hanada K;
DR WPI; 1993-197052/24.
```

```
XX
PT New DNA fragment which codes for tumour cell proliferation inhibiting
PT factor - useful in treatment of leukemia and uterine cancer, and is
PT easily expressed in large amts. using Escherichia coli.
XX
PS Example; Fig 3; 42pp; Japanese.
XX
CC The sequence is that of a PCR primer #4 which was used in the
CC amplification and isolation of DNA encoding a tumour cell proliferation
CC inhibiting factor which can be used in the treatment of leukemia and
CC uterine cancer. The factors can be expressed easily in large amts. using
CC conventional techniques with E. coli. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
XX
QY
Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
2243 CCGTCCATATCAGAACT 2259
DB 18 CCGTCCATGTCAGAACT 2
XX
RESULT 78
AAQ54252
ID AAQ54252 standard; DNA; 20 BP.
XX
AC AAQ54252;
XX
DT 02-AUG-1994 (first entry)
XX
DE Cancer cell growth inhibitor primer.
XX
KM Cancer cell; inhibitor; growth; tumour; leukemia; cervical cancer;
KM uterine cancer; bacillus brevis; transformation; expression; vector;
KM growth inhibiting factor; ss.
XX
OS Synthetic.
XX
PN JP05304962-A.
XX
PD 19-NOV-1993.
XX
PF 05-DEC-1991; 91JP-00321928.
XX
PR 05-DEC-1991; 91JP-00321928.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
DR WPI; 1993-408321/51.
XX
PT Tumour cell growth inhibiting factor for leukemia and cervical, uterine
PT cancer - obtd. by culturing bacillus brevis transformant to express
PT factor and secrete it extracellularly and recovering from culture.
XX
PS Disclosure; Fig 5; 20pp; Japanese.
XX
CC The primers (AAQ54246-56) are used to amplify the cancer cell growth
CC inhibiting factor shown in sequences (AAQ54240-42)
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
XX
QY
Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
2243 CCGTCCATATCAGAACT 2259
DB 3 CCGTCCATGTCAGAACT 19
```

```

RESULT 79
AA054249/C
ID AA054249 standard; DNA; 20 BP.
XX
AC AA054249;
XX
DT 02-AUG-1994 (first entry)
XX
DE Cancer cell growth inhibitor primer.
XX
KW Cancer; cell; inhibitor; growth; tumour; leukaemia; cervical cancer;
KW uterine cancer; bacillus brevis; transformation; expression; vector;
KW growth inhibiting factor; ss.
XX
OS Synthetic.
XX
PN JF05304962-A.
XX
PD 19-NOV-1993.
XX
PF 05-DEC-1991; 91UP-00321928.
XX
PR 05-DEC-1991; 91UP-00321928.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
DR WPI; 1993-408321/51.
XX
PT Tumour cell growth inhibiting factor for leukaemia and cervical, uterine
PT cancer - obd. by culturing bacillus brevis transformant to express
PT factor and secrete it extracellularly and recovering from culture.
XX
PS Disclosure; Fig 5; 20pp; Japanese.
XX
CC The primers (AA054246-56) are used to amplify the cancer cell growth
CC inhibiting factor shown in sequences (AA054240-42)
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2243 CCGTCCATATCAGAACT 2259
DB 18 CCGTCCATGTCAGAACT 2
RESULT 80
AA094242/C
ID AA094242 standard; DNA; 20 BP.
XX
AC AA094242;
XX
DT 14-MAY-1998 (first entry)
XX
DE Primer P1 16 for regulatory p85-alpha subunit of PI3K.
XX
KW PCR primer; detection; regulatory p85-alpha subunit; PI3K; obesity;
KW mutation; phosphatidylinositol 3 kinase; hypertension;
KW non-insulin dependent diabetes; cardiovascular disease; ss.
XX
OS Synthetic.
XX
PN WO9742310-A1.
XX
PD 13-NOV-1997.
XX
PF 02-MAY-1997; 97WO-DK000200.
XX
PR 06-MAY-1996; 96DK-00000539.
XX

```

```

PA (NOVO ) NOVO-NORDISK AS.
XX
PI Hansen T, Andersen CB, Pedersen OB;
XX
DR WPI; 1997-558976/51.
XX
PT Mutant phosphatidylinositol 3 kinase regulatory subunit DNA - useful to
PT detect predileposition to impaired glucose tolerance and reduced insulin
PT sensitivity.
XX
PS Example; Page 19; 34pp; English.
XX
CC The present sequence is a DNA primer used for PCR amplification to detect
CC the regulatory p85-alpha subunit of phosphatidylinositol 3 kinase (PI3K)
CC amino acid substitution at codon 326, preferably Met326Ile, by SSCP gel
CC analysis. A nucleic acid sequence encoding a regulatory subunit of PI3K,
CC and comprising at least 1 mutated nucleotide, can be used as a diagnostic
CC tool, marker or probe. The presence of a mutation in a gene encoding a
CC regulatory subunit of PI3K can be detected by analysing a biological
CC sample for the above nucleic acid sequence, useful to determine
CC predileposition to impaired glucose tolerance (particularly when related
CC to reduced glucose disappearance constant), or decreased glucose
CC efficiency or insulin sensitivity (all of which may develop into non-
CC insulin dependent diabetes, cardiovascular disease, obesity or
CC hypertension
XX
SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1940 AAGAGAGCTTGAGAGAG 1956
DB 18 AAGAGAGCTTGAGAGAG 2
RESULT 81
AA210330/C
ID AA210330 standard; DNA; 20 BP.
XX
AC AA210330;
XX
DT 08-NOV-1999 (first entry)
XX
DE PCR primer used to detect codon 326 polymorphism of P85-alpha.
XX
KW Regulatory p85-alpha subunit; human; phosphatidylinositol 3-kinase; PI3K;
KW growth factor plasma membrane receptor; insulin receptor;
KW tyrosine kinase activity; vesicle trafficking; protein sorting;
KW pinocytic activity; cytoskeletal rearrangement; membrane ruffling;
KW actin reorganization; insulin; glucose disappearance rate;
KW glucose sensitivity; glucose resistance; glucose tolerance;
KW non-insulin dependent diabetes mellitus; cardiovascular disease; obesity;
KW hypertension; glucose metabolism; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5955277-A.
XX
PD 21-SEP-1999.
XX
PF 05-MAY-1997; 97US-00850993.
XX
PR 05-MAY-1997; 97US-00850993.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Hansen T, Pedersen OB, Andersen CB;
XX
DR WPI; 1999-539565/45.
XX

```

PT Altered nucleic acids encoding P85alpha subunits of human  
PT phosphatidylinositol 3-kinase, useful for identifying mutations that may  
PT be associated with impaired glucose transport and metabolism.  
XX  
PS Example; Col 14; 14pp; English.  
XX  
CC The present sequence represents a PCR primer used for PCR amplification  
CC to detect the regulatory P85-alpha subunit of human phosphatidylinositol  
CC 3-kinase (PI3K) amino acid substitution mutation at codon 326. PI3K binds  
CC to growth factor plasma membrane receptors (including insulin receptors)  
CC and signaling motifs in signaling proteins and modulates the activity of  
CC those molecules through tyrosine kinase activity. It is also associated  
CC with vesicle trafficking and protein sorting and therefore acts as a  
CC mediator of insulin action on glucose transport and metabolism. The  
CC specification describes a mutated P85-alpha nucleic acid sequence which  
CC comprises the mutations, relative to the present sequence: C261T, T663G,  
CC A810G, and/or G1020A. The nucleic acids may be used to detect mutated  
CC genes encoding the P85 alpha subunit of PI3K and to identify mutations  
CC which may alter the activity of the polypeptide and result in a disease  
CC state. PI3K is associated with pinocytic activity, cytoskeletal  
CC rearrangements that accompany secretory processes, membrane ruffling,  
CC actin reorganization in KB cells in response to insulin, protein sorting  
CC and in membrane and vesicle trafficking. Therefore, PI3K acts as a  
CC mediator of insulin action on glucose transport and metabolism. Mutations  
CC in the PI3K gene result in decreased glucose disappearance rates.  
CC decreased glucose effectiveness and decreased glucose sensitivity.  
CC Consequently, mutations in PI3K genes are associated with glucose  
CC resistance or (impaired glucose tolerance), non-insulin dependent  
CC diabetes mellitus (NIDDM), cardiovascular disease, obesity and  
CC hypertension and other diseases resulting from altered glucose metabolism  
XX  
SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1940 AAGAGAGCTGGAAGAG 1956  
DB 18 AAGAGAGCTTGAAGAG 2  
XX  
RESULT 82  
AAZ01841  
ID AAZ01841 standard; DNA; 20 BP.  
XX  
AC AAZ01841;  
XX  
DT 07-OCT-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
XX  
KW Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;  
KW paratrachoma; inclusion conjunctivitis; genital disease; perithenitis;  
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
XX  
OS Synthetic.  
OS Chlamydia trachomatis.  
XX  
XX WO9298475-A2.  
XX  
XX 10-UTN-1999.  
XX  
PD 27-NOV-1998; 98WO-1B001939.  
XX  
PF 28-NOV-1997; 97FR-00015041.  
PR 17-DEC-1997; 97FR-00016034.  
PR 04-NOV-1998; 98US-0107077P.  
XX  
XX (GEST ) GENSET.  
PA  
XX Griffais R;  
PI

XX  
DR WPI; 1999-371125/31.  
XX  
XX Genome sequence of Chlamydia trachomatis.  
XX  
PT  
XX  
PS Disclosure; Page 1476; 1755pp; English.  
XX  
CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
CC be used to control growth of the microorganism. Chlamydia trachomatis is  
CC responsible for a large number of diseases, e.g. eye diseases such as  
CC conjunctivitis; genital diseases such as nongonococcal urethritis;  
CC epididymitis; cervicitis; salpingitis; perithenitis; Bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases  
XX  
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 15.4; DB 1; Length 20;  
Best Local Similarity 94.1%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1943 AAGAGCTGGAAGAGTTC 1959  
DB 4 AAGAGCTGGAAGAGTTC 20  
XX  
RESULT 83  
AAZ26981/C  
ID AAZ26981 standard; DNA; 20 BP.  
XX  
AC AAZ26981;  
XX  
DT 25-UTN-1999 (first entry)  
XX  
DE PCR primer used to amplify the signal peptide of LAMP-1 protein.  
XX  
KW MAGE-3 tumour associated gene; human leucocyte antigen Class II;  
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
KW osteosarcoma; leukemia; carcinoma; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9914326-A1.  
XX  
XX 25-MAR-1999.  
XX  
PD 04-SEP-1998; 98WO-US018601.  
XX  
PF 12-SEP-1997; 97US-00928615.  
PR  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (UYVR-) UNIV VIRJIE BRUSSEL.  
XX  
XX Thielemans K, Heirman C, Cortals J, Chauv P, Stroobant V;  
PI Boon-Palleur T, Van Der Bruggen P, Luiten R;  
XX  
XX WPI; 1999-244031/20.  
XX  
DR  
XX  
XX Isolated peptides that bind to human leucocyte antigen class II  
XX molecules.  
XX  
XX Example 5; Page 38; 88pp; English.  
XX  
CC PCR primers AAZ26980-81 were used to amplify DNA encoding the signal  
CC peptide of the LAMP-1 protein. The specification describes a MAGE-3 tumour  
CC associated gene. Peptides that bind human leucocyte antigen (HLA) class  
CC II molecules can be derived from the MAGE-3 protein. These peptides and  
CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA

CC Class II, are used to treat MAGE-3 related diseases, particularly cancers  
 CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
 CC The peptides are also used to produce specific antibodies. Detection of  
 CC of the peptides, e.g. in binding assays, particularly with antibodies, is  
 CC used for diagnosis of such diseases

XX Sequence 20 BP; 1 A; 12 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 77;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGGCGGCCCATGG 463

DB 20 GCCGGGGCGGCCCATGG 4

RESULT 84  
 AAA37934/C

ID AAA37934 standard; DNA; 20 BP.

XX AAA37934;

XX 18-AUG-2000 (first entry)

DE PCR primer used in the construction of pmwG-sig.MAGE-A3.LAMP-1.

XX MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;

KW cancer; human; tumour; tumour associated gene product; PCR primer; ss.

XX Homo sapiens.

PN MO200020581-A1.

PD 13-APR-2000.

PF 15-SEP-1999; 99WO-US021230.

PR 05-OCT-1998; 98US-00166448.

PA (LUDWIG) LUDWIG INST CANCER RES.

PI (UYR-) UNIV VIRITE BROUSEL.

PI Chaux P, Strobant V, Boon-Falleur T, Van Der Bruggen P;

PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;

PI Heitman C;

XX WPI; 2000-317713/27.

XX New MAGE-A3 class II binding peptides, useful to diagnose and treat

XX tumors, are fragments of MAGE-A3 which bind to and are presented to T

XX lymphocytes by human leukocyte antigen class II molecules.

XX Example 6; Page 46; 119pp; English.

XX The present invention relates to MAGE-A3 (tumour associated gene product)

XX human leukocyte antigen (HLA) class II-binding peptides (see AA02566-

XX B02595, and AA02633-B02637). These peptides are presented to T cells in

XX the context of HLA class II molecules. The peptides stimulate the

XX activity and proliferation of CD4+ T lymphocytes. The invention also

XX includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928 and

XX AAA37938-A37940). The peptides and nucleotide sequences can be used to

XX create antibodies against the MAGE-A3 peptides, the antibodies, peptides

XX and nucleotide sequences can be used to create a vaccine. The peptides

XX are used to diagnose or treat a disorder characterized by expression of

Query Match 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 77;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 447 GCCGGGGCGGCCCATGG 463

DB 20 GCCGGGGCGGCCCATGG 4

RESULT 85

AAC83443/C

ID AAC83443 standard; DNA; 20 BP.

XX AAC83443;

XX 27-FEB-2001 (first entry)

XX Primer Ha5.2.

XX Primer; immunization; AIDS; tetanus; tuberculosis; malaria; cancer; ss.

XX Unidentified.

XX MO20006179-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000MO-US012001.

XX 03-MAY-1999; 98US-0132216P.

XX 23-MAR-2000; 2000US-00535149.

XX (UABR-) UAB RES FOUND.

XX Tang DC, Marks DH, Curiel DT, Shi Z, Van Kampen KR;

XX WPI; 2000-687450/67.

XX Non-invasive genetic immunization comprising contacting an animal with a

XX vector containing a nucleic acid, useful for the treatment of e.g.

XX acquired immune deficiency syndrome (AIDS), tuberculosis, malaria,

XX malignant tumors and cancers.

XX Example 18; Page 44; 81pp; English.

XX The present invention relates to a method of non-invasive genetic

XX immunization in an animal and a method of inducing a systemic immune

XX response to a gene product comprising contacting an animal with a vector

XX that contains a nucleic acid encoding the gene product. The non-invasive

XX vaccine may be used for the treatment of acquired immune deficiency

XX syndrome (AIDS), tetanus, tuberculosis, malaria, malignant tumours and a

XX wide variety of cancers. The method allows non-invasive, simple, less

XX effective, economical and painless immunization. The method is less

XX dependent on medical resources and therefore increases the annual

XX utilization rate of vaccinations

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 77;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGGTAAGTAATACCCCA 1825

DB 18 GGGTAAGTAATACCCCA 2

RESULT 86

AAH39578

ID AAH39578 standard; DNA; 20 BP.

XX AAH39578;

XX 27-FEB-2001 (first entry)

XX Primer Ha5.2.

XX Primer; immunization; AIDS; tetanus; tuberculosis; malaria; cancer; ss.

XX Unidentified.

XX MO20006179-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000MO-US012001.

XX 03-MAY-1999; 98US-0132216P.

XX 23-MAR-2000; 2000US-00535149.

XX (UABR-) UAB RES FOUND.

XX Tang DC, Marks DH, Curiel DT, Shi Z, Van Kampen KR;

XX WPI; 2000-687450/67.

XX Non-invasive genetic immunization comprising contacting an animal with a

XX vector containing a nucleic acid, useful for the treatment of e.g.

XX acquired immune deficiency syndrome (AIDS), tuberculosis, malaria,

XX malignant tumors and cancers.

XX Example 18; Page 44; 81pp; English.

XX The present invention relates to a method of non-invasive genetic

XX immunization in an animal and a method of inducing a systemic immune

XX response to a gene product comprising contacting an animal with a vector

XX that contains a nucleic acid encoding the gene product. The non-invasive

XX vaccine may be used for the treatment of acquired immune deficiency

XX syndrome (AIDS), tetanus, tuberculosis, malaria, malignant tumours and a

XX wide variety of cancers. The method allows non-invasive, simple, less

XX effective, economical and painless immunization. The method is less

XX dependent on medical resources and therefore increases the annual

XX utilization rate of vaccinations

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 77;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGGTAAGTAATACCCCA 1825

DB 18 GGGTAAGTAATACCCCA 2

RESULT 86

AAH39578

ID AAH39578 standard; DNA; 20 BP.

XX AAH39578;

XX 27-FEB-2001 (first entry)

XX Primer Ha5.2.

XX Primer; immunization; AIDS; tetanus; tuberculosis; malaria; cancer; ss.

XX Unidentified.

XX MO20006179-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000MO-US012001.

XX 03-MAY-1999; 98US-0132216P.

XX 23-MAR-2000; 2000US-00535149.

XX (UABR-) UAB RES FOUND.

XX Tang DC, Marks DH, Curiel DT, Shi Z, Van Kampen KR;

XX WPI; 2000-687450/67.

XX Non-invasive genetic immunization comprising contacting an animal with a

XX vector containing a nucleic acid, useful for the treatment of e.g.

XX acquired immune deficiency syndrome (AIDS), tuberculosis, malaria,

XX malignant tumors and cancers.

XX Example 18; Page 44; 81pp; English.

XX The present invention relates to a method of non-invasive genetic

XX immunization in an animal and a method of inducing a systemic immune

XX response to a gene product comprising contacting an animal with a vector

XX that contains a nucleic acid encoding the gene product. The non-invasive

XX vaccine may be used for the treatment of acquired immune deficiency

XX syndrome (AIDS), tetanus, tuberculosis, malaria, malignant tumours and a

XX wide variety of cancers. The method allows non-invasive, simple, less

XX effective, economical and painless immunization. The method is less

XX dependent on medical resources and therefore increases the annual

XX utilization rate of vaccinations

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 77;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1809 GGGTAAGTAATACCCCA 1825

DB 18 GGGTAAGTAATACCCCA 2

RESULT 86

AAH39578

DT 14-AUG-2001 (first entry)  
 XX SNP specific lower PCR primer SEQ ID 2374.  
 DE  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
 KM polyarthritis; osteogenesis imperfecta; autoimmune disease;  
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000MO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 PI Picoult-Newburg L, Pohl M;  
 XX  
 DR WPI; 2001-290930/30.  
 XX  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 62; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNP) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 XX  
 SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 QY  
 DB 2266 CAATGCAATCTCTAGCA 2282  
 4 CAATGCAATCTCTAGCA 20  
 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 77;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 87  
 ABL44409/c  
 ID ABL44409 standard; DNA; 20 BP.  
 XX  
 AC ABL44409;

XX 11-APR-2002 (first entry)  
 DT  
 XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1453.  
 DE  
 XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
 KM PCR primer; ss.  
 KM  
 XX Homo sapiens.  
 XX  
 PN JP2001321190-A.  
 XX  
 PD 20-NOV-2001.  
 XX  
 PF 12-MAR-2001; 2001JP-00068285.  
 XX  
 PR 10-MAR-2000; 2000JP-00066716.  
 XX  
 PA (RIKA) RIKAGAKU KENKYUSHO.  
 PA (GENO-) GENOTEX YG.  
 XX  
 DR WPI; 2002-144136/19.  
 XX  
 PT Arraying genome clones.  
 XX  
 PS Claim 4; Page 33; 528pp; Japanese.  
 XX  
 CC The present invention describes a method of arraying genome clones. The  
 CC method comprises: (a) clones of the genomic libraries contained in  
 CC multiwell plates numbered for discrimination are mixed in each of the  
 CC multiwell plates; (b) a primer designed based on the chromosome marker  
 CC sequence is added to the mixture to carry out an amplification reaction;  
 CC (c) a signal corresponding to the marker is detected from the resultant  
 CC amplified product to specify the discrimination Nos. of the multiwell  
 CC plates containing the clones having said marker sequence; (d) the order  
 CC of the markers is changed so that the same discrimination Nos. succeed to  
 CC the maximum in the specified discrimination Nos. to array the multiwell  
 CC plates; (e) the clones in the multiwell plates of the specified  
 CC discrimination Nos. are mixed respectively in each wells of longitudinal  
 CC and lateral directions; (f) the mixed clones are cultured and the  
 CC resultant cultures are amplified by using the above primer; (g) signals  
 CC are detected from the amplified products; (h) the clones in the multiwell  
 CC plates are specified from the detected result; and (i) the clones are  
 CC reconstituted as the positions on the chromosome and arrayed. The  
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
 CC represent PCR primers for human chromosome 21q22.1, which are  
 CC specifically claimed for use in the present invention  
 XX  
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;  
 XX  
 QY  
 DB 1955 AGTTCGACCAAGAGC 1971  
 18 AGTTCGACCAAGAGC 2  
 0.6%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 77;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 88  
 ACC71703/c  
 ID ACC71703 standard; DNA; 20 BP.  
 XX  
 AC ACC71703;  
 XX  
 DT 23-JUL-2003 (first entry)  
 XX  
 DE Interferon Regulatory Factor (IRF)-1/-2 probe.  
 XX  
 KM Antiaesthetic; immunosuppressive; ophthalmological; IRF-1; IRF-2;  
 KM Interferon Regulatory Factor 1; Interferon Regulatory Factor 2; probe;  
 KM Interleukin-4; IL-4; asthma; rhinocconjunctivitis; autoimmune disease; ss.

```

XX OS Synthetic.
XX PN BP1298141-A1.
XX PD 02-APR-2003.
XX PF 27-SEP-2001; 2001EP-00123096.
XX PR 27-SEP-2001; 2001EP-00123096.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX DR WPI; 2003-405560/39.
XX PT New nucleic acid, useful for preparing a medicament for treating a
XX disease associated with a decreased interleukin (IL)-4 expression e.g.
XX asthma, rhinoconjunctivitis and autoimmune disease.
XX PS Example 1; Page 7; 26pp; English.
XX CC The present invention relates to oligonucleotides (ACC71701 and ACC71702)
XX CC which are capable of specifically interacting with Interferon Regulatory
XX CC Factor (IRF)-1 and/or IRF-2. The oligonucleotides are useful for
XX CC preparing a medicament for treating a disease associated with a decreased
XX CC interleukin (IL)-4 expression e.g. asthma, rhinoconjunctivitis and
XX CC autoimmune disease. ACC71701 and ACC71702 were originally located within
XX CC the IL-4 promoter. The present sequence is a probe, which was used in an
XX CC example from the invention
SQ Sequence 20 BP; 5 A; 3 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 878 AGGAAATGAGGCTT 894
DB 17 AGGAAATGAACTTT 1

RESULT 89
AAQ62025/c
ID AAQ62025 standard; DNA; 20 BP.
XX AC AAQ62025;
XX DT 25-MAR-2003 (revised)
XX DT 17-NOV-1994 (first entry)
XX DE Mutant Ki-ras 5'-UTR/5' cap antisense phosphorothioate oligo ref. 6958.
XX KM Antisense; phosphorothioate; H-ras; translation initiation codon;
XX KM codon-12 point mutation; activated; inhibition; ras-luciferase; activity;
XX KM detection; modulation; inhibition; expression; oncogene; proliferation;
XX KM Ki-ras; cancer cell; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_difference 1..20
XX FT /*tag= a
XX FT /note= "Phosphorothioate linkages"
XX PN MO9408003-A1.
XX PD 14-APR-1994.
XX PF 01-OCT-1993; 93WO-US009346.
XX PR 05-OCT-1992; 92US-00958134.
XX PR 21-JAN-1993; 93US-00007996.

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PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Ecker DJ;
XX DR WPI; 1994-135570/16.
XX PT New oligo:nucleotides hybridisable with H-ras or Ki-ras gene nucleic acid
XX PT - in normal or mutated form, for detecting or modulating gene expression,
XX PT specifically inhibiting proliferation of cancer cells.
XX PS Claim 109 and 115; Page 36; 104pp; English.
XX CC The sequences given in AAQ62025-38 are antisense phosphorothioate
XX CC oligonucleotides which are targeted to various regions of Ki-ras
XX CC oncogene. These oligonucleotides gave significant and reproducible
XX CC inhibition of the level of Ki-ras mRNA. These oligonucleotides may be
XX CC used for detecting and modulating, esp. inhibiting, expression of the Ki-
XX CC ras gene, esp. for inhibiting proliferation of cancer cells, and other
XX CC conditions associated with Ki-ras oncogene activation. Activated (mutant)
XX CC Ki-ras can be detected from its differential affinity for particular
XX CC oligos. (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 400 GGGCGTCCGCGGAGGCGAG 419
DB 20 GGGCGGCGGCGGAGGCGAG 1

RESULT 90
AAQ79844/c
ID AAQ79844 standard; DNA; 20 BP.
XX AC AAQ79844;
XX DT 25-MAR-2003 (revised)
XX DT 04-SEP-1995 (first entry)
XX DE K-ras modulating sequence, targeted to 5' UTR/5' cap.
XX KM Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;
XX KM expression; ras gene; mutation; tumour; cancer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /note= "Each base is attached to a N-acetyl(2-amino-
XX FT ethyl)Gly residue through the N-acetyl group"
XX PN MO9428720-A1.
XX PD 22-DEC-1994.
XX PF 10-JUN-1994; 94WO-US006620.
XX PR 11-JUN-1993; 93US-00076234.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Lima W, Monia B, Freier S, Ecker D;
XX DR WPI; 1995-035955/05.
XX PT New peptide nucleic acid oligomers for ras oncogene modulation -
XX PT including specific inhibition of the activated gene, for diagnosis and
XX PT treatment esp. of tumours.

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	Matches	17;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1665	CATGAGAGAGAGGTTGAAG	1664							
Db	1	CACGTAGAGAGAGGTTGAAG	20							
RESULT 92										
ID	AA764699	AA764699 standard; DNA, 20 BP.								
AC	AA764699;									
XX										
XX										
DT	25-MAR-2003	(revised)								
DT	12-FEB-1998	(first entry)								
XX										
DE	Primer D8621	for mapping prostate/colon tumour suppressor gene.								
KX	Prostate/colon tumour suppressor;	allelic loss; prostate cancer;								
KX	colorectal cancer; microsatellite	analysis; sequence tagged site; STS;								
KX	amplification; chromosomal	location 8q22-21; probe; primer; gene mapping;								
KX	diagnosis; treatment; ss.									
XX										
XX	Synthetic.									
OS	Homo sapiens.									
XX										
PN	JPO9098790-A.									
XX										
PD	15-APR-1997.									
XX										
PF	22-FEB-1996;	96JP-00062144.								
XX										
PR	22-MAY-1995;	95US-00445515.								
XX										
PA	(CANT-) CANJI INC.									
PA	(UYJO ) UNIV JOHNS HOPKINS.									
XX										
PI	Isaacs WB, Bookstein R;									
XX										
DR	WPI; 1997-275447/25.									
XX										
PT	New prostate/colon tumour suppressor gene -	mapped to a locus on human								
PT	chromosome 8.									
PS										
PS	Disclosure; Page 25; 45pp; Japanese.									
XX										
CC	The present primer was used in the	mapping of a gene encoding 2 forms of								
CC	a prostate/colon tumour suppressor	(P/CTS). The P/CTS gene was isolated								
CC	by analysis of allelic loss in	patients with prostate cancer, and was								
CC	putatively located to the	chromosomal location 8q22-21 via microsatellite								
CC	analysis and the use of	sequence tagged sites (STS). Primers and probes								
CC	derived from the gene can	be used to screen lambda cDNA libraries for								
CC	genes encoding P/CTS form	1 and 2. The P/CTS or its cDNA can be used in								
CC	the diagnosis and	treatment of prostate and colorectal cancers. (Updated								
CC	on 25-MAR-2003 to	correct PA field.) (Updated on 25-MAR-2003 to correct								
CC	PI field.)									
XX										
XX	Sequence 20 BP, 7 A, 2 C, 8 G, 3 T, 0 U, 0	Other;								
XX										
SO										
Query Match		0.6%; Score 15.2; DB 1; Length 20;								
Best Local Similarity		85.0%; Pred.No. 82;								
Matches	17;	Conservative 0; Mismatches 3; Indels 0; Gaps 0;								
QY	1665	CATGAGAGAGAGGTTGAAG	1664							
Db	1	CACGTAGAGAGAGGTTGAAG	20							
RESULT 93										
ID	AA773572	AA773572 standard; DNA, 20 BP.								
XX										
AC	AA773572;									

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XX 01-OCT-1997 (first entry)
DT
XX Primer UGT184r for STS marker of apomixis gene.
DE
XX Apomixis gene; true-breeding; pearl millet; molecular marker; probe;
KM hybrid seed; transgenic plant; Pennisetum squamulatum;
XX sequence tagged site; STS; polymerase chain reaction; PCR; primer; ss.
OS Synthetic.
XX WO9710704-A1.
XX 27-MAR-1997.
XX 23-SEP-1996; 96WO-US015169.
XX 22-SEP-1995; 95US-00532050.
XX (USDA) US SEC OF AGRIC.
XX Hanna WE, Ozias-Akins P, Dujardin M;
XX WPI; 1997-202528/18.
XX Transgenic apomictic plants, e.g. pearl millet, expressing Pennisetum
PT squamulatum apomixis gene(s) - useful as forage or grain cultivar(s) or
PT to develop true-breeding hybrids.
XX Example 5; Page 39; 87pp; English.
XX Primer pairs UGT184f (AAT73571) and UGT184r (AAT73572), UGT197f
CC (AAT73573) and UGT197r (AAT73574), and UGT1f1 (AAT73575) and UGT1r2
CC (AAT73576) were used to amplify sequence-tagged sites (STS) from
CC Pennisetum genomic DNA. The primers were designed from sequences cloned
CC from a BC3 clonal line K169-46 library. The STS can be used as molecular
CC markers for the identification of Pennisetum apomixis genes. Such genes,
CC esp. from Pennisetum squamulatum, can be transferred to pearl millet to
CC provide apomictic plants useful as forage or grain cultivars or for
CC development of true-breeding hybrids
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CTGCAGAGATGGGCTCTC 686
DB 1 CTGCAGCATATGGGCTCTC 20

RESULT 94
AAV22579/c
ID AAV22579 standard; DNA; 20 BP.
XX
XX AAV22579;
AC
XX 08-UTL-1998 (first entry)
DT
XX Antisense oligonucleotide designed to target the R1 message.
DE
XX R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
KM antisense; growth inhibition; sensitivity; hydroxyurea;
KM chemotherapeutic drug; methotrexate; PAIA; treatment; ss.
XX Synthetic.
XX OS Homo sapiens.
XX WO9805769-A2.
XX 12-FEB-1998.
XX

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PF 01-AUG-1997; 97WO-CA000540.
XX
XX 02-AUG-1996; 96US-0023040P.
PR 07-MAR-1997; 97US-0039599P.
XX
XX (GENE-) GENSENSE TECHNOLOGIES INC.
XX Wright JA, Young AH;
XX WPI; 1998-145609/13.
XX Antisense oligonucleotides to ribonucleotide reductase genes - used to
PT modulate tumour growth and inhibit tumour cell proliferation.
XX
XX Claim 8; Page 49; 79pp; English.
XX AAV2531-89 represent antisense oligonucleotides which are targeted
CC against the mRNA of the R1 subunit sequence of ribonucleotide reductase.
CC aberrant expression of the R2 gene, which encodes the second subunit of
CC the ribonucleotide reductase gene, can determine the malignant
CC characteristics of cells. Suppression of R2 and R1 gene expression was
CC found to reduce transformed properties of tumour cells. The antisense
CC oligonucleotides can be used for modulating tumour cell growth, or for
CC inhibiting tumour cell proliferation. They can also be used for
CC increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
CC (especially to hydroxyurea, methotrexate (MTX), and PAIA). The antisense
CC oligonucleotides may be used to treat proliferative disorders including
CC leukaemias, lymphomas, sarcomas, melanomas, various other forms of
CC cancer, papillomas, arthrosclerosis, psoriasis, polycythemia, mastocytosis,
CC autoimmune diseases, angio genesis, bacterial infections and viral
CC infections (including HIV hepatitis, or herpes infections)
XX
SQ Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1668 GGAAGGAAGAGCTGAGAGCT 1687
DB 20 GGAAGCAGGCTTGAAGACT 1

RESULT 95
AAV84024/c
ID AAV84024 standard; DNA; 20 BP.
XX
XX AAV84024;
AC
XX 05-MAR-1999 (first entry)
DT
XX Antisense oligonucleotide 6958 directed against Ki-ras 5' UTR/5' cap.
DE
XX Antisense oligonucleotide; phosphorothioate; human H-ras;
KM tumour formation; cancer cell proliferation; ss.
XX Synthetic.
XX OS Homo sapiens.
XX WO9849349-A1.
XX 05-NOV-1998.
XX 30-APR-1998; 98WO-US008800.
XX 30-APR-1997; 97US-00848840.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Cook PD, Monia BP, Freier SM, Sanghvi YS;
XX WPI; 1999-024070/02.
XX

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PT New oligonucleotides for inhibiting ras gene in mutant and activated form  
 PT - also used to detect ras genes.  
 XX  
 PS Disclosure; Page 38; 118pp; English.  
 XX  
 CC AAV84024-37 represent antisense phosphorothioate oligonucleotides  
 CC directed against human K1-ras. The oligonucleotides are representative of  
 CC the invention, where each oligonucleotide has at least one portion  
 CC comprising at least one CH2-NH-O-CH2, CH2-O-N(CH3)-CH2, CH2-N(CH3)-N(CH3)  
 CC -CH2 or O-N(CH3)-CH2-CH2 linkage alternating with a phosphorothioate or  
 CC phosphodiester linkage. The oligonucleotides are used for the inhibition  
 CC of expression of the ras gene in both the normal and the activated form,  
 CC the latter of which has been implicated in tumour formation. They are  
 CC also used for the detection of the ras gene in cells and tissues and the  
 CC treatment of conditions arising from the activation of the ras gene i.e.  
 CC to inhibit the proliferation of cancer cells  
 CC  
 XX  
 SQ Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 400 GGCGGTGCGCGCGAGGCGAG 419  
 DB 20 GGCGCGCGCGCGCGAGGCGAG 1  
 RESULT 96  
 AAZ37593  
 ID AAZ37593 standard; DNA; 20 BP.  
 XX  
 AC AAZ37593;  
 XX  
 PN 07-JAN-2000 (first entry)  
 DT  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #123.  
 XX  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;  
 KW hyperproliferation; blood cancer; brain cancer; breast cancer;  
 KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
 KW restenosis; ss.  
 KM  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 XX  
 PN WO9449065-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006702.  
 XX  
 PR 26-MAR-1998; 98US-00048810.  
 XX  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Miraglia LJ, Nero P, Graham MJ, Monica BP, Cowsett LM;  
 XX  
 DR WPI; 1999-610754/52.  
 DR  
 PT New antisense compounds used to treat eg. hyperproliferative conditions.  
 PT  
 PS Example 9; Page 50; 157pp; English.  
 XX  
 CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the  
 CC exemplification of the present invention. The present invention describes  
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
 CC translation termination codon, or 3' untranslated region of a nucleic  
 CC acid encoding human mdm2, that modulates expression of human mdm2. The  
 CC oligonucleotides mediate their effect by antisense inhibition of  
 CC hyperproliferative gene expression. The antisense compound is used to

CC treat an animal having a disease or condition associated with mdm2,  
 CC particularly a hyperproliferative condition, more particularly cancer,  
 CC especially of the blood, brain, breast, lung or soft tissue, or  
 CC psoriasis, fibrosis, atherosclerosis or restenosis  
 CC  
 XX  
 SQ Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1005 GCTTCTCAATGAAGAG 1024  
 DB 1 GCTTCTCAATGAAGAG 20  
 RESULT 97  
 AAZ1620/c  
 ID AAZ1620 standard; DNA; 20 BP.  
 XX  
 AC AAZ1620;  
 XX  
 DT 14-MAY-1999 (first entry)  
 DT  
 XX  
 DE Human K1-ras specific antisense oligo ISIS #6958.  
 XX  
 KW Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;  
 KW diagnostic; therapeutic; tumour; K1-ras; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 XX  
 PN WO9902732-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 06-JUL-1998; 98WO-US013966.  
 XX  
 PR 08-JUL-1997; 97US-00889296.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monica BP, Cowsett LM, Manoharan M;  
 XX  
 DR WPI; 1999-120932/10.  
 DR  
 PT New oligonucleotide targeting human N-ras nucleic acid - is capable of  
 PT inhibiting human N-ras expression, useful for preventing or treating  
 PT conditions arising from the activation of a human N-ras oncogene.  
 XX  
 PS Disclosure; Page 35; 97pp; English.  
 XX  
 CC The invention relates to oligonucleotides, which target a nucleic acid  
 CC encoding human N-ras, and are capable of inhibiting human N-ras  
 CC expression. The antisense oligonucleotides form a pharmaceutical  
 CC composition, which is useful for modulating the expression of human N-  
 CC ras, inhibiting the proliferation of cancer cells, and preventing or  
 CC treating conditions arising from the activation of a human N-ras  
 CC oncogene. The oligonucleotides are also useful in diagnostics,  
 CC therapeutics, and as research reagents and kits. The oligonucleotides  
 CC enable the specific modulation of activated human N-ras expression, which  
 CC is associated with tumour formation. Sequences AAZ1620-633 represent  
 CC antisense oligonucleotides complementary to human K1-ras  
 CC  
 XX  
 SQ Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 400 GGCGGTGCGCGCGAGGCGAG 419  
 DB 20 GGCGCGCGCGCGAGGCGAG 1

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RESULT 98
AAK56984/c
ID AAK56984 standard; DNA; 20 BP.
XX
XX AAK56984;
AC
XX
XX 16-JUL-1999 (first entry)
DT
XX
XX Ras gene modulating liposomal entrapped oligonucleotide primer 28.
DE
XX Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
KM cell growth inhibitor; treatment; cancer; ras protein; ss.
XX
XX Synthetic.
OS
XX WO922772-A1.
PN
XX 14-MAY-1999.
PD
XX 28-OCT-1998; 98MO-US022821.
PF
XX 31-OCT-1997; 97US-00961469.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Hardee GE, Geary RS, Levin A, Templin MV, Howard R, Mehta RC;
PI WPI; 1999-313181/26.
XX
XX Liposome-encapsulated oligonucleotides useful for treating or preventing
PT cancers associated with ras gene activation.
XX
XX Example 1; Page 111; 120pp; English.
XX
XX This invention describes novel compositions comprising oligonucleotides
CC (AAK56984-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with non-
CC encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.
CC
SQ Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 400 GCGCGTCGCGCGAGAGCAG 419
DB 20 GCGCGCGCGCGAGAGCAG 1
RESULT 99
AAA41180
ID AAA41180 standard; DNA; 20 BP.
XX
XX AAA41180;
AC
XX 16-AUG-2000 (first entry)
DT
XX
XX Human TNFalpha antisense oligonucleotide ISIS# 104827.
DE
XX
XX Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KM tumour necrosis factor; alpha; inflammatory bowel disease; diabetes;
KM rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
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XX pancreatitis; atopic dermatitis; allograft rejection; autoimmune disease;
KM inflammatory disease; ss.
XX
XX Synthetic.
OS
XX WO200020645-A1.
PN
XX 13-APR-2000.
PD
XX 05-OCT-1999; 99MO-US023205.
PF
XX 05-OCT-1998; 98US-00166186.
PR 18-MAY-1999; 99US-00313932.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Baker BF, Bennett CF, Butler MM, Shanahan WJ;
PI WPI; 2000-303808/26.
XX
XX Oligonucleotide for treating diseases associated with human tumor
PT necrosis factor-alpha (TNF-alpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNF-alpha.
XX
XX Example 22; Page 105; 283pp; English.
XX
XX This sequence represents an antisense oligonucleotide sequence which
CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
CC in host defence. It is produced mainly in macrophages and monocytes in
CC response to infection, invasion, injury or inflammation. Overexpression
CC of TNFalpha can result in disease states, particularly in infectious,
CC inflammatory and autoimmune diseases. The invention relates to antisense
CC oligonucleotides, such as that represented by the present sequence which
CC are capable of modulating the TNFalpha gene expression. The
CC oligonucleotides optionally have a phosphorothioate backbone, and may
CC also optionally contain at least one 2'-O-methoxyethyl modification. The
CC oligonucleotides are useful for modulating the expression of human
CC TNFalpha in cells and tissues, reducing a human cell inflammatory
CC response, reducing the blood glucose level in a human and treating a
CC human having a disease or condition associated with TNFalpha. Examples of
CC diseases associated with TNFalpha include diabetes, inflammatory bowel
CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
CC The antisense oligonucleotides are also useful for modulating the
CC function of a selected nucleic acid sequence in adipose tissue
CC
SQ Sequence 20 BP; 8 A; 1 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1783 CGGTATGTGAGAGAGAGA 1802
DB 1 CAGTATGTGAGAGAGAGA 20
RESULT 100
AAA94483/c
ID AAA94483 standard; DNA; 20 BP.
XX
XX AAA94483;
AC
XX 09-JAN-2001 (first entry)
DT
XX
XX Antisense oligonucleotide #20922 targeted to human G-alpha-S1.
DE
XX
XX G-alpha-S1; infection; inflammation; tumour; antisense; human;
KM phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KM Gs-alpha short form; ss.
XX
```

```

OS Homo sapiens.
XX Key
XX modified_base
XX 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Optionally the internucleotide linkages are
XX phosphorothioate"
XX modified_base
XX 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "Optionally the nucleotides are 2'-methoxyethyl
XX and cytidine residues are 5-methylcytidines"
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "Optionally the nucleotides are 2'-methoxyethyl
XX and cytidine residues are 5-methylcytidines"
XX US6110664-A.
XX 29-AUG-2000.
XX 25-JUN-1999; 99US-00344914.
XX 25-JUN-1999; 99US-00344914.
XX (ISIS-) ISIS PHARM INC.
XX Cowser LM;
XX WPI; 2000-586346/55.
XX New antisense compounds for modulating the expression of G-alpha-S1,
XX especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
XX prevent or delay infection, inflammation or tumor formation.
XX Claim 3; Col 39; 37pp; English.
XX The present invention relates to antisense compounds 8-30 bases long
XX targeted to a coding region, a stop codon, or a 3' untranslated region of
XX human G-alpha-S1 (see AAA94451). The antisense compounds specifically
XX hybridize with and inhibit the expression of human G-alpha-S1. The
XX antisense compounds are useful for diagnostics, therapeutics and
XX prophylaxis, e.g. to prevent or delay infection, inflammation or tumor
XX formation. Particularly, the antisense oligonucleotides are useful for
XX treating humans prone to a disease or condition associated with
XX expression of G-alpha-S1. The present sequence of human G-alpha-S1
XX oligonucleotide targeted to the coding region of human G-alpha-S1
XX Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 82;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 840 CCATGACATCTTCAGCTCA 859
XX |||||
XX 20 CCGTGCATCATTCAGCGCA 1
XX
XX RESULT 101
XX AAA95858/C
XX ID AAA95858 standard; DNA; 20 BP.
XX
XX AC AAA95858;
XX
XX 18-JAN-2001 (first entry)
XX
XX Human Ki-ras antisense oligonucleotide ISIS #6958.
XX
XX Human; antisense oligonucleotide; ras; H-ras; Ki-ras; N-ras; cytosstatic;
XX phosphorothioate; cancer; ss.

```

```

XX OS Homo sapiens.
XX Key
XX US6117848-A.
XX 12-SEP-2000.
XX 03-AUG-1998; 98US-00128494.
XX 05-OCT-1992; 92US-00958134.
XX 21-JAN-1993; 93US-00007996.
XX 01-OCT-1993; 93WO-US009246.
XX 03-APR-1995; 95US-00411734.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cowser LM, Monia BP;
XX WPI; 2000-610851/58.
XX Oligonucleotides targeted to human H-ras or human Ki-ras coding
XX sequences, useful for treating and preventing cancer.
XX Claim 9; Col 19; 41pp; English.
XX The present sequence was used in methods for the modulation of ras
XX expression. Antisense oligonucleotides were designed to specifically
XX target mRNA encoding human H-ras, Ki-ras and N-ras. The oligonucleotides
XX can be used to inhibit the proliferation of cancer cells and to prevent
XX or treat a condition arising from the activation of a ras oncogene. They
XX may also be used to modulate the expression of human H-ras or human Ki-
XX ras. The antisense oligonucleotides may contain modified backbones,
XX substituted sugar moieties and modified bases. The sequences preferably
XX have a phosphorothioate backbone. They are preferably
XX oligodeoxynucleotides or chimeric oligonucleotides containing 2'-O-methyl
XX ends and a central deoxy gap
XX
XX Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 82;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 400 GCGGCTCCGCGGAGGCGAG 419
XX |||||
XX 20 GCGCCGCGGCGGAGGCGAG 1
XX
XX RESULT 102
XX AAZ72504
XX ID AAZ72504 standard; DNA; 20 BP.
XX
XX AC AAZ72504;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker upstream amplification primer SEQ ID NO:6860.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenocype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX WO954500-A2.
XX 28-OCT-1999.
XX 21-APR-1999; 99WO-1B000822.
XX 21-APR-1998; 98US-0082614P.

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XX 23-NOV-1998; 98US-0109732P.
XX (GERT) GENSET.
XX Cohen D, Blumenfeld M, Chumakov I,
XX WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX Claim 9; Page 1693; 2745pp; English.
CC AA26554 to AA29578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequence. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence listing from the
CC present invention
XX
XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2385 TTACACAGAAATGCTGCTG 2404
DB 1 TGACACAGAAATGAGACTG 20
RESULT 103
AAA90808/c
ID AAA90808 standard; DNA; 20 BP.
XX AAA90808;
AC
XX 20-DEC-2000 (first entry)
DT
XX
DE Ribonucleotide reductase R1 message antisense oligo AS-I-2364-20.
XX
XX Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
KM R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
XX
XX Synthetic.
OS
XX
XX WO200047733-A1.
PN
XX
XX 17-AUG-2000.
PD
XX
XX 09-FEB-2000; 2000WO-CA000120.
PF
XX
XX 11-FEB-1999; 99US-00249730.
PR
XX (GENE-) GENESENSE TECHNOLOGIES INC.
PA
XX
XX Wright JA, Young AH;
PI
XX
XX WPI; 2000-558216/51.
DR
XX
XX New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
PT tumor cell growth.
XX
XX Example 3; Page 32; 137pp; English.
PS

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XX
XX The present sequence is an antisense oligonucleotide directed against the
CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.
CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to
CC their corresponding deoxyribonucleotides and thus plays an important role
CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide
CC reductase is altered in cultured malignant cells and increased levels of
CC R2 protein and R2 mRNA have been found in pre-malignant and malignant
CC tissues as compared to normal control tissue samples. The present
CC antisense sequence is therefore useful for inhibiting tumorigenicity of
CC neoplastic cells and inhibiting metastasis of tumour cells. It is also
CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic
CC drugs, thus allowing chemotherapeutic treatments to be used in patients
CC who have become resistant or less sensitive to chemotherapy. The sequence
CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide
CC analogues
XX
SQ Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1668 GGAAGAGAGGTTGAAGACT 1687
DB 20 GGAAGCAGGGTTGAAGACT 1
RESULT 104
AAA92062
ID AAA92062 standard; DNA; 20 BP.
XX AAA92062;
AC
XX 04-JAN-2001 (first entry)
DT
XX
DE Mammalian Lhx3 PCR primer SEQ ID NO:41.
XX
XX Lhx3; LIM-3; P-LIM; identification; characterisation; diagnosis;
KM chromosome 9; pituitary disease; subtelomeric region; mutation;
KM pituitary trophic hormone gene promoter; PCR primer; ss.
XX
XX Mammalia.
OS
XX
XX WO200050868-A2.
PN
XX
XX 31-AUG-2000.
PD
XX
XX 22-FEB-2000; 2000WO-US004424.
PF
XX
XX 22-FEB-1999; 99US-0121110P.
PR
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA
XX
XX Rhodes SJ, Bridwell JL, Meter BC, Parker GE, Price JR;
PI
XX
XX Showalter AD, Sloop KW;
PI
XX
XX WPI; 2000-594085/56.
DR
XX
XX New isolated nucleic acid encoding mammalian Lhx3 for identifying a human
PT with a disease, disorder, or condition caused by an altered level of
PT expression or binding of Lhx3.
XX
XX Claim 41; Page 12; 239pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
CC mammalian Lhx3. (I) is used in assays to: (1) detect and quantify the
CC presence and level of expression of Lhx3, Lhx3a or Lhx3b, in a sample;
CC (2) identify a compound that affects expression, the level of expression,
CC or the activity of Lhx3, Lhx3a, or Lhx3b in a cell; (3) identify a
CC compound that affects binding or Lhx3 to nucleic acid or Lhx3 induction
CC of a pituitary trophic hormone gene promoter; (4) identify a human
CC afflicted with a disease, disorder, or condition caused by altered

```

CC expression of Lhx3 or altered level of binding of Lhx3 to a nucleic acid;  
CC and (5) detect a mutation in a Lhx3 allele in a human. The coding region  
CC of human Lhx3 has been genomically mapped to the subtelomeric region of  
CC chromosome 9. Lhx3 is also known as P-LIM or LIM-3. The present sequence  
CC represents a specifically claimed PCR primer for a mammalian Lhx3 nucleic  
CC acid, which is given in the present invention

XX Sequence 20 BP; 4 A; 9 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 82;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 469 GGGCCGAGCCCCGACGCG 488  
DB 1 GGCACGAGCCCCGACGACG 20

## RESULT 105

AAA92053  
ID AAA92053 standard; DNA; 20 BP.

XX AAA92053;

XX 04-JAN-2001 (first entry)

DE Mammalian Lhx3 PCR primer SEQ ID NO:44.

XX Lhx3; LIM-3; P-LIM; identification; characterisation; diagnosis;

KW chromosome 9; pituitary disease; subtelomeric region; mutation;

KW pituitary trophic hormone gene promoter; PCR primer; ss.

XX Mammalia.

XX WO200050868-A2.

XX 31-AUG-2000.

XX 22-FEB-2000; 2000WO-US004424.

XX 22-FEB-1999; 99US-0121110P.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX Rhodes SJ, Bridwell JL, Meier BC, Parker GE, Price JR;

XX Showalter AD, Sloop KW;

XX WPI; 2000-594085/56.

XX New isolated nucleic acid encoding mammalian Lhx3 for identifying a human  
XX with a disease, disorder, or condition caused by an altered level of  
XX expression or binding of Lhx3.

XX Claim 25; Page 10; 23pp; English.

XX The present invention describes an isolated nucleic acid (1) encoding a  
XX mammalian Lhx3. (1) is used in assays to: (1) detect and quantify the  
XX presence and level of expression of Lhx3, Lhx3a or Lhx3b, in a sample;  
XX (2) identify a compound that affects expression, the level of expression,  
XX or the activity of Lhx3, Lhx3a, or Lhx3b in a cell; (3) identify a  
XX compound that affects binding of Lhx3 to nucleic acid or Lhx3 induction  
XX of a pituitary trophic hormone gene promoter; (4) identify a human  
XX afflicted with a disease, disorder, or condition caused by altered  
XX expression of Lhx3 or altered level of binding of Lhx3 to a nucleic acid;  
XX and (5) detect a mutation in a Lhx3 allele in a human. The coding region  
XX of human Lhx3 has been genomically mapped to the subtelomeric region of  
XX chromosome 9. Lhx3 is also known as P-LIM or LIM-3. The present sequence  
XX represents a specifically claimed PCR primer for a mammalian Lhx3 nucleic  
XX acid, which is given in the present invention

XX Sequence 20 BP; 4 A; 9 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 82;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 469 GGGCCGAGCCCCGACGCG 488  
DB 1 GGCACGAGCCCCGACGACG 20

## RESULT 106

AA845617/C  
ID AA845617 standard; DNA; 20 BP.

XX AA845617;

XX 18-DEC-2001 (first entry)

DE Human PARP-1 antisense inhibitor ISIS #125978.

XX Human; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;

KW cytosolic; neurotropic; neuroprotective; antiinflammatory; antidiabetic;

KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;

KW oxidative stress; neurological disorder; parkinsonism; apoptosis;

KW meningitis-associated intracranial complication; ischemia; probe;

XX inflammatory disorder; autoimmune disorder; arthritis; diabetes.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

Claim 3; Page 83; 16pp; English.

XX The invention relates to antisense oligonucleotides targeted to human

XX PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly

XX (ADP-ribose) polymerase plays an important role in chromatin

XX decondensation, DNA replication, DNA repair, gene expression, malignant

XX transformation, cellular differentiation and apoptosis. The antisense

XX oligonucleotide inhibitors are useful for inhibiting the expression of

XX PARP in human cells or tissues. They are also useful for treating a human

XX with a disease associated with PARP especially hyperproliferative

XX disorders (e.g. cancer), cellular injury resulting from oxidative stress,

```
CC neurological (e.g parkinsonism, meningitis-associated intracranial
CC complications and ischaemia) , inflammatory and autoimmune disorders (e.g
CC arthritis) and diabetes. The present sequence is an antisense
CC oligonucleotide of the invention
XX
SQ Sequence 20 BP, 6 A, 3 C, 3 G, 3 T, 0 U, 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2297 TCTGAGCCACAGTGGATGA 2316
DB 20 TCTGAGCTTCGTGGATGA 1
RESULT 107
AAF80747
XX AAF80747 standard; DNA, 20 BP.
XX
XX AAF80747;
XX
XX 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #121.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX US6184212-B1.
XX
XX 06-FEB-2001.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX WPI; 2001-190948/19.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
XX acid molecule encoding human mdm-2 useful for modulating the expression
XX of human mdm-2 and reducing hyperproliferation of human cells.
XX
XX Example 9; Col 29; 77BP; English.
XX
XX The present invention relates to an antisense compound 8-30 nucleobases
XX in length targeted to nucleobases 1-308 of the 5' untranslated region,
XX 1776-1806 of the translation termination codon region or 1818-2370 of the
XX 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
XX The invention is useful for reducing hyperproliferation of human cells,
XX modulating the expression of mdm2 in human cells or tissues or in vitro.
XX The hyperproliferative disorder includes cancer or psoriasis
XX
SQ Sequence 20 BP, 7 A, 3 C, 6 G, 4 T, 0 U, 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1005 GCTTCTCAATGAAGAG 1024
DB 1 GCTTTCATCAAGAGAGG 20
RESULT 108
AAH20646
XX AAH20646 standard; DNA, 20 BP.
XX
```

```
AC AAH20646;
XX
XX 13-AUG-2001 (first entry)
XX
XX Human telomeric repeat binding factor 2 oligonucleotide 111374.
XX
XX Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
XX inhibitor; premature aging; hyperproliferative disorder; cancer;
XX cytostatic; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX modified_base 1..3
XX /note= "phosphorothioate backbone"
XX /tag= a
XX /mod_base= OTHER
XX modified_base 13..20
XX /note= "2-O-methoxyethyl"
XX /tag= c
XX /mod_base= OTHER
XX /note= "2-O-methoxyethyl"
XX
XX WO200143752-A1.
XX
XX 21-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-US039354.
XX
XX 17-DEC-1999; 99US-00467642.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowseart LM;
XX WPI; 2001-398071/42.
XX
XX Antisense compounds targeted to nucleic acid encoding telomeric repeat
XX binding factor 2 useful for treating conditions such as premature aging
XX and diseases such as cancer.
XX
XX Claim 3; Page 80; 108BP; English.
XX
XX This invention describes a novel antisense compound (I) 8-30 nucleobases
XX in length targeted to a polynucleotide encoding human telomeric repeat
XX binding factor 2 (II) which specifically hybridizes with, and inhibits
XX the expression of (II). (I) is useful for treating a human having a
XX disease or condition associated with (II) such as premature aging or a
XX hyperproliferative disorder especially cancer, by inhibiting the
XX expression of (II) in human cells or tissues. (I) is useful for
XX diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX The products of the invention have cytostatic activity. This sequence
XX represents an antisense oligonucleotide used to illustrate the method of
XX the invention
XX
SQ Sequence 20 BP, 1 A, 12 C, 5 G, 2 T, 0 U, 0 Other;
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 199 CGCCCGCCGCGCGCTGCC 218
DB 1 CGCCCGCTGCGAGCTGCC 20
RESULT 109
AAS29362
XX AAS29362 standard; DNA, 20 BP.
XX
```



```

KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW disease diagnosis; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX US6251588-B1.
XX
XX 26-JUN-2001.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX (AGIL-) AGILENT TECHNOLOGIES INC.
XX
XX Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
XX WPI; 2001-424456/45.
XX
XX
XX Predicting the potential of an oligonucleotide to hybridize to a target
XX nucleotide sequence, useful for evaluating oligonucleotide probe
XX sequences, by identifying a oligonucleotides based on the evaluation of
XX parameters.
XX
XX Example 2; Col 57; 342pp; English.
XX
XX The present invention describes a method for predicting the potential of
XX an oligonucleotide to hybridize to a (complementary) target nucleotide
XX sequence, involving identifying a subset of oligonucleotides within the
XX predetermined number of unique oligonucleotides based on the evaluation
XX of the parameter. Oligonucleotides in the subset are identified that are
XX clustered along a region of the nucleotide sequence that is hybridisable
XX to the target nucleotide sequence. This is useful for evaluating
XX oligonucleotide probe sequences. The present sequence is an
XX oligonucleotide described in the exemplification of the invention.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 776 CCTTACCTCAAAAGCTGTG 795
DB 1 CCCCACTCAACGAGTGTG 20
XX
RESULT 112
AAD39575
ID AAD39575 standard; DNA; 20 BP.
XX
AC AAD39575;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human SR-cyp antisense oligonucleotide, ISIS #123839.
XX
XX Human; antisense; SR-cyp; C1x-associated RS cyclophilin; inflammation;
XX hyperproliferative disorder; cancer; prophylaxis; infection; therapy;
XX tumour; CAsS-cyp; phosphorothioate backbone; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER

```

```

FT modified_base
FT /note= "2-methoxyethyl nucleotides"
FT /tag= d
FT /mod_base= m5c
FT modified_base
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base
FT 17
FT /note= "2-methoxyethyl nucleotides"
FT /tag= e
FT /mod_base= m5c
FT modified_base
FT 20
FT /tag= f
FT /mod_base= m5c
XX
XX W0200236809-A2.
XX
XX 10-MAY-2002.
XX
XX
XX 30-OCT-2001; 2001MO-US047335.
XX
XX 03-NOV-2000; 2000US-00706197.
XX
XX (ISIS-) ISIS PHARM INC.
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Bennett CF, Spector DL, Wyatt JR;
XX
XX WPI; 2002-479763/51.
XX
XX Novel antisense compounds targeted to nucleic acids encoding SR-cyp, C1x-
XX associated RS cyclophilin for modulating the gene expression and treating
XX hyperproliferative disorders such as cancer.
XX
XX Claim 3; Page 89; 117pp; English.
XX
XX The invention relates to antisense compounds targeted to a nucleic acid
XX molecule encoding human SR-cyp (C1x-associated RS cyclophilin) to inhibit
XX its expression. SR-cyp is also referred to as CAsS-cyp. Antisense
XX compounds of the invention are used for treating diseases or conditions
XX associated with SR-cyp. The diseases treated include hyperproliferative
XX disorders e.g. cancer or hyperproliferative disorders resulting from an
XX alternative splicing event. They are useful for diagnostics, therapeutics
XX and as research reagents, e.g. prophylactically to prevent or delay
XX infection, inflammation or tumour formation. They are also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targeted to human SR-cyp
XX
XX Sequence 20 BP; 3 A; 3 C; 4 G; 10 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1730 TCATTGTTGTTTCACTGC 1749
DB 1 TCTTTGTTGTTTCAACGC 20
XX
RESULT 113
AB288060/c
ID AB288060 standard; DNA; 20 BP.
XX
AC AB288060;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;

```

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PT WPI; 2003-229219/22.  
 DR  
 XX  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 3302; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX  
 SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 DB 20 AGCTCGAGGATCTGGCAGT 1  
 CY 608 AGCTCGAGGATCTGGCAGT 627  
 DB 20 AGCTCGAGGATCTGGCAGT 1  
 RESULT 114  
 AB292114/c  
 ID AB292114 standard; DNA; 20 BP.  
 XX  
 XX AB292114;  
 AC  
 XX  
 XX 17-OCT-2003 (first entry)  
 DT  
 XX  
 XX Human oligonucleotide sequence.  
 DE  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PT WPI; 2003-229219/22.  
 DR  
 XX  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 7356; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX  
 SQ Sequence 20 BP; 10 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 DB 20 AGGAATTTCTCTCTCTTT 1  
 CY 1038 AGGAATTTCTCTCTCTTT 1057  
 DB 20 AGGAATTTCTCTCTCTTT 1  
 RESULT 115  
 AB297778  
 ID AB297778 standard; DNA; 20 BP.  
 XX  
 XX AB297778;  
 AC  
 XX  
 XX 17-OCT-2003 (first entry)  
 DT  
 XX  
 XX Human CCR3 oligonucleotide sequence.  
 DE  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;



KW inflammatory disorder; inflammatory bowel disease; Crohn's disease;  
 KW colitis; rheumatoid arthritis; diabetes; pancreatitis;  
 KW multiple sclerosis; atopic dermatitis; asthma; hepatitis;  
 KW antisense technology; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003022848-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 02-APR-2001; 2001US-00824322.  
 XX  
 PR 05-OCT-1998; 98US-00166186.  
 PR 18-MAY-1999; 99US-00313932.  
 XX  
 PA (BAKE/) BAKER B F.  
 PA (BEN/) BENNETT C F.  
 PA (BUT/) BUTLER M M.  
 PA (SHAN/) SHANAHAN W R.  
 XX  
 PI Baker BF, Bennett CF, Butler MM, Shanahan WR;  
 XX  
 DR WPI; 2003-447433/42.  
 XX  
 PT Treating inflammatory disorders such as inflammatory bowel disease,  
 PT Crohn's disease or rheumatoid arthritis, in a subject, by administering  
 PT oligonucleotide which inhibits expression of human tumor necrosis factor  
 PT alpha.  
 XX  
 PS Example 24; Page 39; 142pp; English.  
 XX  
 CC The invention describes a method of treating an inflammatory disorder in  
 CC an individual, comprising administering to the individual an  
 CC oligonucleotide upto 30 nucleotides in length complementary to a nucleic  
 CC acid molecule encoding human tumor necrosis factor (TNF)-alpha. The  
 CC method is useful for treating an inflammatory disorder such as  
 CC inflammatory bowel disease, Crohn's disease, colitis or rheumatoid  
 CC arthritis, in an individual. The method is also useful for treating  
 CC diabetes, pancreatitis, multiple sclerosis, atopic dermatitis, asthma,  
 CC and hepatitis in an individual. This sequence represents an antisense  
 CC oligonucleotide used to modulate expression of tumor necrosis factor  
 CC alpha (TNF-alpha)  
 CC  
 XX  
 SO Sequence 20 BP; 8 A; 1 C; 8 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1783 CCGTATGTGAGAGAGAG 1802  
 DB 1 CAGTATGTGAGAGAGAGAGA 20  
 XX  
 RESULT 118  
 ADCl0494/c  
 ID ADCl0494 standard; DNA; 20 BP.  
 XX  
 AC ADCl0494;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human NOXV polypeptide gene reverse primer SEQ ID NO: 513.  
 XX  
 KW ss; primary; cytosolic; antidiabetic; anorectic; cerebroprotective;  
 KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;  
 KW thymic; NOXV; pathology; cancer; diabetes; obesity;  
 KW endocrine disorder; CNS disorder; inflammatory disorder;  
 KW chromosome mapping; tissue typing; predictive medicine.  
 XX  
 OS Homo sapiens.  
 XX

PN WO2003000842-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 04-JUN-2002; 2002WO-US017443.  
 XX  
 PR 04-JUN-2001; 2001US-0235607P.  
 PR 04-JUN-2001; 2001US-0235661P.  
 PR 06-JUN-2001; 2001US-0236404P.  
 PR 06-JUN-2001; 2001US-0236418P.  
 PR 07-JUN-2001; 2001US-0236575P.  
 PR 11-JUN-2001; 2001US-0237414P.  
 PR 12-JUN-2001; 2001US-02395573P.  
 PR 12-JUN-2001; 2001US-0237557P.  
 PR 14-JUN-2001; 2001US-0238285P.  
 PR 15-JUN-2001; 2001US-0238528P.  
 PR 18-JUN-2001; 2001US-0239133P.  
 PR 19-JUN-2001; 2001US-0239230P.  
 PR 21-JUN-2001; 2001US-0239949P.  
 PR 22-JUN-2001; 2001US-0300177P.  
 PR 26-JUN-2001; 2001US-0300883P.  
 PR 28-JUN-2001; 2001US-0301530P.  
 PR 28-JUN-2001; 2001US-0301550P.  
 PR 03-JUL-2001; 2001US-0302951P.  
 PR 31-JUL-2001; 2001US-0308890P.  
 PR 14-SEP-2001; 2001US-0322297P.  
 PR 25-SEP-2001; 2001US-0337477P.  
 PR 03-DEC-2001; 2001US-0341552P.  
 PR 14-DEC-2001; 2001US-0341552P.  
 PR 21-FEB-2002; 2002US-0358122P.  
 PR 21-FEB-2002; 2002US-0359122P.  
 PR 22-FEB-2002; 2002US-0359034P.  
 PR 22-FEB-2002; 2002US-0359034P.  
 PR 22-FEB-2002; 2002US-0359121P.  
 PR 22-FEB-2002; 2002US-0359121P.  
 PR 27-FEB-2002; 2002US-0359564P.  
 PR 01-MAR-2002; 2002US-0360858P.  
 PR 12-MAR-2002; 2002US-0363430P.  
 PR 12-MAR-2002; 2002US-0363767P.  
 PR 10-APR-2002; 2002US-0371346P.  
 PR 10-MAY-2002; 2002US-0379444P.  
 PR 04-JUN-2002; 2002US-00379444.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Agee WL, Anderson DW, Berghs C, Casman SJ, Catterton E;  
 PI DiBiase VA, Edinger SR, Eissen A, Ellerman K, Gargolli EA;  
 PI Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;  
 PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CB, Millec I;  
 PI Ort T, Padigaru M, Patuturajan M, Pena CE, Rastelli L, Rieger DK;  
 PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;  
 PI Rytel KA, Store DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
 PI Burgess CE, Lepley DM;  
 XX  
 DR WPI; 2003-210149/20.  
 XX  
 PT New isolated NOXV polypeptides and nucleic acid molecules useful for  
 PT treating, preventing and diagnosing pathological conditions with NOXV-  
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
 PT or CNS diseases.  
 XX  
 PS Example B, SEQ ID NO 513; 772pp; English.  
 XX  
 CC The invention relates to novel isolated polypeptides, mature form of the  
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
 CC polypeptide comprising one or more conservative substitutions. The NOXV  
 CC polypeptide is useful for treating or preventing a pathology associated  
 CC with the polypeptide e.g. disorders associated with aberrant expression  
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
 CC endocrine, CNS and inflammatory disorders. They can also be used in  
 CC various detection and screening assays, chromosome mapping, tissue typing  
 CC and predictive medicine. This sequence corresponds to a primer used to  
 CC amplify and isolate the coding sequence for one of the polypeptides of

CC the invention.

XX Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 15.2; DB 1; Length 20;

XX Best Local Similarity 85.0%; Pred. No. 82;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1277 AGAGACCAGAACGTTCTCAA 1296

Db 20 AAGACCTGAATGTCTCAA 1

RESULT 119

ADD21558

ID ADD21558 standard; DNA; 20 BP.

AC ADD21558;

DT 15-JAN-2004 (first entry)

DE Human mdm2 antisense oligonucleotide #121.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;

XX hyperproliferative disorder; cancer; psoriasis; fibrosis;

XX atherosclerosis; restenosis; apoptosis modulation; p21; ss;

XX 2'-methoxyethoxy-residue; phosphorothioate backbone.

XX Homo sapiens.

XX WO2003048315-A2.

XX 12-JUN-2003.

PF 02-DEC-2002; 2002WO-US038281.

PR 04-DEC-2001; 2001US-00005344.

PA (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero PS, Graham MJ, Monica BP, Koller E, Chiang MY;

PI Manoharan M;

XX MPI; 2003-577263/54.

XX Novel antisense compound targeted to 5' untranslated region, coding

XX region, or intron/exon junction of nucleic acid molecule encoding mdm2.

XX useful for treating e.g. cancer, psoriasis or restenosis by inhibiting

XX mdm2 expression.

XX Example 9; SEQ ID NO 123; 289bp; English.

XX The invention comprises antisense oligonucleotides which are targeted to

XX the human mdm2 gene. The antisense oligonucleotides of the invention are

XX useful for reducing hyperproliferation of human cells. The antisense

XX oligonucleotides are also useful for treating: hyperproliferative

XX disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or

XX restenosis. The antisense oligonucleotides are also useful for modulating

XX apoptosis, and for increasing expression of p21. The present DNA sequence

XX represents a human mdm2 gene antisense oligonucleotide of the invention.

XX The present sequence contains 2'-methoxyethoxy-residues and has a

XX phosphorothioate backbone.

SQ Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;

XX Best Local Similarity 85.0%; Pred. No. 82;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1005 GCTTTCTCAATGAAGAG 1024

Db 1 GCTTCATCAAGAAAGAGG 20

RESULT 120

ADD44374

ID ADD44374 standard; DNA; 20 BP.

AC ADD44374;

DT 15-JAN-2004 (first entry)

DE Staphylococcus aureus enterotoxin A target gene detecting primer enA-1.

XX enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;

XX ice cream; primer; PCR; ss.

XX Staphylococcus aureus.

XX WO2003080865-A1.

XX 02-OCT-2003.

XX 26-MAR-2002; 2002WO-IB001150.

XX 26-MAR-2002; 2002WO-IB001150.

XX (COUL ) COUNCIL SCI &amp; IND RES.

XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraaj MC;

XX MPI; 2003-779273/73.

XX Novel oligonucleotide primers directed against enterotoxin A gene of

XX Staphylococcus aureus and heat stable enterotoxin gene of Yersinia

XX enterocolitica, useful for detecting food poisoning causing bacteria.

XX Claim 1; SEQ ID NO 1; 34bp; English.

XX The invention relates to novel oligonucleotide primers directed against

XX enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable

XX enterotoxin gene (yst) of bacteria Yersinia enterocolitica. The novel

XX oligonucleotide primers are useful for simultaneously detecting food

XX poisoning bacterial species Staphylococcus aureus and/or Yersinia

XX enterocolitica in food systems e.g., milk, fruit juices and ice creams,

XX without prior enrichment for preventing food poisoning outbreak. The PCR

XX detection method is useful for detecting the bacteria strains in quantity

XX as low as one cell. The method can be directly used for detecting

XX bacterial strains. The oligonucleotide primers allow quick and highly

XX sensitive detection of the food poisoning bacterial species. This

XX polynucleotide sequence represents a novel oligonucleotide primer of the

XX invention used for detecting an enterotoxin A target gene in

XX Staphylococcus aureus.

SQ Sequence 20 BP; 9 A; 2 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.2; DB 1; Length 20;

XX Best Local Similarity 85.0%; Pred. No. 82;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 83 GGTGGGAGAACGCGAAGA 102

Db 1 GGTAGCGAGAAAGCGAAGA 20

RESULT 121

ADD42355

ID ADD42355 standard; DNA; 20 BP.

AC ADD42355;

DT 15-JAN-2004 (first entry)

DE Human infertility associated primer SEQ ID 216.

XX primer; male infertility; infertility-associated mutation;

KM azoospermia factor; Y-chromosome;  
 KM cystic fibrosis transmembrane conductance regulator; CTRF;  
 KM Kallmann syndrome; Kall; androgen resistance; steroid 21-hydroxylase;  
 KM CYP21; microarray; quantitative trait locus; in vitro fertilization;  
 KM oligospermia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003050299-A2.  
 XX  
 PD 19-JUN-2003.  
 XX  
 XX 10-DEC-2002; 2002WO-EP013995.  
 XX  
 XX 10-DEC-2001; 2001DE-01060563.  
 XX  
 PA (OGHA-) OGHA GMBH.  
 XX  
 PI Cullen P, Seedorf U;  
 DR WPI; 2003-505402/47.  
 XX  
 PT Investigating male genetic infertility, useful for diagnosis e.g. for  
 PT assessing suitability for in vitro fertilization, based on multifactorial  
 PT analysis of infertility-related mutations.  
 XX  
 PS Claim 13; SEQ ID NO 217; 110pp; German.  
 XX  
 XX This invention describes a novel method for investigating genetic  
 CC infertility or predisposition in males. The method involves selecting at  
 CC least two infertility-associated mutations which are recessive or  
 CC intermediate that are associated with infertility in the heterozygous  
 CC state and/or only in the homozygous state. Preferably at least one  
 CC azoospermia factor is detected which may be lost by microdeletions in  
 CC intervals 5 or 6 of the Y-chromosome. Also any of several hundred  
 CC mutations, listed, present in the cystic fibrosis transmembrane  
 CC conductance regulator (CFTR). Kallmann syndrome (Kall), androgen  
 CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.  
 CC Probes for the mutated genes and/or native nucleic acid, or their  
 CC complementary strands, are fixed to a carrier, particularly as a  
 CC microarray, then tested for hybridization with oligonucleotides from or  
 CC synthesized from, a patient sample and hybridization detected.  
 CC Multifactorial analysis is by standard statistical methods, particularly  
 CC the quantitative trait locus method. The method is used to diagnose  
 CC inherited male infertility or predisposition to its, especially in  
 CC conjunction with in vitro fertilization programs, e.g. for assessing  
 CC subjects with oligospermia for possible application of the  
 CC intracytoplasmic sperm injection method. Analysis of many mutations  
 CC improves diagnosis of the genetic basis of male infertility, including  
 CC polygenic origins (complex interactions between different heterozygotic  
 CC mutations). A chip for analyzing genetic infertility in males comprises  
 CC oligonucleotides that represent known mutations (nonsense or missense,  
 CC insertions, allelic variants deletions or rearrangements) in the cystic  
 CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen  
 CC resistance and steroid 21-hydroxylase genes. ADD2140-ADD4633 represent  
 CC oligonucleotides used in the microarray described in the method of the  
 CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the  
 CC SEQ ID list of the specification.  
 CC  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 1 G; 11 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 DB Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1042 AATTTCATTCTCTTTTAC 1061  
 DB 1 AATTTCATTCTCTTTTAC 20  
 RESULT 122  
 ADD81158  
 ID ADD81158 standard; DNA; 20 BP.

XX  
 AC ADD81158;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX  
 DE HIV PRT antisense derived probe #87.  
 XX  
 KM ss; oligonucleotide hybridisation potential; efficient hybridisation;  
 KM large array; minimum oligonucleotide synthesis; probe.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 XX US2003054346-A1.  
 XX  
 XX 20-MAR-2003.  
 XX  
 XX 15-FEB-2001; 2001US-00784674.  
 XX  
 XX 10-FEB-1998; 98US-00021701.  
 XX  
 PA (SHAN/) SHANNON K W.  
 PA (WOLB/) WOLBER P K.  
 PA (DELE/) DELENSTARR G C.  
 PA (WEBB/) WEBB P G.  
 PA (KINC/) KINCAID R H.  
 XX  
 PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;  
 DR WPI; 2003-743746/70.  
 XX  
 PT Predicting potential of oligonucleotides to hybridize to target  
 PT nucleotide sequence comprises determining and evaluating for each  
 PT oligonucleotide a parameter predictive of the oligonucleotides ability to  
 PT hybridize with target.  
 XX  
 PS Example 2; SEQ ID NO 231; 423pp; English.  
 XX  
 XX The invention relates to a method of predicting the potential of  
 CC oligonucleotides to hybridise to target nucleotide sequences. The method  
 CC is useful for predicting the potential of an oligonucleotide to hybridise  
 CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that  
 CC contains chemically modified nucleotides. The method is also useful for  
 CC predicting the potential of the oligonucleotides to hybridise to a  
 CC complementary target nucleotide sequence. The method is useful to predict  
 CC efficient hybridisation oligonucleotides for each of multiple target  
 CC sequences therefore very large arrays may be constructed and tested with  
 CC HIV PRT antisense derived probe.  
 CC  
 XX  
 SQ Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.6%; Score 15.2; DB 1; Length 20;  
 DB Best Local Similarity 85.0%; Pred. No. 82;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 775 TCCCTACCTCAAGAGCTGTT 794  
 DB 1 TCCCTACCTCAAGAGATGTT 20  
 RESULT 123  
 ADD81159  
 ID ADD81159 standard; DNA; 20 BP.  
 XX  
 AC ADD81159;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE HIV PRT antisense derived probe #88.  
 XX  
 KM ss; oligonucleotide hybridisation potential; efficient hybridisation;  
 KM large array; minimum oligonucleotide synthesis; probe.  
 XX

```

OS Human immunodeficiency virus.
XX
XX US2003054346-A1.
XX
XX 20-MAR-2003.
XX
XX 15-FEB-2001; 2001US-00784674.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX (SHAN/) SHANNON K W.
XX (WOLB/) WOLBER P K.
XX (DELE/) DELENSTARR G C.
XX (WEBB/) WEBB P G.
XX (KINC/) KINCAID R H.
XX
XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
XX nucleotide sequence comprises determining and evaluating for each
XX oligonucleotide a parameter predictive of the oligonucleotides ability to
XX hybridize with target.
XX
XX Example 2; SEQ ID NO 232; 423bp; English.
XX
XX The invention relates to a method of predicting the potential of
XX oligonucleotides to hybridize to target nucleotide sequences. The method
XX is useful for predicting the potential of an oligonucleotide to hybridize
XX to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
XX contains chemically modified nucleotides. The method is also useful for
XX predicting the potential of the oligonucleotides to hybridize to a
XX complementary target nucleotide sequence. The method is useful to predict
XX efficient hybridisation oligonucleotides for each of multiple target
XX sequences therefore very large arrays may be constructed and tested with
XX minimum synthesis of oligonucleotides. The present sequence represents a
XX HIV PRT antisense derived probe.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 82;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 776 CCTTACTCTGAAGCTGTTG 795
XX 1 CCCCACCTCAACAGATGTTG 20
XX
XX RESULT 124
XX AAL29294/C
XX ID AAL29294 standard; DNA; 51 BP.
XX
XX AAL29294;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #2502.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX OS
XX XX WO200147944-A2.
XX
XX

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PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 2099; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukin, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. Rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
XX Sequence 51 BP; 12 A; 19 C; 8 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15.2; DB 1; Length 51;
XX Best Local Similarity 59.1%; Pred. No. 1.2e+02;
XX Matches 26; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX 2337 GCTTCAGCATCTCATGAGGAGAGACGAGCGGAGTGAAG 2380
XX 44 GCTTAAGTTTCTCTGCGAGAAAGAGGTAAAGGGAGTGAAG 1
XX
XX RESULT 125
XX AAF45225
XX ID AAF45225 standard; DNA; 15 BP.
XX
XX AAF45225;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP2 oligonucleotide #64.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiac; vitricide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX OS
XX XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX

```

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XX
PR 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
DR
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 34; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation.
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 200 GCCCGCGCGCGCGCT 214
Db 1 GCCCGCGCGCGCGCT 15
XX
RESULT 126
AAV43464/c
ID AAV43464 standard; RNA; 16 BP.
XX
XX AAV43464;
XX
DT 17-OCT-2003 (revised)
DT 14-SEP-1998 (first entry)
XX
XX HIV-1 beta-chemokine receptor (CCR)-5 target sequence 11.
XX
XX Endo-ribonuclease; ribozyme; cleave; co-receptor RNA; HIV infection;
XX chemokine receptor; CCR; fusin; ss.
XX
OS Human immunodeficiency virus 1.
XX
XX WO9817308-A1.
XX
XX 30-APR-1998.
XX
XX 24-OCT-1997; 97MO-US019923.
XX
XX 25-OCT-1996; 96US-0027875P.
XX 19-DEC-1996; 96US-00770235.
XX
XX (IMMU-) IMMUSOL INC.
XX
PI Leavitt MC, Tritz R, Feng Y, Barber J, Yu M;
XX
XX WPI; 1998-261188/23.

```

```

XX
XX Endo-ribonuclease nucleic acids - which encode ribozymes which cleave co-
PT receptor RNA expressed in cells, used particularly for inhibiting HIV
PT infection of cells.
XX
XX Claim 3; Page 27; 83pp; English.
XX
CC This represents a target sequence of HIV-1 co-receptor beta-chemokine
CC receptor (CCR)-5. The invention provides endo-ribonuclease nucleic acid
CC that encodes a ribozyme which cleaves a co-receptor RNA expressed in a
CC cell. The co-receptor RNA is a member of the seven trans-membrane protein
CC receptor family. This can be used in a method of inhibiting HIV infection
CC of a cell which comprises cleaving a co-receptor mRNA expressed in the
CC cell. The co-receptor mRNA encodes an HIV co-receptor protein selected
CC from fusin, beta-chemokine receptor-5 (CCR-5), CCR-3 and CCR-2b. The
CC cleavage of the co-receptor mRNA inhibits the production of the selected
CC co-receptor protein, thereby inhibiting HIV infection of the cell. The
CC endo-ribonucleases can be used to specifically cleave RNAs. The method
CC can be used for inhibiting HIV infection of cells by inhibiting
CC expression of HIV co-receptor on the surface of cells. Because the level
CC of co-receptor on the surface of the cell is reduced, HIV entry into the
CC cells is inhibited. Cleavage of HIV co-receptor mRNA using targeted
CC ribozymes is not cytotoxic to cells expressing the co-receptor and the
CC cells retain normal immune function. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 16 BP; 0 A; 6 C; 6 G; 0 T; 4 U; 0 Other;
XX
Query Match 0.6%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2034 GCGGCGAGCAGCCGCC 2048
Db 15 GCGGCGAGCAGCCGCC 1
XX
RESULT 127
AAV48449
ID AAV48449 standard; DNA; 18 BP.
XX
XX AAV48449;
XX
XX 15-OCT-1998 (first entry)
XX
XX Transforming growth factor beta-1 antisense oligonucleotide N37.
XX
XX Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX EP856579-A1.
XX
XX PD 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX (BIOG-) BIOGNOSTIK GES BIOKOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiefen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.

```

PS Example 1; Fig 3a; 286pp; English.

XX CC AAV48412-84 represent antisense oligonucleotides directed against

CC transforming growth factor beta-1 (TGF-beta-1). The oligonucleotides

CC exemplify the invention. The specification describes oligonucleotides

CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that

CC contain each form three hydrogen bonds to cytosine; do not contain four

CC consecutive nucleotides able to form three H-bonds each to four

CC nucleotides each able to form three H-bonds to three consecutive

CC cytosines, and the ratio between residues able to form two H-bonds each

CC (2R) or three such bonds (3R) is given by  $2R/3R = 0.33-0.72$ . The

CC oligonucleotides are used to modulate expression of genes, particularly

CC the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or beta 2 to control

CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or

CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The

CC oligonucleotides can also be used to analyse function of proteins (by

CC altering their expression or activity) and therapeutically, e.g. in cases

CC of cancer or (targeting TGF) for stimulating the immune system

CC

SQ Sequence 18 BP; 0 A; 3 C; 15 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GCGCGGCGCGCGCGCG 404

Db 2 GCGCGGCGCGCGCGCG 16

RESULT 128

AAZ74166

ID AAZ74166 standard; DNA; 18 BP.

XX AC AAZ74166;

XX DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO: 8522.

XX KW Human genome; biallelic marker; high density disequilibrium map;

XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX KW haplotyping; hybridisation; identification; characterisation;

XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;

XX KW diagnosis; ss.

XX OS Homo sapiens.

XX PN M0954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99MO-IB000822.

XX PR 21-APR-1998; 98US-0082614P.

XX PR 23-NOV-1998; 98US-0109732P.

XX PA (GEST ) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium

XX PT map of the human genome.

XX PS Claim 8; Page 2047; 2745pp; English.

XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

XX CC invention, which contain a polymorphic base at position 24 of their

XX CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

XX CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses; they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 7 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 CCCGATGAGACCA 878

Db 3 CCCAGATGAGACCA 17

RESULT 129

AAA11058/C

ID AAA11058 standard; DNA; 19 BP.

XX AC AAA11058;

XX DT 28-JUL-2000 (first entry)

XX DE Sequencing primer 1 for exon 3 of HLA-A, -B and -C genes.

XX KW Tissue sample testing; allelic typing; human leukocyte antigen;

XX KW PCR primer; probe; hybridisation; intron; amplification; ss;

XX KW allelic variation; non-classical HLA class I gene; exon.

XX OS Homo sapiens.

XX PN US6030775-A.

XX PD 29-FEB-2000.

XX PF 22-DEC-1995; 95US-00577081.

XX PR 22-DEC-1995; 95US-00577081.

XX PA (CERE/) CERE B N.

XX PA (YANG/) YANG S Y.

XX PI Cereb N, Yang SY;

XX DR WPI; 2000-223158/19.

XX PT Testing a tissue sample to determine the allelic type of a human

XX PT leukocyte antigen class I gene comprises amplification of nucleic acid

XX PT polymers with primers which flank a region including an allelic variation

XX PT of the HLA class I gene.

XX BS Disclosure; Col 9; 90pp; English.

XX CC The invention relates to a method (I) for testing a tissue sample to

XX CC determine the allelic type of a human leukocyte antigen (HLA) class I

XX CC gene in the sample, where the HLA class I gene is selected from HLA-A,

XX CC HLA-B or HLA-C, by: (a) treating the tissue sample to obtain nucleic acid

XX CC polymers suitable for amplification; (b) combining the nucleic acid

XX CC polymers with a primer which hybridizes with a portion of intron 1 or

XX CC intron 3 of the HLA class I gene, and a second primer which hybridizes

XX CC with a different portion of the HLA class I gene and performing

XX CC amplification, where the primers flank a region including at least one

XX CC site of allelic variation in at least one of exons 2 or 3 of the HLA

XX CC class I gene and where the first primer is a locus specific primer which

XX CC hybridizes with intron 1 or 3 of only one of the HLA class I genes; and

CC (c) evaluating the amplified product to determine the allelic type of the  
CC HLA class I gene. The method is useful for testing a tissue sample to  
CC determine the allelic type of a classical or non-classical HLA class I  
CC gene in the sample. The sequences AA11039-11122 represent consensus  
CC sequences of introns and exons of the HLA genes and primers and probes  
CC used to isolate and analyse the HLA genes  
XX  
SQ Sequence 19 BP, 0 A, 4 C, 13 G, 1 T, 0 U, 1 Other;

SQ Sequence 19 BP; 0 A; 4 C; 13 G; 1 T; 0 U; 1 Other;

Query Match	0.6%	Score 15	DB 1	Length 19
Best Local Similarity	88.2%	Pred No. 85		
Matches 15, Conservative		1, Mismatches		0, Gaps 0

```
Qy      471  CCGAGCCCCCGCACCGC  487
          |||||
Db      17  CCGAGCCCCCGYCCCGC  1
```

RESULT 130  
AAT73214/c  
ID AAT73214 standard; DNA; 20 BP.

AC	AAT73214;
XX	
DT	27-AUG-1997 (first entry)

PCR primer corresponds to bases 610-631 of vav.

KM Proto-oncogene; vav; complementary; in vitro; antisense; inhibition; ss  
KM proliferation; leukaemia; erythroid; solid tumour; myelogenous; primer;  
KM expression; lung tumour; polymerase chain reaction; amplification; PCR.

OS Synthetic

PN US5612212-A.

PD 18-MAR-1997.

PF 12-NOV-1993; 93US-00152634.

PR 12-NOV-1993; 93US-00152634.

(TYPE-) UNIV PENNSYLVANIA.

PI	Gew1rtz Al
yy	

DR WPI; 1997-192110/17.

PT Antisense vav proto-oncogene oligo:nucleotide - for inhibiting leukaemic  
PT erythroid and solid tumour cell proliferation.

PS Example 1; Col 18; 12pp; English.

The oligonucleotides AAT73213-5 were used in to detect the amount of vav proto-oncogene expression in mononuclear cells derived from healthy patients or patients suffering from acute or chronic myelogenous leukaemia after treatment with the antisense oligonucleotide (AAT73210) or controls (AAT73211-2). This sequence represents a PCR primer used to amplify the vav proto-oncogene sequence after cDNA syntheses using RNA isolated from the treated cells. Antisense oligonucleotides (especially AAT73210) to the vav proto-oncogene can be used as an *in vitro* antisense agent for inhibiting the proliferation of leukaemic, erythroid or solid tumour cells, especially where the leukaemic cells are chronic or acute myelogenous leukaemia cells and the solid tumour is characterised by low level vav expression (e.g. a lung tumour).

SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match	0.6%;	Score 15;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 88;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2390 CAGAAATGCTGCTGG 2404

Db 19 CAGAATGCTGCTGG

RESULT 131  
AAZ37481/C  
ID AAZ37481 standard; DNA; 20 BP.

AC AAZ37481;

DT 07-JAN-2000 (first entry)

DE Human mcm2 phosphorothioate oligodeoxynucleotide #11. 117

KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer  
 KW anisensin; modulation; oligonucleotide; expression; inhibition;  
 KW hyperproliferation; blood cancer; brain cancer; breast cancer;  
 KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis  
 KW restenosis; ss.

OS Synthetic.  
OS Homo sapiens.

PN W09949065-A1.

PD 30-SEP-1999

PF 26-MAR-1999; 99WO-US006702.

PR 26-MAR-1998; 98US-00048810.

PA (ISIS-) ISIS PHARM INC.  
VV

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM,   
 vv

DR WPI; 1999-610754/52.  
xy

PT New antisense compounds used to treat eg. hyperproliferative conditions

PS Example 2; page 3 /; 15/100; English

CC AA23747-3-AA237738 represent human mdm2 phosphorothioate oligonucleotides.  
CC AA23747-1-AA237739, AA237739, AA237740 and AA237741 are used in the  
CC AA23747-1-AA237739, AA237739, AA237740 and AA237741 are used in the  
CC exemplification of the present invention. The present invention describes  
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
CC translation termination codon, or 3' untranslated region of a nucleic  
CC acid encoding human mdm2, that modulates expression of human mdm2. The  
CC oligonucleotides mediate their effect by antisense inhibition of  
CC hyperproliferative gene expression. The antisense compound is used to  
CC treat an animal having a disease or condition associated with mdm2,  
CC particularly a hyperproliferative condition, more particularly cancer,  
CC especially of the blood, brain, breast, lung or soft tissue, or  
CC psoriasis, fibrosis, atherosclerosis or rheumatism

SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match	0.6%	Score 15	DB 1	Length 20
Best Local Similarity	100.0%	Prod. No. 88		
Matches 15	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1707 TGTACCTACTGATGG 1721  
|||  
Db 19 TGTACCTACTGATGG 5

RESULT 132  
AAZ31280  
ID AAZ31280 standard; DNA; 20 BP.

AC AAZ31280

DT 24-JAN-2000 (first entry)

X

```

DE CCR5 gene inhibiting antisense oligo AS(s)-37.
XX
XX HIV cofactor inhibitor; HIV infection; CXCR4 gene; CCR5 gene;
KM drug composition; antisense; ss.
XX
XX Synthetic.
XX
XX WO951751-A1.
XX
XX 14-OCT-1999.
XX
XX
XX 01-APR-1999; 99WO-JP001722.
XX
XX 02-APR-1998; 98JP-00125452.
XX
XX (MAR-) MARINE BIO CO LTD.
XX
XX Takaku H, Yamamoto N, Kimura T, Takai K, Wada A;
XX
XX WPI; 1999-620207/53.
XX
XX Antisense oligonucleotide-based HIV cofactor inhibitors, as drug
XX compositions for treatment of HIV infection.
XX
XX Claim 6; Page 16; 59pp; Japanese.
XX
XX The invention provides HIV cofactor inhibitors that contain
XX oligonucleotides with a base sequence complementary to the CXCR4 or CCR5
XX genes. Such inhibitors can be formulated into drug compositions for
XX prevention or treatment of HIV infection, with inhibition of expression
XX of CXCR4 or/and CCR5 gene. Sequences AA231244-306 represent antisense
XX oligonucleotides to the CCR5 gene
XX
SQ Sequence 20 BP; 5 A; 8 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2034 GCGGCGAGGACCAAGCC 2048
DB 5 GCGGCGAGGACCAAGCC 19
RESULT 133
AA289069/c
ID AA289069 standard; DNA; 20 BP.
XX
XX AA289069;
XX
XX 01-JUN-2000 (first entry)
XX
XX Human nibrin PCR primer Ex2 R.
XX
XX Nibrin; human; DNA double strand break repair protein; diagnosis;
XX therapy; Nijmegen Breakage Syndrome; gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX DE19818680-C1.
XX
XX 09-MAR-2000.
XX
XX 27-APR-1998; 98DE-01018680.
XX
XX 27-APR-1998; 98DE-01018680.
XX
XX (UYBE ) UNIV BERLIN HUMBOLDT.
XX
XX WPI; 2000-196117/18.
XX
XX A DNA double strand break repair protein, Nibrin, and related DNA useful
XX for diagnosis and therapy of Nijmegen Breakage Syndrome and other
PT

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```

PT diseases influenced by DNA-double-strand break repair.
XX
XX Claim 5; Fig 3B; 32pp; German.
XX
XX This invention describes a novel DNA double strand break repair protein,
XX Nibrin. Nibrin and DNA encoding it are useful for diagnosis and/or
XX therapy of diseases influenced by repair of DNA-double strand breaks, in
XX particular Nijmegen Breakage Syndrome. The product of the invention has
XX applications in gene therapy. AA289048-289103 represent PCR primers used
XX in the amplification of the human nibrin protein described in the
XX invention
XX
SQ Sequence 20 BP; 6 A; 9 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1785 GTATGTGAGAGAGAG 1799
DB 15 GTATGTGAGAGAGAG 1
RESULT 134
AA235001/c
ID AA235001 standard; DNA; 20 BP.
XX
XX AA235001;
XX
XX 28-FEB-2000 (first entry)
XX
XX Nijmegen breakage syndrome NBS1 gene primer Ex2 R.
XX
XX NBS1 gene; nibrin; Nijmegen breakage syndrome; diagnosis; human;
XX gene therapy; cancer; microcephaly; mental retardation;
XX primary ovarian failure; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9955716-A1.
XX
XX 04-NOV-1999.
XX
XX 27-APR-1999; 99WO-US009036.
XX
XX 27-APR-1998; 98US-0083269P.
XX
XX (VIRG-) VIRGINIA MASON RES CENT.
XX
XX Concannon PJ, Vissinga CS, Cerosaletti KM, Varon R, Sperling K;
XX Reis A;
XX
XX WPI; 2000-062015/05.
XX
XX Novel gene useful for detecting mutations or polymorphisms, and
XX diagnosing certain pathological conditions in Nijmegen Breakage syndrome
XX patients.
XX
XX Claim 20; Page 35; 58pp; English.
XX
XX This primer, termed Ex2 R, flanks exon 2 of the human NBS1 gene (see
XX AA234997) that is associated with Nijmegen breakage syndrome (NBS). It is
XX 1 of 38 claimed exon-flanking primers (see AA234998-235035) designed for
XX the 16 exons of the NBS1 gene. The primers can be used to screen NBS
XX patients for mutations of the NBS1 gene, e.g. by PCR, and hence to
XX diagnose a predisposition to a pathological condition such as cancer,
XX microcephaly, mental retardation, and primary ovarian failure
XX
SQ Sequence 20 BP; 6 A; 9 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1795 GTATGTGAGAGAG 1799  
 |||||  
 DB 15 GTATGTGAGAGAG 1

## RESULT 135

AAF80635/c  
 ID AAF80635 standard; DNA; 20 BP.

AC AAF80635;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX

DE Human mdm2 phosphorothioate oligonucleotide #9.

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Homo sapiens.

XX US6184212-B1.

XX 06-FEB-2001.

XX 26-MAR-1999; 99US-00280805.

XX 26-MAR-1998; 98US-00048810.

XX (ISIS-) ISIS PHARM INC.

XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

XX WPI; 2001-190948/19.

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic acid molecule encoding human mdm-2 useful for modulating the expression of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 2; Col 20; 77pp; English.

CC The present invention relates to an antisense compound 8-30 nucleobases in length targeted to nucleobases 1-308 of the 5' untranslated region, CC 1776-1806 of the translation termination codon region or 1818-2370 of the CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2. CC The invention is useful for reducing hyperproliferation of human cells, CC modulating the expression of mdm2 in human cells or tissues or in vitro. CC The hyperproliferative disorder includes cancer or psoriasis

XX Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1707 TGTACTACTGATGG 1721  
 |||||  
 DB 19 TGTACTACTGATGG 5

## RESULT 136

AAD07540/c  
 ID AAD07540 standard; DNA; 20 BP.

AC AAD07540;  
 XX

DT 10-AUG-2001 (first entry)  
 XX

DE Human mdm2 antisense oligonucleotide (ISIS #16514).

XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;

KW tumour; prophylaxis; antisense; ss.

XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

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FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

Location/Qualifiers

1. .20

/tag= a

/mod\_base= OTHER

/note= "phosphorothioate backbone"

1. .6

/tag= b

/mod\_base= OTHER

/note= "2'-methoxyethoxy residues"

3

/tag= c

/mod\_base= m5c

5. .6

/tag= d

/mod\_base= m5c

15. .20

/tag= e

/mod\_base= OTHER

/note= "2'-methoxyethoxy residues"

18

/tag= f

/mod\_base= m5c

US6238921-B1.

29-MAY-2001.

26-MAR-1998; 98US-00048810.

26-MAR-1998; 98US-00048810.

(ISIS-) ISIS PHARM INC.

XX Miraglia LJ, Nero P, Graham MJ, Monia BP;

XX WPI; 2001-366477/38.

PT New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and 16524, PT which inhibits human mdm2 expression, useful for inhibiting, diagnosing PT or treating abnormal proliferative conditions associated with mdm2.

XX Example 2; Col 16; 19pp; English.

CC The present invention relates to compositions and methods for modulating CC the expression of human mdm2 gene, a naturally present cellular gene CC implicated in abnormal cell proliferation and tumour formation. The CC invention also provides antisense oligonucleotides which are targeted to CC the mdm2 gene and are capable of inhibiting the expression of mdm2 gene. CC The oligonucleotides are useful in diagnostics, therapeutics, prophylaxis CC and as research reagents. They are especially useful for inhibiting, CC diagnosing and treating abnormal proliferative conditions associated with CC mdm2. The method is useful for detecting and determining the role of mdm2 CC expression in various cell functions and physiological processes and CC conditions, and for diagnosing conditions associated with mdm2 CC expression. The present sequence is human mdm2 antisense oligonucleotide CC (ISIS #16514) with a phosphorothioate backbone. This sequence is CC targeted to the coding region of the mdm-2 gene

XX Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1707 TGTACTACTGATGG 1721  
 |||||  
 DB 19 TGTACTACTGATGG 5

## RESULT 137

AAS29250/c

```

ID  AAS29250 standard; DNA; 20 BP.
XX
AC  AAS29250;
XX
DT  21-NOV-2001 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide 16514.
XX
KW  Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW  atherosclerosis; tumour; cytostatic; anti psoriatic;
KW  anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS  Homo sapiens.
XX
FH  Key
FT  modified_base 1..20
FT  /**tag= a
FT  /mod_base= OTHER
FT  /note= "OTHER= All phosphorothioate linkages,
FT  additionally bases 1-6 and bases 15-20 are 2'-O-
FT  methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
PN  US2001016575-A1.
XX
PD  23-AUG-2001.
XX
PF  02-JAN-2001; 2001US-00752983.
XX
PR  26-MAR-1998; 98US-00048810.
XX  26-MAR-1999; 99US-00280805.
XX
PA  (MIRA/) MIRAGLIA L J.
PA  (NERO/) NERO P.
PA  (GRAH/) GRAHAM M J.
PA  (MONI/) MONIA B P.
PA  (COMS/) COMSERT L M.
XX
PI  Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM,
XX  WPI; 2001-535565/59.
XX
PT  An antisense compound, useful for treating e.g. cancer, comprises
PT  nucleobases targeted a region (e.g. translation termination codon region)
PT  of a nucleic acid encoding human mdm2.
XX
PS  Example 2; Page 11; 81pp; English.
XX
CC  The present invention relates to antisense compounds, 8-30 nucleobases in
CC  length targeted to the 5' untranslated region, coding region or translation start
CC  codon region, 3' untranslated region, coding region or translation termination
CC  site of a nucleic acid encoding human mdm2, where the antisense compound
CC  modulates the expression of human mdm2. The antisense oligonucleotides of
CC  the invention are useful for encoding human mdm2 and for inhibiting the
CC  expression of human mdm2. They may be used for treating an animal having
CC  a disease or condition associated with amplification of mdm2 gene or
CC  overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC  (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC  fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC  and chronic myelogenous leukemia. The antisense compound may be
CC  administered with a chemotherapeutic agent to overcome drug resistance.
CC  The antisense compound reduces hyperproliferation of human cells. The
CC  method, which involves the use of the antisense compound, is also useful
CC  for detecting the role of mdm2 expression in various cell functions and
CC  physiological processes and useful in both clinical research and
CC  diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC  oligonucleotides of the present invention
XX
SQ  Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1707 TGTACTACTGATGG 1721
DB 19 TGTACTACTGATGG 5
XX
RESULT 138
ID ABT07408 standard; DNA; 20 BP.
XX
AC ABT07408;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human protein phosphatase 2 oligo inhibitor SEQ ID No 22.
XX
KW Cytostatic; antidiabetic; antisense therapy; aberrant insulin regulation;
KW protein phosphatase 2 catalytic beta subunit; antisense compound; cancer;
KW hyperproliferative disorder; diabetes; inflammation; tumour; human; ds.
XX
OS Homo sapiens.
XX
PN WO200264737-A2.
XX
PD 22-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002805.
XX
PR 09-FEB-2001; 2001US-00780045.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX  WPI; 2002-657588/70.
XX
PT New antisense oligonucleotides targeted to nucleic acid encoding Protein
PT Phosphatase 2 catalytic subunit beta, useful for treating diseases
PT related to Protein Phosphatase 2 catalytic subunit beta expression, such
PT as cancer.
XX
PS Claim 3; Page 94; 137pp; English.
XX
CC The invention relates to a novel compound 8-50 nucleotides in length
CC targeted to a nucleic acid molecule encoding a protein phosphatase 2
CC catalytic beta subunit, where the compound specifically hybridises with
CC and inhibits the expression of protein phosphatase 2 catalytic beta
CC subunits, or specifically hybridises with at least an 8-nucleotide
CC portion of an active site on a nucleic acid molecule encoding a protein
CC phosphatase 2 catalytic beta subunit. The antisense compounds are useful
CC for modulating the expression of protein phosphatase 2 catalytic beta
CC subunits and for treating diseases or conditions associated with
CC expression of protein phosphatase 2 catalytic beta subunits, e.g.
CC aberrant insulin regulation or diabetes or a hyperproliferative disorder,
CC particularly cancer. The antisense compounds are also useful for
CC diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay
CC infection, inflammation or tumour formation, as research reagents and
CC kits, and in distinguishing between functions of various members of a
CC biological pathway. This polynucleotide sequence represents an
CC oligonucleotide inhibitor of human protein phosphatase 2 catalytic beta
CC subunit mRNA levels of the invention. NOTE: This oligonucleotide contains
XX phosphorothioate residues and has 2' - MOE wings with a deoxy gap
XX
SQ Sequence 20 BP; 0 A; 13 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 283 CCGGCCCGGCCCGGC 297
DB 2 CCGGCCCGGCCCGGC 16

```

RESULT 139  
 AB284858/C  
 ID AB284858 standard; DNA; 20 BP.  
 XX  
 AC AB284858;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIC-) EPIDEMESIS PHARM INC.  
 XX  
 PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Claim 15; SEQ ID NO 100; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end, genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pat\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2051 CAGCAGCCCAAGCTT 2065  
 DB 16 CAGCAGCCCAAGCTT 2

RESULT 140  
 ADD21446/C  
 ID ADD21446 standard; DNA; 20 BP.  
 XX  
 AC ADD21446;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide #9.  
 XX  
 KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
 KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
 KW 2'-methoxyethoxy-residue; phosphorothioate backbone.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003048315-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038281.  
 XX  
 PR 04-DEC-2001; 2001US-00005344.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Miraglia LJ, Nero PS, Graham MJ, Morita BP, Koller E, Chiang MY;  
 PI Maronaran M;  
 XX  
 DR WPI; 2003-577263/54.  
 XX  
 PT Novel antisense compound targeted to 5' untranslated region, coding  
 PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
 PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
 PT mdm2 expression.  
 XX  
 PS Example 2; SEQ ID NO 11; 289pp; English.  
 XX  
 CC The invention comprises antisense oligonucleotides which are targeted to  
 CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
 CC useful for reducing hyperproliferation of human cells. The antisense  
 CC oligonucleotides are also useful for treating: hyperproliferative  
 CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
 CC restenosis. The antisense oligonucleotides are also useful for modulating  
 CC apoptosis, and for increasing expression of p21. The present DNA sequence  
 CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
 CC The present sequence contains 2'-methoxyethoxy-residues and has a  
 CC phosphorothioate backbone.  
 XX  
 SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.6%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1707 TGTACTACTGATGG 1721  
 DB 19 TGTACTACTGATGG 5  
 XX  
 RESULT 141  
 ADE86164  
 ID ADE86164 standard; DNA; 20 BP.  
 XX  
 AC ADE86164;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE HRAS gene regulatory region quadruplex DNA.  
 XX  
 KW HRAS; quadruplex DNA; gene therapy; cancer; cytostatic; oncogene; human;  
 KW ds.

```

XX OS Homo sapiens.
XX PN WO2003087317-A2.
XX XX 23-OCT-2003.
XX PD 04-APR-2003; 2003WO-US010658.
XX PF 05-APR-2002; 2002US-0370358P.
XX PR 20-AUG-2002; 2002US-0404966P.
XX PR 20-MAR-2003; 2003US-0456637P.
XX PA (CYTE-) CYTERNEX INC.
XX PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX PI Siddiqui-Jain A, Grand CL, Bears DJ, Hurley LH, Farrell TJ;
XX DR WPI; 2003-853947/79.
XX DR
XX PT Identifying a compound that modulates the biological activity of a native
XX PT quadruplex DNA for treating colorectal cancer comprises determining the
XX PT presence or absence of interaction between the candidate compound and the
XX PT test quadruplex DNA.
XX PS Claim 3; Page 46; 69pp; English.
XX CC The present sequence is from the upstream regulatory region of the HRAS
XX CC gene. The sequence is involved in the regulation of transcription. It
XX CC forms a quadruplex structure through the formation of guanine tetrads.
XX CC The sequence provides an example of intramolecular chair quadruplex DNA
XX CC structures that have been identified as oncogene regulators. Certain
XX CC mutations in quadruplex forming nucleotides sequences have been shown to
XX CC destabilise quadruplex structure and are associated with cancer. Methods
XX CC are provided for identifying quadruplex nucleotide sequences having
XX CC destabilising guanine substitutions, for determining whether a subject is
XX CC at risk of developing or having cancer, pharmacogenomic methods for
XX CC targeting appropriate prevention or therapeutic regimens, methods for
XX CC screening molecules that interact with stabilised and destabilised
XX CC quadruplexes, and therapeutic methods for treating cancers, such as
XX CC antisense nucleic acid cancer therapy that specifically targets DNA in
XX CC subjects having a quadruplex-destabilising mutation.
XX SQ Sequence 20 BP; 0 A; 3 C; 17 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 88;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 390 GCGCGGCGCGCGCGG 404
XX Db |||||
XX 4 GCGCGGCGCGCGCGG 18
XX
XX RESULT 142
XX ADS86160
XX ID ADS86160 standard; DNA; 20 BP.
XX AC ADE86160;
XX DT 29-JAN-2004 (first entry)
XX DE RET gene regulatory region quadruplex DNA.
XX KW Platelet derived growth factor alpha; PDGF; quadruplex DNA; gene therapy;
XX KW cancer; cytoskeletal; oncogene; human; ds.
XX OS Homo sapiens.
XX PN WO2003087317-A2.
XX PD 23-OCT-2003.
XX PA

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XX PF 04-APR-2003; 2003WO-US010658.
XX XX
XX PR 05-APR-2002; 2002US-0370358P.
XX PR 20-AUG-2002; 2002US-0404966P.
XX PR 20-MAR-2003; 2003US-0456637P.
XX XX
XX PA (CYTE-) CYTERNEX INC.
XX PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX PI Siddiqui-Jain A, Grand CL, Bears DJ, Hurley LH, Farrell TJ;
XX DR WPI; 2003-853947/79.
XX DR
XX PT Identifying a compound that modulates the biological activity of a native
XX PT quadruplex DNA for treating colorectal cancer comprises determining the
XX PT presence or absence of interaction between the candidate compound and the
XX PT test quadruplex DNA.
XX PS Claim 3; Page 46; 69pp; English.
XX CC The present sequence is from the upstream regulatory region of the RET.
XX CC It forms a chair quadruplex structure ADE86192 with 2 stable tetrads that
XX CC regulates transcription. The sequence provides an example of
XX CC intramolecular chair quadruplex DNA structures that have been identified
XX CC as oncogene regulators. Certain mutations in quadruplex forming
XX CC nucleotide sequences have been shown to destabilise quadruplex structure
XX CC and are associated with cancer. Methods are provided for identifying
XX CC quadruplex nucleotide sequences having destabilising guanine
XX CC substitutions, for determining whether a subject is at risk of developing
XX CC or having cancer, pharmacogenomic methods for targeting appropriate
XX CC prevention or therapeutic regimens, methods for screening molecules that
XX CC interact with stabilised and destabilised quadruplexes, and therapeutic
XX CC methods for treating cancers, such as antisense nucleic acid cancer
XX CC therapy that specifically targets DNA in subjects having a quadruplex-
XX CC destabilising mutation.
XX SQ Sequence 20 BP; 0 A; 3 C; 17 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 88;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 390 GCGCGGCGCGCGCGG 404
XX Db |||||
XX 4 GCGCGGCGCGCGCGG 18
XX
XX RESULT 143
XX AAT30416
XX ID AAT30416 standard; DNA; 18 BP.
XX AC AAT30416;
XX DT 28-JAN-1997 (first entry)
XX DE Compound simple sequence repeat primer (TG)4.5(AG)4.5.
XX KW Detection; polymorphism; perfect compound simple sequence repeat;
XX KW adaptor directed primer; genome; genetic; fingerprinting;
XX KW amplified fragment length polymorphism assay; microsatellite region;
XX KW genetic trait marking; germplasm comparisons; compound; ss.
XX OS Synthetic.
XX PN WO9617082-A2.
XX PD 06-JUN-1996.
XX PF 21-NOV-1995; 95WO-US015150.
XX PR 28-NOV-1994; 94US-00346456.
XX PA (DUPO ) DU POINT DE MEMOIRS & CO E I.

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XX MORGANCE M, Vogel JM;  
XX WPI: 1996-277795/28.  
XX Modified amplified fragment length polymorphism assay - for detection of  
XX polymorphism esp. in microsatellite regions.  
XX Example 2, Page 84; 173pp; English.  
XX  
XX Detecting polymorphisms between 2 nucleic acid samples, esp. in  
XX microsatellite regions, comprises digesting the nucleic acid to generate  
XX fragments, ligating adaptor segments to their ends, amplifying them using  
XX primer directed amplification and comparing the products to detect  
XX differences. The primers used in the amplification comprise a primer  
XX consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
XX directed primer, comprising a sequence complementary to an adaptor  
XX segment. The present sequence is an example of a compound SSR primer. The  
XX method represents a modified amplified fragment length polymorphism  
XX assay, which is partic. useful for genome fingerprinting, i.e. for  
XX genetic trait marking and germplasm comparisons  
SQ Sequence 18 BP; 5 A; 0 C; 9 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1785 GTATGTGAGAGAGAGA 1802  
DB 1 GTGTGTGAGAGAGAGA 18  
  
RESULT 144  
AAK58119/C  
ID AAK58119 standard; DNA; 18 BP.  
XX  
XX AAK58119;  
XX  
XX 21-JUL-1999 (first entry)  
XX  
XX PCR primer for human GABAB receptor coding sequence.  
XX  
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;  
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;  
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
XX autoimmune disease; neoplastic disease; infectious disease; therapy;  
XX PCR primer; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX WO9921890-A1.  
XX  
XX 06-MAY-1999.  
XX  
XX 27-OCT-1998; 98WO-SE001947.  
XX  
XX 27-OCT-1997; 97SE-00003914.  
XX 16-MAR-1998; 98SE-00000864.  
XX 17-JUL-1998; 98SE-00002575.  
XX  
XX (ASTR ) ASTRA AB.  
XX  
XX Ekstrand J;  
XX  
XX WPI: 1999-302985/25.  
XX  
XX Polynucleotides encoding human and canine gamma aminobutyric acid type B  
XX receptors, used to screen for compounds that are inhibitors of transient  
XX lower esophageal sphincter relaxations.

PS Example 8; Page 30; 222pp; English.  
XX  
XX This sequence represents a PCR primer for DNA encoding a human gamma  
XX aminobutyric acid type B (GABAB) receptor of the invention. Nucleic acid  
XX molecules encoding GABAB receptors can be used to screen for compounds  
XX that are inhibitors of transient lower oesophageal sphincter relaxations  
XX (TLESR). They can also be used to screen for agonists or antagonists of  
XX the GABAB receptors. Inhibitors of TLESR are useful for treating gastro-  
XX oesophageal reflux disease. Other uses of GABAB receptors, such as human  
XX GABAB dysfunction, e.g. epilepsy, psychiatric disorders, emesis,  
XX irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies,  
XX autoimmune diseases, neoplastic diseases, pain and infectious disease  
XX  
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2304 CACAGTGGATGATGACAG 2321  
DB 18 CACATGGAGAGAACAG 1  
  
RESULT 145  
AAK58106/C  
ID AAK58106 standard; DNA; 18 BP.  
XX  
XX AAK58106;  
XX  
XX 21-JUL-1999 (first entry)  
XX  
XX PCR primer for human GABAB receptor coding sequence.  
XX  
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;  
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;  
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
XX autoimmune disease; neoplastic disease; infectious disease; therapy;  
XX PCR primer; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX WO9921890-A1.  
XX  
XX 06-MAY-1999.  
XX  
XX 27-OCT-1998; 98WO-SE001947.  
XX  
XX 27-OCT-1997; 97SE-00003914.  
XX 16-MAR-1998; 98SE-00000864.  
XX 17-JUL-1998; 98SE-00002575.  
XX  
XX (ASTR ) ASTRA AB.  
XX  
XX Ekstrand J;  
XX  
XX WPI: 1999-302985/25.  
XX  
XX Polynucleotides encoding human and canine gamma aminobutyric acid type B  
XX receptors, used to screen for compounds that are inhibitors of transient  
XX lower esophageal sphincter relaxations.  
XX  
XX Example 3; Page 18; 222pp; English.  
XX  
XX This sequence represents a PCR primer for DNA encoding a human gamma  
XX aminobutyric acid type B (GABAB) receptor of the invention. Nucleic acid  
XX molecules encoding GABAB receptors can be used to screen for compounds  
XX that are inhibitors of transient lower oesophageal sphincter relaxations  
XX (TLESR). They can also be used to screen for agonists or antagonists of  
XX the GABAB receptors. Inhibitors of TLESR are useful for treating gastro-

CC oesophageal reflux disease. Other uses of GABAB receptors, such as human  
CC GABAB R1c or 1d, comprise diagnosis or treatment of conditions related to  
CC GABAB dysfunction, e.g. epilepsy, psychiatric disorders, emesis,  
CC irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies,  
CC autoimmune diseases, neoplastic diseases, pain and infectious disease  
XX  
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGATGAACCG 2321  
DB 18 CACATTGGAGGAGAACCG 1

RESULT 146  
ID AAX58109 standard; DNA; 18 BP.  
XX AAX58109;  
AC AAX58109;  
XX 21-JUL-1999 (first entry)

DE PCR primer for human GABAB receptor coding sequence.

XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;  
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLRSR;  
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
XX autoimmune disease; neoplastic disease; infectious disease; therapy;  
XX PCR primer; ss.

OS Synthetic.  
OS Homo sapiens.

PN WO921890-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-SE001947.

XX 27-OCT-1997; 97SE-00003914.

XX 16-MAR-1998; 98SE-00000864.

XX 17-JUL-1998; 98SE-00002575.

XX (ASTR ) ASTRA AB.

XX Bkstrand J;

XX WPI; 1999-302985/25.

XX Polynucleotides encoding human and canine gamma aminobutyric acid type B  
XX receptors, used to screen for compounds that are inhibitors of transient  
XX lower esophageal sphincter relaxations.

XX Example 3; Page 20; 222pp; English.

XX This sequence represents a PCR primer for DNA encoding a human gamma  
XX aminobutyric acid type B (GABAB) receptor of the invention. Nucleic acid  
XX molecules encoding GABAB receptors can be used to screen for compounds  
XX that are inhibitors of transient lower oesophageal sphincter relaxations  
XX (TLRSR). They can also be used to screen for agonists or antagonists of  
XX the GABAB receptors. Inhibitors of TLRSR are useful for treating gastro-  
XX oesophageal reflux disease. Other uses of GABAB receptors, such as human  
XX GABAB R1c or 1d, comprise diagnosis or treatment of conditions related to  
XX GABAB dysfunction, e.g. epilepsy, psychiatric disorders, emesis,  
XX irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies,  
XX autoimmune diseases, neoplastic diseases, pain and infectious disease  
XX  
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGATGAACCG 2321  
DB 18 CACATTGGAGGAGAACCG 1

RESULT 147  
ID AAX58117 standard; DNA; 18 BP.  
XX AAX58117;  
AC AAX58117;  
XX 21-JUL-1999 (first entry)

DE PCR primer for human GABAB receptor coding sequence.

XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;  
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLRSR;  
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
XX autoimmune disease; neoplastic disease; infectious disease; therapy;  
XX PCR primer; ss.

OS Synthetic.  
OS Homo sapiens.

PN WO921890-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-SE001947.

XX 27-OCT-1997; 97SE-00003914.

XX 16-MAR-1998; 98SE-00000864.

XX 17-JUL-1998; 98SE-00002575.

XX (ASTR ) ASTRA AB.

XX Bkstrand J;

XX WPI; 1999-302985/25.

XX Polynucleotides encoding human and canine gamma aminobutyric acid type B  
XX receptors, used to screen for compounds that are inhibitors of transient  
XX lower esophageal sphincter relaxations.

XX Example 7; Page 28; 222pp; English.

XX This sequence represents a PCR primer for DNA encoding a human gamma  
XX aminobutyric acid type B (GABAB) receptor of the invention. Nucleic acid  
XX molecules encoding GABAB receptors can be used to screen for compounds  
XX that are inhibitors of transient lower oesophageal sphincter relaxations  
XX (TLRSR). They can also be used to screen for agonists or antagonists of  
XX the GABAB receptors. Inhibitors of TLRSR are useful for treating gastro-  
XX oesophageal reflux disease. Other uses of GABAB receptors, such as human  
XX GABAB R1c or 1d, comprise diagnosis or treatment of conditions related to  
XX GABAB dysfunction, e.g. epilepsy, psychiatric disorders, emesis,  
XX irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies,  
XX autoimmune diseases, neoplastic diseases, pain and infectious disease  
XX  
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 CACAGTGGATGAACCG 2321  
DB 18 CACATTGGAGGAGAACCG 1

RESULT 148  
AAZ71698  
ID AAZ71698 standard; DNA; 18 BP.  
XX  
XX AAZ71698;  
AC  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker upstream amplification primer SEQ ID NO:6054.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO954500-A2.  
PN  
XX 28-OCT-1999.  
PD  
XX 21-APR-1999; 99WO-IB000822.  
PF  
XX 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
DR  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
XX Claim 8; Page 1521; 2745pp; English.  
PS  
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ6579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 18 BP; 10 A; 0 C; 8 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX  
XX Human biallelic marker downstream amplification primer SEQ ID NO:8778.  
DE  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO954500-A2.  
PN  
XX 28-OCT-1999.  
PD  
XX 21-APR-1999; 99WO-IB000822.  
PF  
XX 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
DR  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
XX Claim 8; Page 2102; 2745pp; English.  
PS  
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ6579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 687 CGAGTCAACAGATTCAGG 704  
DB 18 CAAGTCAACAGATTCAGG 1  
XX  
RESULT 150  
AAZ77163/C  
ID AAZ77163 standard; DNA; 18 BP.  
XX  
XX AAZ77163;  
AC  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker downstream amplification primer SEQ ID NO:11519.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.

```

XX OS Homo sapiens.
XX XX
XX PN WD9954500-A2.
XX XX
XX PD 28-OCT-1999.
XX XX
XX PF 21-APR-1999; 99WO-IB000822.
XX XX
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX XX
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I,
XX XX
XX DR WPI; 2000-013267/01.
XX XX
XX PT Novel diallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX XX
XX PS Claim 9; Page 2686; 2745PP; English.
XX XX
XX CC AA265654 to AA269578 represent human diallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AA269579 to AA277440 represent amplification
XX CC primers for the diallelic markers. The diallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterization of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence listing from the
XX CC present invention
XX XX
XX SQ Sequence 18 BP; 4 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX XX
XX Query Match 0.6%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 87;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
QY 1930 GAGGACTTTAAGAGAC 1947
DB 18 GAGGCGCTTTAAGAGAC 1
XX XX
RESULT 151
AAA48762
ID AAA48762 standard; DNA; 18 BP.
XX XX
XX AC AAA48762;
XX XX
XX DT 08-SEP-2000 (first entry)
XX XX
XX DE Human G-alpha-16 antisense oligonucleotide ISIS# 20819.
XX XX
XX KM Human; G-alpha-16; G protein; cytosolic; hyperproliferative disorder;
XX KM cancer; inflammation; infection; antisense inhibition; se.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200032817-A1.
XX XX
XX PD 08-JUN-2000.
XX XX
XX PF 25-AUG-1999; 99WO-US019613.
XX PR 03-DEC-1998; 98US-00205143.
XX XX

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PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cowsett LM;
XX XX
XX DR WPI; 2000-412354/35.
XX XX
XX PF A new antisense compound for inhibiting the expression of human G-alpha-
XX PT 16 and treating, preventing or delaying infections, inflammation or
XX PT hyperproliferative disorders such as cancer.
XX XX
XX PS Example 15; Page 72; 100pp; English.
XX XX
XX CC The present sequence is an antisense oligonucleotide used to modulate
XX CC expression of G-alpha-16. G-alpha-16 is a human G protein which interacts
XX CC differentially with several receptor types including members of the
XX CC opioid and chemokine receptor families. A series of antisense
XX CC oligonucleotides have been designed to target different regions of the
XX CC human G-alpha-16 RNA. They may be used to inhibit the expression of G-
XX CC alpha-16 in human cells and tissues and thus to treat diseases associated
XX CC with G-alpha-16, such as hyperproliferative disorders, especially cancer.
XX CC Infections, inflammation or tumour formation can be prevented or delayed.
XX CC The compounds can be used in research and diagnostics in sandwich and
XX CC other assays. Note: The sequence has a phosphorothioate backbone and may
XX CC be either an oligodeoxynucleotide or a chimeric oligonucleotide
XX CC containing 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS
XX CC number given above corresponds to the oligodeoxynucleotide sequence
XX XX
XX SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 0.6%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 87;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
QY 2149 GACTTCGATGCTTAAC 2166
DB 1 GACTTCCTTCCTGAAC 18
XX XX
RESULT 152
ABA82560/C
ID ABA82560 standard; DNA; 18 BP.
XX XX
XX AC ABA82560;
XX XX
XX DT 25-JAN-2002 (first entry)
XX XX
XX DE Zmax1 gene region physical map preparation STS marker #519.
XX XX
XX KM Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
XX KM sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
XX KM antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
XX KM sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN WO200177327-A1.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 21-JUN-2000; 2000WO-US016951.
XX XX
XX PR 05-APR-2000; 2000US-00543771.
XX PR 05-APR-2000; 2000US-00544398.
XX XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX XX
XX PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX XX
XX DR WPI; 2001-657171/75.
XX XX
XX PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX PT modulating bone mass for the treatment of e.g. osteoporosis.

```

XX PS Disclosure; Page 37; 443pp; English.  
XX CC The present invention describes the human Zmax1 gene and the high bone  
XX mass (HBM) gene, which are found on chromosome 11q12.3. The Zmax1 and HBM  
XX genes have osteopathic activities. The genes can be used in gene therapy,  
XX antisense therapy and in the production of vaccines. They can be used in  
XX the diagnosis and treatment of bone disorders including osteoporosis,  
XX Paget's disease, sclerosteosis, osteomalacia and fibrous dysplasia.  
XX CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in  
XX the exemplification of the present invention.  
XX SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 0.6%; Score 14.8; DB 1; Length 18;  
XX Best Local Similarity 88.9%; Pred. No. 87;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2400 GCTGGCCAAATAGCCAAAG 2417  
DB 18 GCTGTCCAAATAGCCAAAG 1  
RESULT 153  
ID ABAK23357/C  
XX ABAK23357 standard; DNA; 18 BP.  
XX AC ABAK23357;  
XX DT 09-APR-2002 (first entry)  
XX DE Human Zmax1 cDNA forward PCR primer #260.  
XX DE Human Zmax1 cDNA forward PCR primer #260.  
XX DE Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;  
XX lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;  
XX osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;  
XX neurovascular condition; wound healing; gene therapy; PCR primer; probe;  
XX bone development disorder; antiarteriosclerotic; cardiovascular;  
XX osteopathic; cerebroprotective.  
XX OS Homo sapiens.  
XX OS WO200192891-A2.  
XX PN 06-DEC-2001.  
XX PD 25-MAY-2001; 2001WO-US016946.  
XX PF 25-MAY-2001; 2001WO-US016946.  
XX PR 26-MAY-2000; 2000US-00578900.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PA (UYCR-) UNIV CRIGHTON SCHOOL MEDICINE.  
XX PI Carulli JP, Little RD, Recker ER, Johnson ML;  
XX WPI; 2002-097784/13.  
XX PT Identifying molecules involved in lipid regulation, useful for  
XX diagnosing, treating or preventing e.g., arteriosclerosis, comprises  
XX identifying a molecule that binds to high bone mass gene or its  
XX corresponding wild type gene.  
XX PS Disclosure; Page 42; 409pp; English.  
XX CC The invention relates to a method for identifying a molecule involved in  
XX lipid regulation comprising identifying a molecule that binds to or  
XX inhibits binding of a molecule to high bone mass (HBM) or its wild type  
XX gene, Zmax1. Compounds identified by the method are useful for treating,  
XX diagnosing, preventing or screening for normal and abnormal lipid-  
XX associated conditions, including arteriosclerosis, cardiovascular  
XX disease, stroke, and osteoporosis. The compounds may also be used in the  
XX treatment or prevention of diabetic atherosclerosis, neurovascular  
XX conditions caused by plaque build-up, poor circulation due to plaque

CC build-up and associated poor wound healing. The methods may be used in  
CC gene therapy, pharmaceutical development, and diagnostic assays for bone  
CC development disorders. Molecules identified by comparison of Zmax1 and  
CC HBM systems can be used as surrogate markers in pharmaceutical  
CC treatment, in diagnosis of human or animal bone disease, and in the  
CC treatment of bone diseases. Sequences ABAK22776-ABAK23411 represent cDNA  
XX molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers  
XX and adapters of the invention.  
XX SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 0.6%; Score 14.8; DB 1; Length 18;  
XX Best Local Similarity 88.9%; Pred. No. 87;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2400 GCTGGCCAAATAGCCAAAG 2417  
DB 18 GCTGTCCAAATAGCCAAAG 1  
RESULT 154  
ID ABAQ78618  
XX ABAQ78618 standard; DNA; 18 BP.  
XX AC ABAQ78618;  
XX DT 25-NOV-2002 (first entry)  
XX DE PCR primer ERCC1-504R used to amplify a 71 bp fragment of ERCC1 gene.  
XX DE Excision repair cross-complementing gene; ERCC1 gene; tumour;  
XX clinical resistance; platinum-based chemotherapy; genotoxin; PCR; primer;  
XX ss.  
XX OS Homo sapiens.  
XX OS WO200261128-A2.  
XX PN 08-AUG-2002.  
XX PD 23-NOV-2001; 2001WO-US044519.  
XX PR 01-DEC-2000; 2000US-0250121P.  
XX PR 04-DEC-2000; 2000US-0250470P.  
XX PR 02-MAR-2001; 2001US-00796491.  
XX PR 11-JUN-2001; 2001US-00877095.  
XX PR 20-NOV-2001; 2001US-00988784.  
XX PA (RESP-) RESPONSE GENETICS INC.  
XX PI Daneberg KD;  
XX WPI; 2002-643370/69.  
XX PT Determining excision repair cross-complementing expression in fixed  
XX paraffin embedded tissue sample, by isolating mRNA, amplifying it using  
XX primers and determining quantity of mRNA relative to that of internal  
XX control.  
XX PS Claim 13; Page 50; 51pp; English.  
XX CC PCR primers ABAQ78617-18 were used to amplify a 71 bp fragment of the  
XX human excision repair cross-complementing (ERCC1) gene. The primers are  
XX used for determining the level ERCC1 expression in fixed paraffin  
XX embedded tissue samples, and determine a platinum-based chemotherapy by  
XX examination of the amount of ERCC1 mRNA in a patient's tumour cells and  
XX comparing it to a predetermined threshold expression level. This is  
XX useful for making prognosis concerning clinical resistance of a tumour to  
XX a particular genotoxin or the survivability of patient receiving a  
XX particular genotoxin.  
XX SQ Sequence 18 BP; 5 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

410 GCGAGGCGAGGAGAGAG 427  
 1 GCGAGGCGCTGAGGAGACG 18

Db

RESULT 155  
 AB211033/c  
 ID AB211033 standard; DNA; 18 BP.  
 XX  
 AC AB211033;  
 XX  
 DT 16-JAN-2003 (first entry)  
 XX  
 DE Haematopoietic cell proliferation disorder related oligonucleotide #1173.  
 XX  
 KM Human, haematopoietic cell proliferation disorder; cytostatic;  
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KM cytosine methylation state; probe; primer; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN MO200277272-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002MO-EP003401.  
 XX  
 PR 26-MAR-2001; 2001US-0278333P.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Berlin K, Braun A, Distler J, Gnetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwöpe I, Ziebarth H;  
 XX  
 DR WPI; 2003-018942/01.  
 XX  
 PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX  
 PS Claim 15; Page 77; 117pp; English.  
 XX  
 CC The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB211118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 XX Sequence 18 BP; 2 A; 6 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

89 GAGAACGCGGAGAGACGC 106  
 18 GAGAAATGCGAAGATAGC 1

Db

RESULT 156  
 AB210446  
 ID AB210446 standard; DNA; 18 BP.  
 XX  
 AC AB210446;  
 XX  
 DT 16-JAN-2003 (first entry)  
 XX  
 DE Haematopoietic cell proliferation disorder related oligonucleotide #586.  
 XX  
 KM Human, haematopoietic cell proliferation disorder; cytostatic;  
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KM cytosine methylation state; probe; primer; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN MO200277272-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002MO-EP003401.  
 XX  
 PR 26-MAR-2001; 2001US-0278333P.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Berlin K, Braun A, Distler J, Gnetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwöpe I, Ziebarth H;  
 XX  
 DR WPI; 2003-018942/01.  
 XX  
 PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX  
 PS Claim 15; SEQ ID NO 586; 117pp; English.  
 XX  
 CC The present invention describes a method for detecting and  
 CC differentiating between hematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB211118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 XX

Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

39 GTGTAGGTCGGCTTGTT 56  
 1 GTGTAGGTCGGCTTGTT 18

RESULT 157  
 AB211020.

ID AB211020 standard; DNA; 18 BP.

AB211020;

16-JAN-2003 (first entry)

Haematopoietic cell proliferation disorder related oligonucleotide #1160.

Human; haematopoietic cell proliferation disorder; cytostatic;  
 gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 cytosine methylation state; probe; primer; ss.

Homo sapiens.  
 Synthetic.

WO200277272-A2.

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P.

(EPIG-) EPIGENOMICS AG.

Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
 Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pellet C;  
 Schwabe I, Ziebarth H;

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative  
 disorders, comprises contacting a target nucleic acid with a reagent that  
 distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 15; Page 44; 117pp; English.

The present invention describes a method for detecting and  
 differentiating between haematopoietic cell proliferative disorders  
 associated with at least 1 gene and/or their regulatory regions in a  
 subject. The method comprises contacting a target nucleic acid in a  
 biological sample obtained from the subject with at least 1 reagent,  
 which distinguishes between methylated and non-methylated CpG  
 dinucleotides within the target nucleic acid. AB209861 to AB211118  
 represent specifically claimed nucleotide sequences from the present  
 invention. Oligonucleotides from the present invention can be used: for  
 differentiating between healthy haematopoietic cells and proliferative  
 disorder haematopoietic cells; for differentiating between acute  
 lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 determining the cytosine methylation state and/or single nucleotide  
 polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 related sequences and their complements; and as primers for the  
 amplification of haematopoietic cell proliferation disorder related DNA  
 sequences. The nucleotide sequences from the present invention can also  
 be used for detecting a predisposition to, differentiation between  
 subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 haematopoietic cell proliferative disorders. The present method enables a  
 highly specific classification of haematopoietic cell proliferative  
 disorders allowing for improved and informed treatment of patients

Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

39 GTGTAGGTCGGCTTGTT 56  
 1 GTGTAGGTCGGCTTGTT 18

RESULT 158  
 AB210449

ID AB210449 standard; DNA; 18 BP.

AB210449;

16-JAN-2003 (first entry)

Haematopoietic cell proliferation disorder related oligonucleotide #589.

Human; haematopoietic cell proliferation disorder; cytostatic;  
 gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 cytosine methylation state; probe; primer; ss.

Homo sapiens.  
 Synthetic.

WO200277272-A2.

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P.

(EPIG-) EPIGENOMICS AG.

Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
 Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pellet C;  
 Schwabe I, Ziebarth H;

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative  
 disorders, comprises contacting a target nucleic acid with a reagent that  
 distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 15; Page 44; 117pp; English.

The present invention describes a method for detecting and  
 differentiating between haematopoietic cell proliferative disorders  
 associated with at least 1 gene and/or their regulatory regions in a  
 subject. The method comprises contacting a target nucleic acid in a  
 biological sample obtained from the subject with at least 1 reagent,  
 which distinguishes between methylated and non-methylated CpG  
 dinucleotides within the target nucleic acid. AB209861 to AB211118  
 represent specifically claimed nucleotide sequences from the present  
 invention. Oligonucleotides from the present invention can be used: for  
 differentiating between healthy haematopoietic cells and proliferative  
 disorder haematopoietic cells; for differentiating between acute  
 lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 determining the cytosine methylation state and/or single nucleotide  
 polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 related sequences and their complements; and as primers for the  
 amplification of haematopoietic cell proliferation disorder related DNA  
 sequences. The nucleotide sequences from the present invention can also  
 be used for detecting a predisposition to, differentiation between  
 subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 haematopoietic cell proliferative disorders. The present method enables a  
 highly specific classification of haematopoietic cell proliferative

CC disorders allowing for improved and informed treatment of patients  
 XX  
 SQ Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 88 GGAGAACAGCGAGACAG 105  
 Db 1 GGAGATAGCGAGATAG 18

RESULT 159  
 ABZ11022/c  
 ID ABZ11022 standard; DNA; 18 BP.

XX  
 AC ABZ11022;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related oligonucleotide #1162.

XX Human; haematopoietic cell proliferation disorder; cytostatic;

KM Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

XX cytosine methylation state; probe; primer; ss.

OS Homo sapiens.

XX Synthetic.

PN W0200277272-A2.

XX 03-OCT-2002.

PF 26-MAR-2002; 2002MO-EP003401.

PR 26-MAR-2001; 2001US-0278333P.

PA (EPIC-) EPIDENOMICS AG.

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwöpe I, Ziebarth H;

XX MPI; 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.

PS Claim 15; Page 76; 117pp; English.

XX The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a

CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 SQ Sequence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 39 GTGTAGTGGCGTTGGTT 56  
 Db 18 GTGTAGTGGTTGGTT 1

RESULT 160  
 ABZ11031  
 ID ABZ11031 standard; DNA; 18 BP.

XX  
 AC ABZ11031;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related oligonucleotide #1171.

XX Human; haematopoietic cell proliferation disorder; cytostatic;

KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

XX cytosine methylation state; probe; primer; ss.

OS Homo sapiens.

XX Synthetic.

PN W0200277272-A2.

XX 03-OCT-2002.

PF 26-MAR-2002; 2002MO-EP003401.

PR 26-MAR-2001; 2001US-0278333P.

PA (EPIC-) EPIDENOMICS AG.

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwöpe I, Ziebarth H;

XX MPI; 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.

PS Claim 15; Page 77; 117pp; English.

XX The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of

CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 SQ Sequence 18 BP; 8 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 GGAACACGACGACACG 105  
 DB 1 GAGAAATAGCGAAGATAGC 18

## RESULT 161

ACC45940/c  
 ID ACC45940 standard; DNA; 18 BP.

AC ACC45940;

DT 02-JUN-2003 (first entry)

DE Human HEM STS marker forward primer #260.

XX Human; high bone mass; HBM; LRPS; LRPE; transgenic; bone mass modulation;  
 KW gene therapy; bone density modulation; bone strength; trabecular number;  
 KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;  
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

OS Homo sapiens.

PN WO200292764-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014876.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMRP) MYETH.

PI Babilj P, Bex FJ, Yaworsky PJ, Bodine PV;

PI WPI; 2003-129278/12.

PT New transgenic animals (e.g. mice), useful as models for studying bone  
 PT density modulation, developing drugs for treating or preventing bone  
 PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by  
 PT reduced bone density.

PS Disclosure; Page 58; 603pp; English.

CC The invention relates to novel transgenic animals expressing the high  
 CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,  
 CC comprising an alteration of the gene encoding LRPS or LRPE, or expressing  
 CC an LRPS that is modulated by an altered gene control sequence introduced  
 CC by homologous or non-homologous recombination. The transgenic animals are  
 CC for the study of bone density modulation or bone mass modulation. The  
 CC invention has osteopathic and cytostatic activity. The polynucleotides of  
 CC the invention may have a use in gene therapy. The transgenic animals and  
 CC nucleic acids are for the study of bone density modulation, where the  
 CC bone mass is modulated relative to non-transgenic animals of the same  
 CC species in more than one parameter selected from bone density, bone  
 CC strength, trabecular number, bone size, or bone tissue connectivity. The  
 CC transgenic animals, nucleic acids and methods are useful for identifying  
 CC molecules involved in bone development, and for developing pharmaceutical  
 CC compositions, which may be employed for treating or preventing bone  
 CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or

CC neoplasms of the bone. The transgenic animals and nucleic acids are also  
 CC useful in methods for diagnosing diseases involved in bone development,  
 CC or characterised by reduced bone density or mass. The present sequence is  
 CC used in the exemplification of the invention  
 XX

SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 87;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2400 GCTGCCAATAGCAAG 2417  
 DB 18 GCTGCCAATAGCAAG 1

## RESULT 162

ADB68489/c  
 ID ADB68489 standard; DNA; 18 BP.

AC ADB68489;

DT 04-DEC-2003 (first entry)

DE Antisense HYPNA-pRNA oligomer targeted to zebrafish chordin 4-mis DNA.

XX hydroxyproline nucleic acid; HYPNA; PNA; peptide nucleic acid;  
 KW gene expression; respiration; secretion; signaling;  
 KW ion-channel activity; cell motility; developmental phenotype;  
 KW tumour regression; ss; phosphono-peptide nucleic acid; PPNNA;  
 KW chordin 4-mis; zebrafish; antisense.

OS Synthetic.

OS Danio rerio.

PN WO2003068798-A2.

PD 21-AUG-2003.

PF 07-FEB-2003; 2003WO-US003904.

PF 09-FEB-2002; 2002US-00072975.

PA (ACTI-) ACTIVE MOTIF.

PI Eftimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;

PI WPI; 2003-689653/65.

PT Method of inhibiting expression of genes or RNA transcripts, useful for  
 PT therapy and determining effects of genes, by administering oligomers  
 PT containing hydroxyproline nucleic acid.

PS Example 37; Page 188; 240pp; English.

CC The invention relates to a novel method of inhibiting the expression of  
 CC one or more genes or RNA transcripts by administering at least one  
 CC oligonucleotide analogue that includes at least one hydroxyproline  
 CC nucleic acid (HYPNA) monomer to a cell or organism or their extracts. The  
 CC oligonucleotides of the invention may be used to monitor properties  
 CC including gene expression, respiration, secretion, signaling, ion-  
 CC channel activity, cell motility, developmental phenotype and tumour  
 CC regression. Furthermore, they may be utilised to determine the effects of  
 CC particular genes, as antisense or homologous recombination constructs  
 CC e.g. for creating animal models of disease and finally, for increasing  
 CC the activity of some enzymes, such as polymerases. The current sequence  
 CC is that of the antisense HYPNA-pRNA oligomer of the invention which was

CC targeted to the zebrafish chordin 4-mis DNA.

SQ Sequence 18 BP; 0 A; 9 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 87;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 421 GGAGAGGAGGAGGAGGAGC 438

DB 18 GGAGAGAGGAGGAGGAGC 1

RESULT 163

ID ADB98638/C

AC ADB98638; DNA; 18 BP.

DT 04-DEC-2003 (first entry)

DE Sequence tagged site #519 used to prepare Zmax1 (LRP5) gene region map.

KM Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;

KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.

OS Homo sapiens.

PN MO200292000-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014877.

PR 11-MAY-2001; 2001US-0290077P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0351293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;

DR WPI, 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for

PT diagnosing a HBM-like phenotype in a subject and for preparing a

PT composition for modulating bone mass and/or lipid levels in a subject

PT suffering from e.g. osteoporosis.

PS Example 2; Page 64; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and

CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a

CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid

CC level modulation. The invention is useful for diagnosing a HBM-like

CC phenotype in a subject and for preparing a composition for modulating

CC bone mass and/or lipid levels in a subject suffering from e.g.

CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)

CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene

CC region.

SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 87;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2400 GGTGGCAATATGCAAG 2417

DB 18 GGTGTCATAATGCAAG 1

RESULT 164

ID ADE84342

AC ADE84342;

DT 29-JAN-2004 (first entry)

DE Human lymphoid cell proliferative disorder gene Cpg analysis oligo #48.

KM lymphoid cell proliferative disorder; methylation;

KM methylated Cpg dinucleotide; single nucleotide polymorphism; SNP;

KM diffuse large B-cell lymphoma; mantle cell lymphoma;

KM chronic lymphocytic leukemia; small lymphocytic lymphoma;

XX follicular lymphoma; diagnosis; prognosis; primer; ss.

OS Homo sapiens.

PN WO2003044226-A2.

PD 30-MAY-2003.

PF 25-NOV-2002; 2002WO-EP013265.

PR 23-NOV-2001; 2001DE-01057491.

PR 28-DEC-2001; 2001DE-01064501.

PA (EPIC-) EPIDEMIOLOGICS AG.

PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;

DR WPI; 2003-457521/43.

XX Detecting and differentiating between lymphoid cell proliferative

PT disorders comprises contacting a target nucleic acid with at least one

PT reagent that distinguishes between methylated and non-methylated Cpg

PT dinucleotides.

PS Claim 30; SEQ ID NO 338; 448pp; English.

XX The invention relates to a method of detecting and differentiating

CC between lymphoid cell proliferative disorders associated with at least

CC one gene and/or their regulatory regions in a subject by contacting a

CC target nucleic acid in a biological sample obtained from the subject with

CC at least one reagent or series of reagents that distinguish between

CC methylated and non-methylated Cpg dinucleotides within the target nucleic

CC acid. The genes and/or their regulatory regions are preferably selected

CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, Gpib beta, MYO1, CDH3,

CC MYC11, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,

CC GSTP1, HIC-1, MGMT, MDM1, MDS, MYC, PTEN, RBL2, TGFBR2, TP53, CDKN1C,

CC GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic

CC acid (PNA)-oligomers and/or isolated nucleic acids based on all the

CC Cpg dinucleotides within one or more the sequences, or their complements,

CC for determining the cytosine methylation state and/or single nucleotide

CC polymorphisms (SNPs), and for differentiating at least two of the medical

CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,

CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular

CC lymphoma. They are also useful for detecting of a predisposition to,

CC differentiation between subclasses, diagnosis, prognosis, treating and/or

CC monitoring of lymphoid cell proliferative disorder. This sequence

CC represents an oligonucleotide used to analyse of Cpg positions within the

CC above mentioned genes.

SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 87;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 39 GTGTAGTCTGCGCTTGATT 56

DB 18 GTGTAGTCTGCGCTTGATT 1

Db 1 GTGTAGTGTGTTGTT 18

## RESULT 165

ADBE84345 ADEB84345 standard; DNA; 18 BP.

AC ADEB84345;

DT 29-JAN-2004 (first entry)

DE Human lymphoid cell proliferative disorder gene Cpg analysis oligo #51.

XX lymphoid cell proliferative disorder; methylation;  
XX methylated Cpg dinucleotide; single nucleotide polymorphism; SNP;  
XX diffused large B-cell lymphoma; mantle cell lymphoma;  
XX chronic lymphocytic leukemia; small lymphocytic lymphoma;  
XX follicular lymphoma; diagnosis; prognosis; primer; ss.

OS Homo sapiens.

PN W02003044226-A2.

PD 30-MAY-2003.

PF 25-NOV-2002; 2002W0-EP013265.

PR 23-NOV-2001; 2001DE-01057491.

PR 28-DEC-2001; 2001DE-01064501.

PA (EPIC-) EPICENOMICS AG.

PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;

DR WPI; 2003-457621/43.

PT Detecting and differentiating between lymphoid cell proliferative  
PT disorders comprises contacting a target nucleic acid with at least one  
PT reagent that distinguishes between methylated and non-methylated Cpg  
PT dinucleotides.

PS Claim 30; SEQ ID NO 341; 448bp; English.

XX The invention relates to a method of detecting and differentiating  
XX between lymphoid cell proliferative disorders associated with at least  
XX one gene and/or their regulatory regions in a subject by contacting a  
XX target nucleic acid in a biological sample obtained from the subject with  
XX at least one reagent or series of reagents that distinguish between  
XX methylated and non-methylated Cpg dinucleotides within the target nucleic  
XX acid. The genes and/or their regulatory regions are preferably selected  
XX from MD1, CSN2B, BCR4, AR, CDK4, RB2, CDC25A, Gpib beta, MYO1, CDH3,  
XX MYO1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,  
XX GSTP1, HIC-1, MGMT, MLI1, MOS, MYC, PTEN, RB1, TGFBR2, TP73, CDKN1C,  
XX GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic  
XX acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences  
XX of the genes are useful for detecting the methylation state of all the  
XX Cpg dinucleotides within one or more the sequences, or their complements,  
XX for determining the cytosine methylation state and/or single nucleotide  
XX polymorphisms (SNPs), and for differentiating at least two of the medical  
XX conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
XX chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular  
XX lymphoma. They are also useful for detecting of a predisposition to,  
XX differentiation between subclasses, diagnosis, prognosis, treating and/or  
XX monitoring of lymphoid cell proliferative disorder. This sequence  
XX represents an oligonucleotide used to analyse of Cpg positions within the  
XX above mentioned genes.

XX Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 88 GGAGAACAGCGAAGACAG 105  
Db 1 GGAGAAATAGCGAAGATAG 18

## RESULT 166

AA13267 AA13267 standard; cDNA; 19 BP.

AC AA13267;

DT 25-JUL-2000 (first entry)

DE PCR primer #2 used in GnRH-I and GnRH-II expression determination.

XX Gonadotropin-releasing hormone; GnRH; differentiation modulator;  
XX osteoporosis; bone metabolism; bone repair; osteogenesis imperfecta;  
XX osteomalacia; bone loss; fracture healing; PCR primer; ss.

OS Synthetic.

PN GB2343182-A.

PD 03-MAY-2000.

PF 27-OCT-1998; 98GB-00023515.

PR 27-OCT-1998; 98GB-00023515.

PA (FERR) FERRING BV.

PI Akinsanya K, Hayward A, Qi S;

DR WPI; 2000-331495/29.

PT Composition containing gonadotropin-releasing hormone II peptide, useful  
PT e.g. for treating osteoporosis and for accelerating bone repair.  
PT Example 4; Page 12; 16pp; English.

XX This sequence represents a PCR primer used in the expression  
XX determination of gonadotropin-releasing hormone (GnRH) I and II. GnRH is  
XX released by the hypothalamus and acts on the pituitary to stimulate the  
XX release of luteinizing hormone and follicle stimulating hormone. GnRH is  
XX capable of modulating the differentiation of bone precursor cells, and  
XX inducing the expansion of osteoblast populations. The invention relates  
XX to GnRH-II peptide analogues that can be used in compositions for  
XX treating osteoporosis (and other diseases of bone metabolism) and for the  
XX acceleration of bone repair. The compositions have osteogenic activity.  
XX The compositions are used to treat or prevent osteoporosis, other  
XX disorders of bone metabolism (e.g. osteogenesis imperfecta, osteomalacia  
XX or bone loss resulting from prolonged periods of immobility), and to  
XX accelerate bone growth and repair (e.g. for healing fractures)

XX Sequence 19 BP; 0 A; 5 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 GCGGCGCGCGCGCGCTCG 407  
Db 2 GCGGCGCGCGCGCTCG 19

## RESULT 167

AA243816 AA243816 standard; DNA; 19 BP.

AC AA243816;

DT 10-MAR-2000 (first entry)

```

DE Human fetal brain cDNA clone vb9_1 DNA probe.
XX
XX Human; secreted protein; treatment; nutritional activity; cytokine;
KM cell proliferation; cell differentiation; hematopoiesis regulation;
KM tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic;
KM thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
KM gene therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN MO955721-A1.
PD 04-NOV-1999.
XX
XX 23-APR-1999; 99WO-US008504.
PF
XX 24-APR-1998; 98US-0082904P.
PR 11-JUN-1998; 98US-0088994P.
PR 12-JUN-1998; 98US-0089278P.
PR 02-JUL-1998; 98US-0091647P.
PR 24-AUG-1998; 98US-0097639P.
PR 22-APR-1999; 99US-00097639.
XX
XX (ALPH-) ALPHAGEN INC.
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
DR WPI; 2000-052801/04.
XX
XX New polynucleotides encoding secreted human proteins, derived from human
PT fetal brain, adult skin, adult brain, adult heart, adult thymus and adult
PT aorta cDNA libraries.
XX
XX Disclosure; Page 266; 282pp; English.
PS
XX This invention describes novel human secreted proteins which are encoded
CC by polynucleotides obtained from fetal brain, adult skin, adult brain,
CC adult heart, adult thymus and adult aorta cDNA libraries. The
CC polynucleotides and proteins are predicted to have biological activities
CC which would make them suitable for treating, preventing or ameliorating
CC medical conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, hematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumor
CC invasion suppressor activity, and tumor inhibition activity. The
CC polynucleotides are also stated to be useful for gene therapy. AA243809-
CC 243840 represent DNA probes used to isolate the polynucleotides
CC represented in AA243777-243808 which encode the secreted proteins
CC represented in AA250905-Y50947
XX
SQ Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1090 TCTGATGAGCATGATGCG 1107
DB 2 TCTGATGAGCATGATGCG 19

```

```

DE Cdc 25 hs ribozyme binding site #243.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
OS Mammalia.
XX
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
DR WPI; 2000-412314/35.
XX
XX Disclosure; Page 103; 109pp; English.
PS
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 6 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1685 ACTTCTTACTGAAGAGC 1702
DB 2 ACTTCTTCTGAAGAGC 19

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RESULT 169
AA82502/C
ID AA82502 standard; DNA; 19 BP.
XX
XX AAA82502;
AC
XX 04-DEC-2000 (first entry)
DT
XX
XX cdk1 ribozyme binding site #88.
DE
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
OS Mammalia.
XX
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
DR WPI; 2000-412314/35.

```

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.  
XX  
PS Disclosure; Page 47, 109pp; English.  
XX  
CC The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AA82415 to AA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment  
CC  
XX Sequence 19 BP; 0 A; 7 C; 3 G; 9 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 1988 AGAAGAGCAAGAGGAGA 2005  
DB 18 AGCAGAGCAACAGGAGAGA 1  
RESULT 170  
AAH57664/C  
ID AAH57664 standard; DNA; 19 BP.  
XX  
AC AAH57664;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cell-cycle dependent kinase cdk1 ribozyme binding site SEQ ID NO:88.  
XX  
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
XX recognition site; target; ribozyme binding site; eye disease; vulnery;  
XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
XX antiproliferative; dermatological; keratolytic; gene therapy; viral wart;  
XX antisticking; ophthalmological; keratolytic; gene therapy; viral wart;  
XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
XX basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
XX sickle cell retinopathy; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200130362-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WC-US029500.  
XX  
PR 26-OCT-1999; 99US-0161532P.  
XX  
PA (IMMU-) IMMUSOL INC.  
XX  
PI Robbins JM, Tiltz R;  
XX  
DR WPI; 2001-300427/31.  
XX  
PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
PS Example 1; Page 78; 408pp; English.  
XX  
CC The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (i) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (ii) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (i). (i) can have antiproliferative,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,  
CC ophthalmological, vulnery, keratolytic and vitruide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (i) can be used  
CC in gene therapy. (i) and (ii) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seboreic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
CC  
XX Sequence 19 BP; 0 A; 7 C; 3 G; 9 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 1988 AGAAGAGCAAGAGGAGA 2005  
DB 18 AGCAGAGCAACAGGAGAGA 1  
RESULT 171  
AAH61297  
ID AAH61297 standard; DNA; 19 BP.  
XX  
AC AAH61297;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cdc25 hs ribozyme binding site SEQ ID NO:3721.  
XX  
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
XX recognition site; target; ribozyme binding site; eye disease; vulnery;  
XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
XX antiproliferative; dermatological; antiseborrheic; antidiabetic; vitruide;  
XX antisticking; ophthalmological; keratolytic; gene therapy; viral wart;  
XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
XX basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
XX sickle cell retinopathy; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200130362-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WC-US029500.  
XX  
PR 26-OCT-1999; 99US-0161532P.  
XX  
PA (IMMU-) IMMUSOL INC.  
XX  
PI Robbins JM, Tiltz R;  
XX  
DR WPI; 2001-300427/31.  
XX  
PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
PS Example 1; Page 342; 408pp; English.  
XX

CC The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antiapoptotic, anti-  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,  
CC ophthalmological, vulvetary, keratolytic and virucide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH52099 represent sequences used in the  
CC exemplification of the present invention

SQ Sequence 19 BP; 6 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1685 ACTTCTTATGAGAGC 1702  
Db 2 ACTTCTTCTGAGAGC 19

RESULT 172  
ADE30092/C  
ID ADE30092 standard; RNA; 19 BP.

AC ADE30092;

DT 29-JAN-2004 (first entry)

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:714.

XX short interfering nucleic acid; siNA; downregulation; inhibition;  
XX mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
XX cytoskeletal; anorectic; antidiabetic; antiinflammatory; antisthmatic;  
XX immunosuppressive; antibacterial; antineuritic; antitumour;  
XX antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
XX inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
XX psoriasis; inflammatory bowel disease; drug screening;  
XX genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic.

PN WO2003072590-A1.

PD 04-SEP-2003.

PF 28-JAN-2003; 2003WO-US002510.

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-036782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409239P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PA Mcswiggen J, Beigelman L, Usman N, Haeblerl P, Chowrira B;

PI WPI; 2003-683980/65.

DR New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer, downregulates expression of mitogen-activated  
PT protein kinase genes.

XX Example 3; SEQ ID NO 714; 164bp; English.

CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of a mitogen-activated protein kinase  
CC (MAPK) genes by RNA interference. Also described: (1) a method for  
CC modulating expression of MAPK genes in cells, tissue explants or  
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
CC vectors that express siNA and cells containing these vectors. MAPK siNA  
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
CC antisthmatic, immunosuppressive, antibacterial, antineuritic,  
CC antitumour, antipsoriatic and gastrointestinal activities. The MAPK  
CC siNA can be used to modulate the expression of MAPK genes, in cells,  
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
CC disease). They can also be used for drug screening; diagnosis; target  
CC identification and validation; genetic engineering; pharmacogenomic;  
CC studying gene function and gene mapping (e.g. of single-nucleotide  
CC polymorphisms). The present sequence represents a MAPK siNA which is used  
CC in the exemplification of the present invention.

SQ Sequence 19 BP; 4 A; 5 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.6%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 301 TTGGCCGCGGCGCGC 318  
Db 19 TTTCGAGCGGCGCGC 2

RESULT 173  
ADE30301  
ID ADE30301 standard; RNA; 19 BP.

AC ADE30301;

DT 29-JAN-2004 (first entry)

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:923.

XX short interfering nucleic acid; siNA; downregulation; inhibition;  
XX mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
XX cytoskeletal; anorectic; antidiabetic; antiinflammatory; antisthmatic;  
XX immunosuppressive; antibacterial; antineuritic; antitumour;  
XX antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
XX inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
XX psoriasis; inflammatory bowel disease; drug screening;  
XX genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic.

PN WO2003072590-A1.

PD 04-SEP-2003.

PF 28-JAN-2003; 2003WO-US002510.

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-036782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409239P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PI Mcswiggen J, Beigelman L, Usman N, Haeblerli P, Chowitra B;  
 XX MPI; 2003-689980/65.  
 XX  
 XX New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer, downregulates expression of mitogen-activated  
 PT protein kinase genes.  
 XX  
 XX Example 3; SEQ ID NO 923; 164bp; English.  
 XX  
 CC The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of a mitogen-activated protein kinase  
 CC (MAPK) genes by RNA interference. Also described: (1) a method for  
 CC modulating expression of MAPK genes in cells, tissue explants or  
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
 CC antiasthmatic, immunosuppressive, antibacterial, antihemmatic,  
 CC antiarthritic, antiproliferative and gastrointestinal activities. The MAPK  
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
 CC tissue explants or organisms, e.g. for treating obesity, diabetes types I  
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
 CC disease). They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents a MAPK siNA which is used  
 CC in the exemplification of the present invention.  
 CC  
 SQ Sequence 19 BP; 2 A; 8 C; 5 G; 0 T; 4 U; 0 Other;  
 QY  
 Query Match 0.6%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 90;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Db 301 TTTCGCCGCGCAGCCGC 318  
 1 UUUUCGAGCGCGCAGCCGC 18  
 RESULT 174  
 ABQ72279  
 ID ABQ72279 standard; DNA; 15 BP.  
 XX  
 AC ABQ72279;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human CYP2D6 allele-specific oligonucleotide (ASO) primer, SEQ ID NO:66.  
 XX  
 KW Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;  
 KW chromosome 22q13.1; drug metabolism; detoxification; mono-oxigenase;  
 KW anticholinergic; arrhythmia; adrenoceptor antagonist; hypertension;  
 KW tricyclic antidepressant; procainamide; drug induced lupus syndrome;  
 KW environmentally linked disease; Parkinson's disease; haplotyping;  
 KW genotyping; haplotype; genetic variant; single nucleotide polymorphism;  
 KW SNP; drug screening; drug discovery; allele-specific oligonucleotide;  
 KW ASO; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200238589-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 PF 09-NOV-2001; 2001WO-US047396.  
 XX  
 PR 09-NOV-2000; 2000US-0247943P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Anastasio AE, Chew A, Choi JY, Denton RR, Nandabalan K;

PI Petersen N, Rounds E;  
 XX  
 DR MPI; 2002-519292/55.  
 XX  
 XX Novel genetic variants of Cytochrome P450, Subfamily IID, Polypeptide 6  
 PT isoenzymes, useful for improving efficiency and reliability in drug  
 PT development for treating hypertension, arrhythmias and Parkinson's  
 PT disease.  
 XX  
 XX Claim 15; Page 18; 156pp; English.  
 XX  
 CC The invention relates to a method for haplotyping the cytochrome P450,  
 CC subfamily IID, polypeptide 6 (CYP2D6) gene (ABQ72315, ABQ72364) of an  
 CC individual, and also describes 29 novel polymorphic sites within the  
 CC human CYP2D6 gene. The CYP2D6 gene is located on chromosome 22q13.1 and  
 CC contains 9 exons which encode a 497 amino acid protein (ABR09563). CYP2D6  
 CC is a mono-oxigenase involved in the detoxification of many drugs and  
 CC environmental chemicals. It plays a role in the metabolism of drugs such  
 CC as antiarrhythmics, adrenoceptor antagonists and tricyclic  
 CC antidepressants, and is also involved in the formation of a metabolite  
 CC linked to the drug-induced lupus syndrome observed with procainamide.  
 CC Variations in CYP2D6 activity or expression may also influence an  
 CC individual's susceptibility to environmentally-linked diseases, and it  
 CC has been demonstrated that CYP2D6 activity may be involved in the  
 CC pathogenesis of Parkinson's disease, with individuals with a less active  
 CC form of the enzyme tending to have an earlier onset of this condition.  
 CC CYP2D6 nucleic acid sequences are useful in studying the expression and  
 CC function of CYP2D6, and in expressing CYP2D6 protein for use in screening  
 CC drugs for the treatment of CYP2D6-associated diseases (e.g.,  
 CC hypertension, atrial and ventricular arrhythmias, Parkinson's disease,  
 CC and drug-induced lupus syndrome) or which are metabolised by CYP2D6.  
 CC CYP2D6 nucleic acids and proteins are also useful in studying the effect  
 CC of polymorphisms on the biological activity of CYP2D6. Polymorphisms in  
 CC the target region may be determined by the use of allele-specific  
 CC oligonucleotides (ASOs; ABQ72217-ABQ72303) as probes and primers, and by  
 CC primer extension using oligonucleotide primers comprising sequences  
 CC ABQ72304-ABQ72361. The method of the invention is useful for haplotyping  
 CC the CYP2D6 gene in populations and in individuals, enabling decisions to  
 CC be made as to whether CYP2D6 is a likely therapeutic target for a disease  
 CC of interest, and to control for genetically-based bias in the design of  
 CC drugs that target or are metabolised by CYP2D6. In addition, transgenic  
 CC animals comprising a human CYP2D6 gene are useful for studying the  
 CC expression of CYP2D6 isoenzymes in vivo, for in vivo screening and testing  
 CC of drugs targeted to or metabolised by CYP2D6, and for testing the  
 CC efficacy of therapeutic agents and compounds for treating CYP2D6-  
 CC associated conditions in a biological system. Sequences ABQ72246-  
 CC ABQ72303 represent specifically claimed allele-specific oligonucleotide  
 CC (ASO) primers used for detecting polymorphisms in the CYP2D6 gene  
 XX  
 SQ Sequence 15 BP; 1 A; 7 C; 3 G; 3 T; 0 U; 1 Other;  
 QY  
 Query Match 0.6%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 81;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 987 CTCGCCCACTCGG 1001  
 1 CTCGCCCACTCGG 15  
 RESULT 175  
 ABL45856  
 ID ABL45856 standard; DNA; 15 BP.  
 XX  
 AC ABL45856;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 DE Human EDG6 gene allele specific primer SEQ ID NO: 50.  
 XX  
 KW Human; endothelial differentiation; G-protein coupled receptor 6; EDG6;  
 KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;  
 KW cytostatic; antiinflammatory; gene therapy; SNP;

KW single nucleotide polymorphism; primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200206446-A2.  
 PN  
 XX 24-JAN-2002.  
 PD  
 XX  
 XX 17-JUL-2001; 2001WO-US022523.  
 PF  
 XX 17-JUL-2000; 2000US-0218727P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 PI Klem SE, Koshy B;  
 XX  
 XX WPI; 2002-171804/22.  
 DR  
 XX  
 XX New genetic variants of endothelial differentiation; G-protein coupled  
 PT receptor-6 gene for studying expression, function of the gene and  
 PT expressing EDG6 protein for use in screening drugs to treat cancer,  
 PT inflammation.  
 XX  
 XX Claim 16; Page 14; 11pp; English.  
 PS  
 XX  
 CC The present invention provides the gene, protein and cDNA sequences of  
 CC the human endothelial differentiation; G-protein coupled receptor 6  
 CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found  
 CC within the sequences. The sequences can be used in the identification of  
 CC the haplotype of an individual, and in the treatment of cancer,  
 CC angiogenesis and inflammation. The present sequence is an allele specific  
 CC primer for the EDG6 gene, which is found on chromosome 19p13.3  
 CC  
 XX  
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 0 T; 0 U; 1 Other;  
 Query Match 0.6%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 81;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2047 CCAGCAGCAGCCCA 2061  
 Db 1 CCAGCAGCAGCCCA 15  
 RESULT 176  
 AA04098  
 ID AA04098 standard; DNA; 16 BP.  
 XX  
 AC AA04098;  
 XX  
 DT 12-APR-1999 (first entry)  
 XX  
 DE PUR element conservation oligonucleotide #6.  
 XX  
 KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;  
 KW monoclonal antibody; identification; characterisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5869622-A.  
 PN  
 XX 09-FEB-1999.  
 PD  
 XX  
 XX 07-JUN-1995; 95US-00466809.  
 PF  
 XX 28-AUG-1992; 92US-00938189.  
 PR 02-FEB-1993; 93US-00014943.  
 PR 06-JUN-1995; 95US-00470911.  
 XX  
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.  
 XX  
 PI Bergemann AD, Johnson EM;  
 XX

DR WPI; 1999-152881/13.  
 XX  
 XX Monoclonal antibody specific for PUR protein - useful for treating  
 PT cancer.  
 PT  
 XX  
 XX Disclosure; Col 13; 64pp; English.  
 PS  
 XX  
 CC The present invention describes a monoclonal antibody that specifically  
 CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR  
 CC protein and neutralise PUR activity may be used to treat  
 CC hyperproliferative diseases such as cancer. PUR antibodies may be used  
 CC diagnostically to detect aberrant expression of the PUR protein and/or  
 CC mutations in the PUR gene. The present sequence represents an  
 CC oligonucleotide from the present invention  
 CC  
 XX  
 SQ Sequence 16 BP; 5 A; 1 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 415 GGCAGAGGAGAGGGA 430  
 Db 1 GGCAGAGGAGAGGGA 16  
 RESULT 177  
 AA297911/c  
 ID AA297911 standard; DNA; 16 BP.  
 XX  
 AC AA297911;  
 XX  
 DT 15-SEP-2003 (revised)  
 DT 26-APR-2000 (first entry)  
 XX  
 DE HIV-1 protease gene probe SEQ ID NO:401.  
 XX  
 KW Human immunodeficiency virus; HIV; protease; probe; detection;  
 KW drug selected mutation; hybridisation; genotyping; infection;  
 KW drug resistance; ss.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX WO9967428-A2.  
 PN  
 XX 29-DEC-1999.  
 PD  
 XX 22-JUN-1999; 99WO-EP04317.  
 PF  
 XX 24-JUN-1998; 98EP-00870143.  
 PR  
 XX (INNO-) INNOGENETICS NV.  
 PA  
 PI Stuyver L;  
 XX  
 DR WPI; 2000-147219/13.  
 XX  
 XX Detection of drug-selected mutations in the HIV protease gene used to  
 PT treat HIV infections.  
 PT  
 XX  
 XX Claim 3; Page 42; 76pp; English.  
 PS  
 XX  
 CC The present invention describes the detection of drug-selected mutations  
 CC in the HIV protease gene. The method of detection allows the simultaneous  
 CC characterisation of a range of codons involved in drug resistance using  
 CC sets of probes optimised to function together in a reverse-hybridisation  
 CC assay. AA297517 to AA297997 represent specifically claimed probes for use  
 CC in the assay, and AA297479 to AA297501 represent specifically claimed HIV  
 CC protease gene polymorphic nucleotide sequences. AA297502 to AA297515, and  
 CC AA298004 to AA298007, represent PCR primers for the HIV protease gene,  
 CC and AA297516 represents an HIV protease probe used in an example from the  
 CC present invention. The method, probes and primers can be used for the  
 CC detection of drug-selected mutations in the HIV protease gene. The method

CC allows the simultaneous characterisation of a range of codons involved in  
 CC drug resistance. The method may also be used for HIV protease genotyping  
 CC assays. The probes are able to discriminate between wild type and mutated  
 CC protease sequences. The method allows rapid and reliable detection of  
 CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS  
 CC field)

CC Sequence 16 BP; 4 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 684 CTCGAGTCACAGAT 699

DB 16 CTCGAGTCACAGAT 1

RESULT 178

AA092117  
 ID AA092117 standard; DNA; 17 BP.

AC AA092117;

DT 11-JAN-1996 (first entry)

DE P53 detection probe, (codon 151 CCC to CAC).

XX primer; polymerase chain reaction; amplify; mutant; K-ras; PCR;  
 KW flanking region; amplification; probe; detection; sputum; diagnosis;  
 KW benign; malignant; neoplasm; lung; lung cancer; head; neck; ss.

OS Synthetic.

PN WO9513397-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; 94WO-US012947.

PR 12-NOV-1993; 93US-00152313.

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.

PI Sidransky D;

DR WPI; 1995-194114/25.

PT Detecting target nucleic acid in mammalian sputum - particularly for  
 PT diagnosis of lung neoplasia involving mutation(s) in the K-ras oncogene  
 PT or p53 tumour suppressor.

PS Example 1; Page 29; 122pp; English.

CC The sequences given in AA092112-21 are probes which were used in the  
 CC detection of a mutant p53 gene sequence. The DNA to be detected is  
 CC amplified using PCR and then these probes which are pref. labeled using  
 CC 32-P gamma-ATP are used to detect the mutant sequences. The primers and  
 CC probes given in AA092098-219 are used in the method of the invention for  
 CC detecting mammalian target DNA in sputum samples. Analysis of the target  
 CC DNA is used to diagnose benign or malignant neoplasms of the lung. It is  
 CC also useful for screening people at high risk or for monitoring progress  
 CC of treatment of lung neoplasms. The method is based on the discovery that  
 CC mutant target DNA associated with lung cancer is present at detectable  
 CC levels in sputum. Cells shed into sputum from head and neck cancers may  
 CC also be detected

CC Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.6%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 275 TCCGACACCCGCCG 290

DB 2 TCCGACACCCGCCG 17

RESULT 179

AA071513/C  
 ID AA071513 standard; RNA; 17 BP.

AC AA071513;

DT 28-JUL-1999 (first entry)

DE Human KDR VEGF receptor hammerhead ribozyme substrate #525.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

OS Homo sapiens.

PN WO9715662-A2.

PD 01-MAY-1997.

PF 25-OCT-1996; 96NO-US017480.

PR 26-OCT-1995; 95US-0005974P.

PR 11-JAN-1996; 96US-00584040.

PA (RIBO-) RIBOZYME PHARM INC.

PA (CHIR ) CHIRON CORP.

PI Pavco P, Meswigen J, Stinchcomb D, Escobedo J;

DR WPI; 1997-259017/23.

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

PS Claim 4; Page 113; 218pp; English.

CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis), ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AA067275 to AA075752 represent specific examples  
 CC of nucleic acid molecules from the present invention

CC Sequence 17 BP; 8 A; 0 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 TCTTCATCAGCTCTTA 1404

DB 17 TCTTCATCAGCTCTTA 2

RESULT 180

AAA25224  
 ID AAA25224 standard; DNA; 17 BP.

AC AAA25224;

DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1722.  
 XX  
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorochioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelsky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 72; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA. In the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
 XX  
 OY Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 2268 ATGCAGTCTGAGCAC 2283  
 1 ATACAGTTCTGAGCAC 16  
 XX  
 RESULT 181  
 ID AAA25223  
 XX AAA25223 standard; DNA; 17 BP.  
 AC  
 XX AAA25223;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1721.  
 XX  
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorochioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelsky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 72; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA. In the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 OY Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 2268 ATGCAGTCTGAGCAC 2283  
 2 ATACAGTTCTGAGCAC 17  
 XX  
 RESULT 182  
 ID AB064171  
 XX AB064171 standard; DNA; 17 BP.  
 AC  
 XX AB064171;  
 XX  
 DT 20-AUG-2002 (first entry)  
 XX  
 DE Human KTM01a portion (AB063232) probe # 884.  
 XX

KW Human; K10M1a; K10M1; kidney tumour overexpressed membrane; cytoskeletal;  
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200224750-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-US029656.  
 XX  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 28-AUG-2001; 2001US-0315676P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhang J;  
 XX  
 DR WPI; 2002-479509/51.  
 XX  
 PT New human kidney tumor overexpressed membrane (K10M1) protein and nucleic  
 PT acids encoding the protein, useful for treating subjects having defects  
 PT in K10M1 which can manifest as cancer of the kidney, or as a disorder of  
 PT e.g., liver or bone.  
 XX  
 PS Example 2; Page 273; 418bp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid encoding human  
 CC K10M1 (kidney tumour overexpressed membrane) protein. The protein of the  
 CC invention has cytoskeletal activity. The nucleotide may have a use in gene  
 CC therapy. The K10M1 nucleic acids may be used to diagnose, treat or  
 CC monitor a disease caused by altered expression of human K10M1.  
 CC Compositions comprising the nucleic acids, proteins or antibodies may be  
 CC used to treat subjects having defects in K10M1 which can manifest as  
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
 CC function. The sequence represents a probe used in the invention to scan  
 CC the nt 1-1001 portion of human K10M1a (AB063232)  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 7 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 DB 247 CTGTGGCTGTGGCTG 262  
 2 CTGTGGCTGTGGCTG 17  
 XX  
 RESULT 183  
 ID AB064172 standard; DNA; 17 BP.  
 XX  
 AC AB064172;  
 XX  
 DT 20-AUG-2002 (first entry)  
 XX  
 DE Human K10M1a portion (AB063232) probe # 885.

XX  
 KW Human; K10M1a; K10M1; kidney tumour overexpressed membrane; cytoskeletal;  
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200224750-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-US029656.  
 XX  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 28-AUG-2001; 2001US-0315676P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhang J;  
 XX  
 DR WPI; 2002-479509/51.  
 XX  
 PT New human kidney tumor overexpressed membrane (K10M1) protein and nucleic  
 PT acids encoding the protein, useful for treating subjects having defects  
 PT in K10M1 which can manifest as cancer of the kidney, or as a disorder of  
 PT e.g., liver or bone.  
 XX  
 PS Example 2; Page 273; 418bp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid encoding human  
 CC K10M1 (kidney tumour overexpressed membrane) protein. The protein of the  
 CC invention has cytoskeletal activity. The nucleotide may have a use in gene  
 CC therapy. The K10M1 nucleic acids may be used to diagnose, treat or  
 CC monitor a disease caused by altered expression of human K10M1.  
 CC Compositions comprising the nucleic acids, proteins or antibodies may be  
 CC used to treat subjects having defects in K10M1 which can manifest as  
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
 CC function. The sequence represents a probe used in the invention to scan  
 CC the nt 1-1001 portion of human K10M1a (AB063232)  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 7 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 DB 247 CTGTGGCTGTGGCTG 262  
 1 CTGTGGCTGTGGCTG 16  
 XX  
 RESULT 184  
 ID ABV78892 standard; DNA; 17 BP.  
 XX  
 AC ABV78892;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE



AC ABR19384;  
 XX  
 DT 09-APR-2002 (first entry)  
 DE Human ERG Amberzyme target sequence Seq ID No 2031.  
 XX  
 XX Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;  
 XX ophthalmological; antiarthritic; antipsoriatic; vitruicide; osteopathic;  
 XX vulnerrary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 XX tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 XX neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 XX angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;  
 XX Sturge Weber syndrome; Kippel-Trenauay-Weber syndrome; leukaemia; ss;  
 XX Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
 XX amberzyme.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200188124-A2.  
 XX  
 XX 22-NOV-2001.  
 XX  
 XX 16-MAY-2001; 2001WO-US015866.  
 XX  
 XX 16-MAY-2000; 2000US-00572021.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (GLAXO) GLAXO GROUP LTD.  
 XX  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 XX  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 XX useful for treating cancer, diabetic retinopathy, macular degeneration,  
 XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 XX Claim 4; Page 127; 149pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule (I) which down regulates  
 XX expression of an Ets-related gene (ERG). (I) is useful for treating  
 XX conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 XX tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 XX neovascular glaucoma, myopic degeneration, arthritis, psoriasis, Sturge  
 XX vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge  
 XX Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-rendu  
 XX syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 XX treating a patient having a condition associated with the level of ERG,  
 XX by contacting cells of the patient with (I) under conditions suitable for  
 XX the treatment. The method comprises the use of one or more therapies  
 XX under conditions suitable for the treatment. Leukaemia or tumour  
 XX angiogenesis is treated by administering (I) to the patient in  
 XX conjunction with one or more of other therapies such as radiation or  
 XX chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 XX cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 XX ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 XX cation such as Mg2+. (I) is useful for diagnosis of conditions and  
 XX diseases related to the expression of ERG, and as diagnostic tool to  
 XX examine genetic drift and mutations within diseased cells or to detect  
 XX the presence of ERG RNA in a cell. (I) is useful for specifically  
 XX targeting genes that share homology with ERG gene or ERG fusion genes.  
 XX ABR17354-ABR22719 represent nucleic acids, including antisense and  
 XX enzymatic nucleic acid molecules which regulate expression of ERG, and  
 XX related PCR primers of the invention  
 XX  
 XX Sequence 17 BP; 7 A; 0 C; 9 G; 0 T; 1 U; 0 Other;  
 XX  
 XX Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 XX Best Local Similarity 87.5%; Pred. No. 95;  
 XX Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1136 TGAAGATTGAGGGA 1151  
 XX :|||||

Db 2 UGAAGAAGAGAGAGA 17  
 RESULT 187  
 ABR19385  
 ID ABR19385 standard; RNA; 17 BP.  
 XX  
 XX ABR19385;  
 XX  
 XX 09-APR-2002 (first entry)  
 XX  
 XX Human ERG Amberzyme target sequence Seq ID No 2032.  
 XX  
 XX Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;  
 XX ophthalmological; antiarthritic; antipsoriatic; vitruicide; osteopathic;  
 XX vulnerrary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 XX tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 XX neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 XX angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;  
 XX Sturge Weber syndrome; Kippel-Trenauay-Weber syndrome; leukaemia; ss;  
 XX Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
 XX amberzyme.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200188124-A2.  
 XX  
 XX 22-NOV-2001.  
 XX  
 XX 16-MAY-2001; 2001WO-US015866.  
 XX  
 XX 16-MAY-2000; 2000US-00572021.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (GLAXO) GLAXO GROUP LTD.  
 XX  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 XX  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 XX useful for treating cancer, diabetic retinopathy, macular degeneration,  
 XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 XX Claim 4; Page 127; 149pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule (I) which down regulates  
 XX expression of an Ets-related gene (ERG). (I) is useful for treating  
 XX conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 XX tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 XX neovascular glaucoma, myopic degeneration, arthritis, psoriasis, Sturge  
 XX vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge  
 XX Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-rendu  
 XX syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 XX treating a patient having a condition associated with the level of ERG,  
 XX by contacting cells of the patient with (I) under conditions suitable for  
 XX the treatment. The method comprises the use of one or more therapies  
 XX under conditions suitable for the treatment. Leukaemia or tumour  
 XX angiogenesis is treated by administering (I) to the patient in  
 XX conjunction with one or more of other therapies such as radiation or  
 XX chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 XX cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 XX ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 XX cation such as Mg2+. (I) is useful for diagnosis of conditions and  
 XX diseases related to the expression of ERG, and as diagnostic tool to  
 XX examine genetic drift and mutations within diseased cells or to detect  
 XX the presence of ERG RNA in a cell. (I) is useful for specifically  
 XX targeting genes that share homology with ERG gene or ERG fusion genes.  
 XX ABR17354-ABR22719 represent nucleic acids, including antisense and  
 XX enzymatic nucleic acid molecules which regulate expression of ERG, and  
 XX related PCR primers of the invention  
 XX  
 XX Sequence 17 BP; 8 A; 0 C; 8 G; 0 T; 1 U; 0 Other;  
 XX  
 XX

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 95;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1136 TGAAGATGAGGAGA 1151  
 : |||||  
 Db 1 UGAAGAAGAGAGAGA 16

RESULT 188  
 ABR57154/c  
 ID ABR57154 standard; RNA; 17 BP.  
 AC ABR57154;  
 XX  
 XX 02-JUL-2002 (first entry)  
 DE Human CLCA1 gene enzymatic nucleic acid #1525.  
 XX  
 XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KM acetylcysteine.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200211674-A2.  
 PN  
 XX 14-FEB-2002.  
 PD  
 XX 09-AUG-2001; 2001MO-US024970.  
 PF  
 XX 09-AUG-2000; 2000US-0224383P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT) SYNTX USA LLC.  
 PA (THOM/) THOMPSON J.  
 PI Thompson J, Mowigen J, McKenzie T, Ayers D, Szymkowski DE;  
 PI Grube A;  
 XX WPI; 2002-217145/27.  
 DR  
 XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.  
 PS  
 XX Claim 4; Page 97; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention

SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 TGAACAGCTCTCTCG 1192  
 : |||||  
 Db 16 TGAACAGCTCTCTAG 1

RESULT 189  
 ABR57671/c  
 ID ABR57671 standard; RNA; 17 BP.  
 AC ABR57671;  
 XX  
 XX 02-JUL-2002 (first entry)  
 DE Human CLCA1 gene enzymatic nucleic acid #2042.  
 XX  
 XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KM acetylcysteine.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200211674-A2.  
 PN  
 XX 14-FEB-2002.  
 PD  
 XX 09-AUG-2001; 2001MO-US024970.  
 PF  
 XX 09-AUG-2000; 2000US-0224383P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT) SYNTX USA LLC.  
 PA (THOM/) THOMPSON J.  
 PI Thompson J, Mowigen J, McKenzie T, Ayers D, Szymkowski DE;  
 PI Grube A;  
 XX WPI; 2002-217145/27.  
 DR  
 XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.  
 PS  
 XX Claim 4; Page 132; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention

SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1178 GGAACAGCTCTCTCGT 1193



ID ABK57267 standard; RNA; 17 BP.  
 XX  
 AC ABE57267;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human CLCA1 gene enzymatic nucleic acid #1638.  
 XX  
 KM Human: chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KM acetylcysteine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200211674-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 09-AUG-2001; 2001WO-US024970.  
 XX  
 PR 09-AUG-2000; 2000US-0224383P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT) SYNTEX USA LLC.  
 PA (THOM/) THOMPSON J.  
 XX  
 PI Thompson J, Mswiggen J, McKenzie T, Ayers D, Szymkowski DB;  
 PI Grupe A;  
 XX  
 DR WPI; 2002-217145/27.  
 XX  
 PT Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.  
 XX  
 PS Claim 4; Page 110; 152pp; English.  
 XX  
 CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell or  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 0 T; 2 U; 0 Other;  
 QY  
 Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 95;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 DB 1997 AGAGGAGATGTACAG 2012  
 1 ACAGGAGAGUUCACAG 16  
 RESULT 193  
 ACC67338  
 ID ACC67338 standard; DNA; 17 BP.  
 XX  
 AC ACC67338;

XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4585.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN MO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-333167/31.  
 XX  
 DR New isolated nucleic acid, useful for treating viral diseases associated  
 DR with tumours and cell degeneration, also related polypeptides, antibodies  
 DR and transfected cells.  
 XX  
 PS Disclosure; Page 567; 738pp; French.  
 XX  
 CC The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterized by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
 QY  
 Query Match 0.6%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 95;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 DB 2249 ATATCAGAACTGCGC 2264  
 2 ATCTCAGAACTGCGC 17  
 RESULT 194  
 ADB43111  
 ID ADB43111 standard; DNA; 17 BP.  
 XX  
 AC ADB43111;  
 XX  
 DT 18-DEC-2003 (revised)  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Tumour suppression/reversion associated nucleotide #3434.  
 XX  
 KM cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KM diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2003040369-A2.

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XX 15-MAY-2003.
PD 17-SEP-2002; 2002WO-IB004219.
XX PF 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
DR New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PS Disclosure; Page 433; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
SQ Sequence 17 BP; 2 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
QY Query Match 0.6%; Score 14.4; DB 1; Length 17;
DB Best Local Similarity 93.8%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2072 ATCCCTTTACCTC 2087
DB 2 ATCCCTTTACCTC 17
RESULT 195
ADB44910
ID ADB44910 standard; DNA; 17 BP.
XX AC ADB44910;
XX DT 18-DEC-2003 (first entry)
DE Tumour suppression/reversion associated nucleotide #5233.
XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX Homo sapiens.
XX OS
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PR 17-SEP-2002; 2002WO-IB004219.
PF (MOLE-) MOLECULAR ENGINES LAB.

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XX 17-SEP-2001; 2001FR-00011981.
XX PF (MOLE-) MOLECULAR ENGINES LAB.
XX PA Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
DR New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PS Disclosure; Page 643; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
QY Query Match 0.6%; Score 14.4; DB 1; Length 17;
DB Best Local Similarity 93.8%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2249 ATATCAGAACTGTGCC 2264
DB 2 ATCTCAGAACTGTGCC 17
RESULT 196
ADB45378/C
ID ADB45378 standard; DNA; 17 BP.
XX AC ADB45378;
XX DT 18-DEC-2003 (first entry)
DE Tumour suppression/reversion associated nucleotide #5701.
XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX Homo sapiens.
XX OS
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.

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CC with hyper-reactive airways  
 XX Sequence 18 BP; 0 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1989 GAAGAGCAAGAGGAG 2004  
 |||||  
 18 GAAGAGCAAGAGGAG 3

RESULT 199  
 AAV16023/C  
 ID AAV16023 standard; DNA; 18 BP.  
 XX  
 XX AAV16023;  
 AC  
 XX  
 XX 21-MAY-1998 (first entry)  
 DT  
 XX  
 XX PCR primer used to identify Sox-2 gene mutations in mice.  
 DE  
 XX Mutation; Sox-2; mutational screening; recessive; phenotypic alteration;  
 XX mouse model; FGF-4; PCR primer; amplify; ss.  
 KW  
 XX  
 XX Synthetic.  
 OS  
 XX Mus sp.  
 XX  
 XX WO9744485-A1.  
 XX  
 XX 27-NOV-1997.  
 PD  
 XX  
 XX 16-MAY-1997; 97WO-GB001354.  
 PF  
 XX  
 XX 17-MAY-1996; 96GB-00010355.  
 PR  
 XX  
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.  
 PA  
 XX  
 XX Goodfellow PN;  
 PI  
 XX  
 XX WPI; 1998-018536/02.  
 DR  
 XX  
 XX Identification of mutation(s) in genes of interest - without prior  
 PT observation of phenotypic alteration in the mutated organism or cell.  
 XX  
 XX Example 6; Page 43; 66pp; English.  
 PS  
 XX  
 XX PCR primers AAV16019-36 were used to identify mutations in Sox-2 using  
 CC the method of the invention. The method comprises testing a nucleic acid  
 CC sample from a mutated organism for a mutation in a gene of interest  
 CC without the prior observation of a phenotypic alteration in the mutated  
 CC organism resulting from the mutation. Sox-2 is a member of the Sox gene  
 CC family, and is involved in transcriptional regulation of the FGF-4 gene.  
 CC FGF-4 codes for a signalling protein whose expression is essential for  
 CC postimplantation mouse development, and, at later embryonic stages, for  
 CC limb patterning and growth. Mutagenised mice in which a Sox-2 mutation is  
 CC identified can be studied and provide a mouse model for a mutant human  
 CC Sox-2 gene. The method provides mutational screening based on genomic and  
 CC genetic techniques rather than on phenotypic observation. The method  
 CC identifies and characterises genes via mutagenesis to identify genes  
 CC encoding products which may have therapeutic benefit. The method also  
 CC identifies the presence of mutations in a gene which do not rely solely  
 CC upon prior matching of a gene with a disease. Heterozygotic organisms can  
 CC also be screened to identify those carrying a mutation in a copy of a  
 CC gene of interest even though the gene may be recessive and therefore  
 CC causes no phenotypic alteration  
 CC  
 XX  
 XX Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 GATTCTCTGGGCCAT 730  
 |||||  
 DB 17 GATTCTCTGGGCCAT 2

RESULT 200  
 AAX35925  
 ID AAX35925 standard; DNA; 18 BP.  
 XX  
 XX AAX35925;  
 AC  
 XX  
 XX 15-JUL-1999 (first entry)  
 DT  
 XX  
 XX PCR primer for granulocyte colony-stimulating factor (G-CSF) DNA.  
 DE  
 XX Granulocyte colony-stimulating factor; G-CSF; feline tumour;  
 XX long-term chemotherapy; serious infection; cancer therapy;  
 XX neutrophilic leukocyte production; early hematopoiesis;  
 KW bone marrow transplant; antibody; diagnosis; cat; PCR primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9920652-A1.  
 PN  
 XX 29-APR-1999.  
 PD  
 XX  
 XX 23-OCT-1998; 98WO-JP004809.  
 PF  
 XX  
 XX 23-OCT-1997; 97JP-00291055.  
 PR  
 XX  
 XX (NIPP) NIPPON INST BIOLOGICAL SCIENCE.  
 PA  
 XX  
 XX Yamamoto A, Tuchiya K, Iwata A, Ueda S;  
 PI  
 XX WPI; 1999-288274/24.  
 DR  
 XX  
 XX Novel feline protein useful in treating feline tumors.  
 PT  
 XX  
 XX Disclosure; Page 12; 28pp; English.  
 PS  
 XX  
 XX The present primer is used to amplify DNA encoding a granulocyte colony-  
 CC stimulating factor (G-CSF). The specification describes a feline G-CSF  
 CC protein. The products can be used to treat feline tumors, to support  
 CC long-term chemotherapy, to treat serious infection during cancer therapy,  
 CC and to boost up neutrophilic leukocyte production and early hematopoiesis  
 CC after bone marrow transplant. Antibodies against the protein are  
 CC applicable for diagnosis of neutrophilic leukocyte production in cats  
 CC  
 XX  
 XX Sequence 18 BP; 2 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

607 CAGCTGCAGGCTTGG 622  
 |||||  
 DB 1 CAGCTGCAGGCTTGG 16

RESULT 201  
 AAX54144/C  
 ID AAX54144 standard; DNA; 18 BP.  
 XX  
 XX AAX54144;  
 AC  
 XX  
 XX 05-JUL-1999 (first entry)  
 DT  
 XX  
 XX Human fibronectin antisense oligonucleotide fragment.  
 DE  
 XX Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO933886-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-US019419.  
 XX  
 PR 17-SEP-1997; 97US-0059160P.  
 PR 09-JUN-1998; 98US-00093972.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 1999-229400/19.  
 XX  
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.  
 XX  
 PS Disclosure; Page 55; 120pp; English.  
 XX  
 XX The specification describes antisense oligonucleotides (AA52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of mRNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the junction between coding and non-coding regions and all  
 CC segments of mRNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AA55180-271. These multiple target oligonucleotides  
 CC (specifically AA55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 CC  
 XX  
 SQ Sequence 18 BP; 0 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1989 GAAGAGCAAGAGGAG 2004  
 DB 18 GAAGAGCAAGAGGAG 3  
 RESULT 202  
 AAA33588/c  
 ID AAA33588 standard; DNA; 18 BP.  
 XX  
 AC AAA33588;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Low adenosine antisense oligonucleotide SEQ ID NO:1277.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphorocholate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antispasmodic; cytosolic; analgesic; impaired airway;  
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US017712.  
 XX  
 PR 03-AUG-1998; 98US-0095212P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-205971/18.  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Claim 18; Page 424; 1343pp; English.  
 XX  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antispasmodic, cytosolic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ON reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AA32313 to AA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 18 BP; 0 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1989 GAAGAGCAAGAGGAG 2004  
 DB 18 GAAGAGCAAGAGGAG 3  
 RESULT 203  
 AA243282/c  
 ID AA243282 standard; DNA; 18 BP.  
 XX  
 AC AA243282;

XX 11-FEB-2000 (first entry)  
 DT Murine Sox2 gene PCR primer 5.  
 DE Screening, mutation, treatment, disease; drug discovery; PCR primer; ss.  
 XX Mus musculus.  
 XX US9594075-A.  
 XX 30-NOV-1999.  
 XX 16-MAY-1997; 97US-00857946.  
 XX 17-MAY-1996; 96US-0017824P.  
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.  
 XX Goodfellow PN;  
 PI WPI; 2000-038255/03.  
 DR Identifying a mutation in a gene of interest in an organism useful for  
 PT identifying genes encoding products which may have therapeutic benefits.  
 XX Example 7; Col 69-70; 70PP; English.  
 XX This invention describes a novel mutational screening method based on  
 CC genomic and genetic techniques to identify and characterize a mutation in  
 CC a gene of interest without first selecting a phenotypic characteristic.  
 CC The screening methods are useful for identifying genes encoding products  
 CC which may have therapeutic benefit for treating human or animal diseases.  
 CC The method can be used for the DNA mutation screening of a class or a  
 CC family of genes providing a rapid assay for identifying mutant genes. The  
 CC methods produce organisms which can be used for drug discovery e.g.  
 CC providing a model for the study and treatment of a disease state, allow  
 CC in vitro assessment of drug activity and interbreeding of mutants which  
 CC allow investigation of gene interactions in the overall phenotype. A  
 CC range of phenotypes associated with different mutations, and specified  
 CC mutations in a gene of interest can be determined. The method can be  
 CC adapted to screen for a mutation in two or more genes of interest in an  
 CC organism. The methods allow mutations in a gene of interest to be  
 CC identified without having to rely on matching a gene with a disease.  
 CC AA243260-243421 represent PCR primers used in the method of the invention  
 XX Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 715 GATTCTCCTGGGCCAT 730  
 DB 17 GGTTCTCTGGGCCAT 2  
 RESULT 204  
 ID AAA05267 standard; DNA; 18 BP.  
 AC AAA05267;  
 XX 19-MAY-2000 (first entry)  
 DT PCR primer C-F used in Sox-2 amplicon generation.  
 XX PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; C-kit; Tryp-1;  
 KW Pax-6; mutation detection; therapeutic target identification; mouse;  
 KW mast cell growth factor; ss.  
 XX Mus sp.  
 OS  
 XX

PN US6015670-A.  
 XX 18-JAN-2000.  
 XX 14-NOV-1997; 97US-00970740.  
 XX 17-MAY-1996; 96US-0017824P.  
 XX 16-MAY-1997; 97US-00857946.  
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.  
 XX Goodfellow PN;  
 PI WPI; 2000-161139/16.  
 DR Detecting mutations in selected genes, useful e.g. for identifying  
 PT therapeutic targets or products, by analyzing DNA in mutated embryonic  
 PT stem cells without phenotypic characterization.  
 XX Example 6; Col 32; 66PP; English.  
 XX PCR primers AAA05245-A05406 are used to generate amplicons from the mouse  
 CC Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry gene,  
 CC MGF (mast cell growth factor) gene, C-kit gene, and the Pax-6 gene. The  
 CC primers are used in a method for the identification of a mutation in a  
 CC selected gene in a tissue without the prior observation of a phenotypic  
 CC alteration in the mutated organism or cell. The method is used to  
 CC identify mutations in a selected gene that encode products of potential  
 CC therapeutic activity or that are potential targets, particularly where  
 CC the gene of interest has been identified as a candidate gene by  
 CC positional cloning. Other applications are determining functions of genes  
 CC in a particular gene and identification of particular mutations. Animals  
 CC containing an identified mutation are used as models for studying  
 CC diseases or their treatment, and cells from them for in vitro assessment  
 CC of drug action. Interbreeding of mutant mice is used to investigate  
 CC genetic interaction in the overall phenotype  
 XX Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 715 GATTCTCCTGGGCCAT 730  
 DB 17 GGTTCTCTGGGCCAT 2  
 RESULT 205  
 ID AAF19710 standard; DNA; 18 BP.  
 AC AAF19710;  
 XX 14-MAR-2001 (first entry)  
 DT Human fibronectin polynucleotide fragment #1277.  
 XX Low adenosine antisease oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200062736-A2.  
 PN

XX 26-OCT-2000.  
 PD 26-OCT-2000.  
 XX 24-MAR-2000; 2000MO-US008020.  
 PF 24-MAR-2000; 2000MO-US008020.  
 XX 06-APR-1999; 99US-0127958P.  
 PR 06-APR-1999; 99US-0127958P.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX NYCE JW;  
 PI NYCE JW;  
 XX WPI; 2000-679539/66.  
 DR WPI; 2000-679539/66.  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX Claim 14; Page 220; 1592pp; English.  
 PS The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 CC  
 XX Sequence 18 BP; 0 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1989 GAAGGCAAGAGGAG 2004  
 DB 18 GAAGGCAAGAGGAG 3

RESULT 206  
 AB295404/C  
 ID AB295404 standard; DNA; 18 BP.  
 XX AB295404;  
 AC AB295404;  
 XX 17-OCT-2003 (first entry)  
 DT 17-OCT-2003 (first entry)  
 XX Human fibronectin antisense fragment no.1268.  
 DE Human fibronectin antisense fragment no.1268.  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KM antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KM antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KM lung inflammation; respiratory disease; da.  
 XX Homo sapiens.  
 CS Homo sapiens.  
 XX WO200285308-A2.  
 PN WO200285308-A2.  
 XX 31-OCT-2002.  
 PD 31-OCT-2002.  
 XX 23-APR-2002; 2002MO-US013135.  
 PF 23-APR-2002; 2002MO-US013135.  
 XX 24-APR-2001; 2001US-0286137P.  
 PR 24-APR-2001; 2001US-0286137P.  
 XX (EPIC-) EPICENESIS PHARM INC.  
 PA (EPIC-) EPICENESIS PHARM INC.  
 XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahbuddin S;  
 XX WPI; 2003-229219/22.  
 DR WPI; 2003-229219/22.  
 XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' and genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiallergic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 18 BP; 0 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1989 GAAGGCAAGAGGAG 2004  
 DB 18 GAAGGCAAGAGGAG 3

RESULT 207  
 ABX80015  
 ID ABX80015 standard; cDNA; 18 BP.  
 XX ABX80015;  
 AC ABX80015;  
 XX 17-APR-2003 (first entry)  
 DT 17-APR-2003 (first entry)  
 XX EST polymorphic DNA repeat polynucleotide #340.  
 DE EST polymorphic DNA repeat polynucleotide #340.  
 XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;

KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KM Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KM Friedreich's ataxia; myotonic dystrophy; hyperandrogenemia;  
 KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 OS Homo sapiens.  
 XX US6472154-B1.  
 PN 29-OCT-2002.  
 PD 31-DEC-1999; 99US-00475947.  
 PF 31-DEC-1999; 99US-00475947.  
 PR 31-DEC-1999; 99US-00475947.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA Garner HR, Wren JD, Minna JD, Fondon JW;  
 PI WPI; 2003-208818/20.  
 DR Identifying a candidate polymorphic repeat within a coding sequence, for  
 PT understanding or treating genetic disease, comprises detecting tandem  
 PT repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability.  
 PS Example; Col 1165; 588bp; English.  
 XX The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs  
 XX Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2048 CAGCAGCAGCCAGC 2063  
 DB 2 CAGCAGCAGCCAGC 17

RESULT 208  
 ADCT0002  
 ID ADCT0002 standard; DNA; 18 BP.  
 AC ADCT0002;  
 XX 18-DEC-2003 (first entry)  
 DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 491).  
 XX PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;  
 KM adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;  
 XX cytosine methylation state.  
 OS Unidentified.  
 XX W02003052135-A2.  
 PN  
 XX

PD 26-JUN-2003.  
 XX 10-DEC-2002; 2002WO-EP014026.  
 PF 14-DEC-2001; 2001DE-01061625.  
 PR (EPIC-) EPICENOMICS AG.  
 XX Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;  
 PI Nimmrich I;  
 PI WPI; 2003-533029/50.  
 DR Detecting and differentiating cytosine methylation state of genomic DNA,  
 PT useful for diagnosing, treating, prognosticating and/or monitoring lung  
 PT cell proliferative disorders e.g. adenocarcinoma and squamous cell  
 PT carcinoma.  
 PS Claim 15; SEQ ID NO 491; 58bp; English.  
 XX This invention relates to a novel method for detecting and  
 CC differentiating between lung cell proliferative disorders associated with  
 CC at least one gene and/or their regulatory regions. Specifically, it  
 CC refers to a method comprising contacting a target nucleic acid in a  
 CC biological sample with at least one reagent, wherein the reagent is able  
 CC to distinguish between methylated and non-methylated CpG dinucleotides  
 CC present in the target DNA. As such, it is possible to further  
 CC differentiate and diagnose medical conditions including adenocarcinoma  
 CC and squamous cell carcinoma, and their respective adjacent lung tissue.  
 CC The present invention describes cytosine oligomers and PNA-oligomers  
 CC that are useful as probes for determining the cytosine methylation state  
 CC of single nucleotide polymorphisms (SNPs) of the target sequence. This  
 CC oligonucleotide sequence is a primer oligomer used for the analysis of  
 CC CpG positions within genomic DNA, used in an exemplification of the  
 CC invention.  
 XX Sequence 18 BP; 3 A; 0 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 165 TTGTGGATTGATTAAT 180  
 DB 3 TTGTGGATTGATTAAT 18

RESULT 209  
 AAX59110  
 ID AAX59110 standard; DNA; 19 BP.  
 AC AAX59110;  
 XX 31-AUG-1999 (first entry)  
 DE Human nuclear receptor NRK5 PCR primer RSK4.  
 XX Nuclear receptor protein; NRK5; human; retina; eye disease; therapy;  
 KM diagnosis; PCR; primer; ss.  
 OS Synthetic.  
 XX Homo sapiens.  
 PN W09929725-A1.  
 PD 17-JUN-1999.  
 PF 11-DEC-1998; 98WO-US026422.  
 PR 12-DEC-1997; 97US-0069379P.  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX

PI Chen F;  
 XX  
 DR WPI; 1999-385576/32.  
 XX  
 PT DNA encoding human nuclear receptor NRNS.  
 XX  
 PS Example 1; Page 32; 57pp; English.  
 CC This oligonucleotide comprises PCR primer R5R4, which was used with  
 CC primer R5R3 (see AAX59109) to define the intron-exon boundary in a cDNA  
 CC clone (see AAX59096) that had been isolated from a human retina cDNA  
 CC library and which coded for a novel member of the nuclear receptor  
 CC superfamily. An intronless clone (see AAX59095) was subsequently  
 CC amplified from the retina cDNA library. This encoded NRNS (see AAY06301),  
 CC a novel member of the human nuclear factor superfamily. NRNS is expressed  
 CC at high levels in the retina and may therefore play a role in eye  
 CC function. The invention also provides recombinant vectors and host cells,  
 CC methods of screening for modulators of NRNS activity, and production of  
 CC antibodies against NRNS  
 CC  
 SQ Sequence 19 BP; 2 A; 7 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1968 GAGCCGAGCTGGGCA 1963  
 DB 4 GAGCCGAGCTGGGCA 19  
 RESULT 210  
 ID AAZ29215 standard; DNA; 19 BP.  
 AC AAZ29215;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE Primer IFN6 used for amplification of human IFNA2 genomic DNA.  
 XX  
 KW Interferon alpha 2; IFNA2; genomic sequence; transcription start site;  
 KW upstream; targeting sequence; regulatory sequence; marker gene; PCR;  
 KW homologous recombination; recombinant cell; gene therapy; DNA construct;  
 KW Papilloma virus; Hepatitis B virus; Hepatitis C virus; Vaccinia virus;  
 KW Herpes simplex virus; Herpes zoster; varicellous virus; Rhinovirus;  
 KW Primer IFN6; human leukocyte genomic library lambda; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO957292-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 05-MAY-1999; 99WO-US009925.  
 XX  
 PR 07-MAY-1998; 98US-0084648P.  
 PR 21-MAY-1998; 98US-0086555P.  
 XX  
 PA (TRAN-) TRANSCRIPTIONAL THERAPIES INC.  
 XX  
 PI Treco DA, Heartlein MW, Selden RF;  
 XX  
 DR WPI; 2000-072236/06.  
 XX  
 PT Novel genomic sequences used to treat human diseases and disorders.  
 XX  
 PS Disclosure; Page 12; 68pp; English.  
 CC The present DNA sequence is the primer IFN6, that is used to amplify the  
 CC human genomic sequence of interferon alpha 2 (IFNA2). This primer is used  
 CC to generate an oligonucleotide probe, to screen the human leukocyte

CC genomic library lambda, to obtain the genomic DNA upstream of the coding  
 CC region of the IFNA2 gene. The 5' end of the primer corresponds to position  
 CC +69 of IFNA2  
 CC  
 SQ Sequence 19 BP; 5 A; 7 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2287 GTCAAGCTGCTGTGAG 2302  
 DB 19 GTCAAGCTGCTGTGAG 4  
 RESULT 211  
 ID AAA84742 standard; DNA; 19 BP.  
 AC AAA84742;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Cyclin F ribozyme binding site #10.  
 XX  
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200032765-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 06-DEC-1999; 99WO-US028772.  
 XX  
 PR 04-DEC-1998; 98US-0110954P.  
 XX  
 PA (IMMU-) IMMUSOL INC.  
 XX  
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;  
 XX  
 DR WPI; 2000-412314/35.  
 XX  
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis; cleaves  
 FT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 FT PCNA and Cyclin B1.  
 XX  
 PS Disclosure; Page 81; 109pp; English.  
 XX  
 CC The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 CC  
 SQ Sequence 19 BP; 8 A; 1 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1137 GAGGATGAGAGAGAG 1152  
 DB 3 GAGGATGAGAGAGAG 18  
 RESULT 212  
 ID AAA83615 standard; DNA; 19 BP.  
 XX

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AC AAA83615;
XX
XX 04-DEC-2000 (first entry)
XX
XX cdk-we-hu ribozyme binding site #80.
DE
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX Mammalia.
OS
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 64; 109pp; English.
XX
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AA82415 to AA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.6%; Score 14.4; DB 1; Length 19;
XX Best Local Similarity 93.8%; Pred. No. 1e+02;
XX Matches 15; Conservative < 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 622 GGCAGTGATTATGAGC 637
XX | | | | | | | | | | | | | | | | |
XX 1 GCCAGTGATTATGAGC 16
XX
XX
XX RESULT 213
XX AA845588/c
XX ID AA845588 standard; DNA; 19 BP.
XX
XX AA845588;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human PARP-2 RT-PCR reverse primer.
XX
XX Human; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
XX cytoskeletal; nocotropic; neuroprotective; antiinflammatory; antidiabetic;
XX immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
XX oxidative stress; neurological disorder; parkinsonism; apoptosis;
XX meningitis-associated intracranial complication; ischaemia; PCR primer;
XX inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX
XX Homo sapiens.
XX
XX WO200164955-A1.
XX
XX 07-SEP-2001.
XX

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PF 01-MAR-2001; 2001MO-US006572.
XX
XX 02-MAR-2000; 2000US-00517467.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Popoff I, Cowest LM;
XX
XX WPI; 2001-602570/68.
XX
XX Antisense compound useful for treating hyperproliferative, neurological,
XX inflammatory and autoimmune disorders and diabetes inhibits human PARP.
XX
XX Example 13; Page 80; 168pp; English.
XX
XX The invention relates to antisense oligonucleotides targeted to human
XX PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
XX (ADP-ribose) polymerase) plays an important role in chromatin
XX decondensation, DNA replication, DNA repair, gene expression, malignant
XX transformation, cellular differentiation and apoptosis. The antisense
XX oligonucleotide inhibitors are useful for inhibiting the expression of
XX PARP in human cells or tissues. They are also useful for treating a human
XX with a disease associated with PARP especially hyperproliferative
XX disorders (e.g. cancer), cellular injury resulting from oxidative stress,
XX neurological (e.g. parkinsonism, meningitis-associated intracranial
XX complications and ischaemia), inflammatory and autoimmune disorders (e.g
XX arthritis) and diabetes. The present sequence is an RT-PCR (reverse
XX transcriptase PCR) primer used to quantitate PARP mRNA levels
XX
XX Sequence 19 BP; 4 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.6%; Score 14.4; DB 1; Length 19;
XX Best Local Similarity 93.8%; Pred. No. 1e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 244 TGCGTGTGGCTGTGG 259
XX | | | | | | | | | | | | | | | | |
XX 16 TGCGTGTGGCTGTGGAGG 1
XX
XX
XX RESULT 214
XX AAH58777
XX ID AAH58777 standard; DNA; 19 BP.
XX
XX AAH58777;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cdk-we-hu ribozyme binding site SEQ ID NO:1201.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX recognition site; target; ribozyme binding site; eye disease; vulneryary;
XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX antipsoriatic; dermatological; antiseborrheic; antidiabetic; vitinude;
XX antisticking; ophthalmological; keratolytic; gene therapy; viral wart;
XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
XX sickle cell retinopathy; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000MO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX
XX (IMMU-) IMMUSOL INC.
XX

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XX  Robbins JM, Tritz R;
XX  MPI; 2001-300427/31.
XX
XX  Treating proliferative skin or eye diseases and scarring, using ribozymes
XX  that cleave RNA encoding cytokines involved in inflammation, matrix
XX  metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX  Example 1; Page 159; 408pp; English.
XX
XX  The present invention describes a method for treating a proliferative
XX  skin or eye disease and scarring. The method involves administering a
XX  ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX  inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX  dependent kinase, growth factor or a reductase, or administering a
XX  nucleic acid molecule (II) comprising a promoter operably linked to a
XX  nucleic acid segment encoding (I). (I) can have antiproliferative,
XX  dermatological, cytostatic, antiseborrheic, antidiabetic, antistickling,
XX  ophthalmological, vulnary, keratolytic and vitruclide activities, and
XX  cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX  in gene therapy. (I) and (II) are useful for treating proliferative skin
XX  diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX  squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX  also be used for treating proliferative eye diseases such as diabetic
XX  retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX  prematurity and retinal detachment, and for treating and preventing
XX  scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX  scar. AAH57577 to AAH62099 represent sequences used in the
XX  exemplification of the present invention.
XX
XX  Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX  Query Match          0.6%; Score 14.4; DB 1; Length 19;
XX  Best Local Similarity 93.8%; Pred. No. 1e+02;
XX  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  622 GGCAGTGATTATGAGC 637
XX      |||||
XX  1 GCCAGTGATTATGAGC 16
XX
XX  RESULT 215
XX  AAH59904
XX  ID AAH59904 standard; DNA; 19 BP.
XX
XX  AAH59904;
XX
XX  10-SEP-2001 (first entry)
XX
XX  Cyclin F ribozyme binding site SEQ ID NO:2328.
XX
XX  Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX  recognition site; target; ribozyme binding site; eye disease; vulnary;
XX  proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX  cytokine; inflammation; cell-cycle dependent kinase; cyclin MMP;
XX  matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX  antiproliferative; dermatological; antiseborrheic; antidiabetic; vitruclide;
XX  antistickling; ophthalmological; keratolytic; gene therapy; viral wart;
XX  atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX  basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX  sickle cell retinopathy; ss.
XX
XX  Homo sapiens.
XX  Synthetic.
XX
XX  WO200130362-A2.
XX
XX  03-MAY-2001.
XX
XX  26-OCT-2000; 2000WO-US029500.
XX
XX  26-OCT-1999; 99US-0161532P.

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XX  (IMMU-) IMMUSOL INC.
XX
XX  Robbins JM, Tritz R;
XX  MPI; 2001-300427/31.
XX
XX  Treating proliferative skin or eye diseases and scarring, using ribozymes
XX  that cleave RNA encoding cytokines involved in inflammation, matrix
XX  metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX  Example 1; Page 241; 408pp; English.
XX
XX  The present invention describes a method for treating a proliferative
XX  skin or eye disease and scarring. The method involves administering a
XX  ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX  inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX  dependent kinase, growth factor or a reductase, or administering a
XX  nucleic acid molecule (II) comprising a promoter operably linked to a
XX  nucleic acid segment encoding (I). (I) can have antiproliferative,
XX  dermatological, cytostatic, antiseborrheic, antidiabetic, antistickling,
XX  ophthalmological, vulnary, keratolytic and vitruclide activities, and
XX  cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX  in gene therapy. (I) and (II) are useful for treating proliferative skin
XX  diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX  squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX  also be used for treating proliferative eye diseases such as diabetic
XX  retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX  prematurity and retinal detachment, and for treating and preventing
XX  scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX  scar. AAH57577 to AAH62099 represent sequences used in the
XX  exemplification of the present invention.
XX
XX  Sequence 19 BP; 8 A; 1 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX  Query Match          0.6%; Score 14.4; DB 1; Length 19;
XX  Best Local Similarity 93.8%; Pred. No. 1e+02;
XX  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1137 GAGAAATGAGAGAG 1152
XX      |||||
XX  3 GAGAAATGAGAGAG 18
XX
XX  RESULT 216
XX  AB297252
XX  ID AB297252 standard; DNA; 19 BP.
XX
XX  AB297252;
XX
XX  17-OCT-2003 (first entry)
XX
XX  Human nucleic acid sequence.
XX
XX  Human; antiseize; lung dysfunction; nasal airway dysfunction;
XX  antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX  antistimatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX  antiseize gene therapy; respiratory; lung; adenosine sensitivity;
XX  adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX  lung inflammation; respiratory disease; ds.
XX
XX  Homo sapiens.
XX
XX  WO200285308-A2.
XX
XX  31-OCT-2002.
XX
XX  23-APR-2002; 2002WO-US013135.
XX
XX  24-APR-2001; 2001US-0286137P.
XX
XX  (EPIC-) EPIGENESIS PHARM INC.
XX

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PI NYCE JW, Li Y, Sendaasagra A, Ketz E, Pabalan J, Aguilar D  
PI Miller S, Tang L, Shahabuddin S,  
XX  
DR WPI: 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 12494; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an anti-inflammatory steroid and ubiquinone. A composition of the invention has anti-inflammatory, antiasthmatic, antiallergic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an anti-inflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [http://www.wipo.int/pub/published\\_pct\\_sequences](http://www.wipo.int/pub/published_pct_sequences)

Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other,

Query Match	0.6%;	Score 14.4;	DB 1;	Length 19;
Best Local Similarity	93.8%;	Pred. No. 1e+02;		
Matches 15;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

QY	134	CTCGCCCGGCTTCTCT	149
Db	4	CACGCCCGGCTTCTCT	19

RESULT 217

ID ABZ97333 standard; DNA; 19 BP.

AC ABZ97333

DT 17-OCT-2003 (first entry)

DE Human IL4-R oligonucleotide sequence

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens

PN WO200285308-A2

PD 31-OCT-2002

PF 23-APR-2002; 2002WO-US013135

PR 24-APR-2001; 2001US-0286137P.

PA (EPIC-) EPIGENESIS PHARM INC.

XX

PI NYCE JW, Li Y, Sandasgrä A, Katz E, Pabalan J, Agullar D,  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI, 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
respiration, has also(s) antihemse to specific gene(s) or its  
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
ubiquinone.

Disclosure; SEQ ID NO 12575; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone  
CC or receptor producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WHO  
CC at ftp.who.int/pub/published\_pat\_sequences

Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other,

Query Match	0.6%;	Score 14.4;	DB 1;	Length 19;
Best Local Similarity	93.8%;	Pred. No. 1e+02;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	134	CTCGCCCGGCTTCTCT	145
Db	4	CACGCCCGGCTTCTCT	19

RESULT 218

ID ADE27352 standard; RNA; 19 BP.

AC ADE27352;

DT 29-JAN-2004 (first entry  
...

DE Stearoyl-CoA desaturase SINA oligonucleotide SEQ ID NO:296

KM short interfering nucleic acid, siNA; downregulation; inhibition; SCB  
KM stearyl-CoA desaturase; RNA interference; anorectic; anti-diabetic;  
KM antihypercholesterolemic; cyrostatic; virucide; obesity; diabetes;  
KM atherosclerosis; cancer; viral infection; drug screening;  
KM genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic

PN W02003070885-A2.

PD 28-AUG-2003

PF 13-FEB-2003; 2003WO-US004317

PR 20-FEB-2002; 2002US-0358580P

PR 06-JUN-2002; 2002US-0386782P

PR 05-SEP-2002; 2002US-0408378P

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PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI, 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 296; 139pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virocidic activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 4 C; 7 G; 0 T; 6 U; 0 Other;

Query Match      0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 186 AGCTGATTGCCGCGC 201
DB 2 AGCTGATTGCCGCGC 17

RESULT 219
ADE27062/C
ID ADE27062 standard; RNA; 19 BP.
AC
AC ADE27062;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearyl-CoA desaturase siNA oligonucleotide SEQ ID NO:6.
XX
XX short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
XX stearyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
XX antiarteriosclerotic; cytostatic; virocidic; obesity; diabetes;
XX atherosclerosis; cancer; viral infection; drug screening;
XX genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
XX WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

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PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI, 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 6; 139pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virocidic activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 4 G; 0 T; 2 U; 0 Other;

Query Match      0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 186 AGCTGATTGCCGCGC 201
DB 18 AGCTGATTGCCGCGC 3

RESULT 220
AAV48449/C
ID AAV48449 standard; DNA; 18 BP.
AC
AC AAV48449;
XX
DT 15-OCT-1998 (first entry)
XX
DE Transforming growth factor beta-1 antisense oligonucleotide N37.
XX
XX Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-00101531.
XX
PR 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiefen K, Brysch W;
XX
DR WPI, 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of

```

PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.

XX Example 1; Fig 3a; 286pp; English.

CC AAV48412-84 represent antisense oligonucleotides directed against  
CC transforming growth factor beta-1 (TGF beta-1). The oligonucleotides  
CC exemplify the invention. The specification describes oligonucleotides  
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that  
CC can each form three hydrogen bonds to cytosine; do not contain four  
CC consecutive nucleotides able to form three H-bonds each to four  
CC consecutive cytosines; do not contain two sequences of three consecutive  
CC nucleotides each able to form three H-bonds to three consecutive  
CC cytosines, and the ratio between residues able to form two H-bonds each  
CC (2R) or three such bonds (3R) is given by  $2R/3R = 0.33-0.72$ . The  
CC oligonucleotides are used to modulate expression of genes, particularly  
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control  
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or  
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The  
CC oligonucleotides can also be used to analyse function of proteins (by  
CC altering their expression or activity) and therapeutically, e.g. in cases  
CC of cancer or (targeting TGF) for stimulating the immune system  
XX

SQ Sequence 18 BP; 0 A; 3 C; 15 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 1.2e+02;

QY 477 CCCCCGACCCGCGCGCC 493

Db 18 CCCCCGCGCGCGCGCGCC 2

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: September 20, 2004, 10:06:54

Job time : 7 secs

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